

November 2005

Published_Applications Nucleic Acid and Published_Applications Amino Acid database searches now generate two sets of results each. The Published_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published_Applications_New databases; older published applications make up the Published_Applications_Main databases.

Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions **.rnpbm** (Published_Applications_NA_Main) and **.rnpbn** (Published_Applications_NA_New).

Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions **.rapbm** (Published_Applications_AA_Main) and **.rapbn** (Published_Applications_AA_New).

This Page Blank (uspto)

STIC-Biotech/ChemLib

175918

LB

From: Kelly, Robert
Sent: Monday, January 09, 2006 8:22 AM
To: STIC-Biotech/ChemLib
Subject: 10/801,648

CITE

Please search:

- (i) nucleic acids matching SEQ ID NO: 1; and
- (ii) nucleic acids encoding SEQ ID NO: 2.

Robert M. Kelly, Ph.D.
Art Unit 1633
Room 2C55, Remsen Bldg.
Mailbox 2C70
(571) 272-0729

10801648

1-1547 NA
2-396a
LB

Searcher: _____
Searcher Phone: _____
Date Searcher Picked up: _____
Date completed: 1/11
Searcher Prep Time: _____
Online Time: _____

Type of Search
NA# _____ AA# _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other (Specify): _____

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 10, 2006, 19:34:29 ; Search time 5436 Seconds
(without alignments)
16176.751 Million cell updates/sec

Title: US-10-801-648-1
Perfect score: 1547
Sequence: 1 ggggactcttgaacttgc.....aatacataatatatatata 1547

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 117666282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl.*
1: gb_ba.*
2: gb_in.*
3: gb_env.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pr.*
9: gb_ro.*
10: gb_scs.*
11: gb_sy.*
12: gb_un.*
13: gb_vi.*
14: gb_htg.*
15: gb_pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|--------|-------------|--------|----|--------------------|
| 1 | 1547 | 100.0 | 1547 | 6 | CQ875282 Sequence |
| 2 | 1547 | 100.0 | 1547 | 6 | CS031823 Sequence |
| 3 | 1547 | 100.0 | 1547 | 6 | CS040775 Sequence |
| 4 | 1547 | 100.0 | 1547 | 6 | I78455 Sequence 2 |
| 5 | 1547 | 100.0 | 1547 | 6 | AX775087 Sequence |
| 6 | 1547 | 100.0 | 1547 | 8 | HUMBMP2A |
| 7 | 1547 | 100.0 | 1581 | 6 | CS038212 Sequence |
| 8 | 1547 | 100.0 | 1607 | 6 | ARI57708 Sequence |
| 9 | 1547 | 100.0 | 3266 | 6 | AR447458 Sequence |
| 10 | 1545.4 | 99.9 | 1607 | 6 | AR031482 Sequence |
| 11 | 1545.4 | 99.9 | 1607 | 6 | ARI30859 Sequence |
| 12 | 1545.4 | 99.9 | 1607 | 6 | ARI353792 Sequence |
| 13 | 1543.8 | 99.8 | 1607 | 6 | I08630 Sequence 32 |
| 14 | 1543.8 | 99.8 | 2041 | 8 | BC069214 Homo sapi |
| 15 | 1542.2 | 99.7 | 1547 | 6 | CQ728408 Sequence |
| 16 | 1314.8 | 85.0 | 2154 | 6 | CS031821 Sequence |
| 17 | 1314.8 | 85.0 | 2154 | 6 | CS040773 Sequence |
| 18 | 1314.8 | 85.0 | 2154 | 6 | AX201366 Sequence |

| | | | | | |
|----|--------|------|--------|----|--------------------|
| 19 | 1233.8 | 79.8 | 2502 | 4 | DSPBMP2 |
| 20 | 1227.2 | 79.3 | 1260 | 6 | AR075478 |
| 21 | 1227.2 | 79.3 | 1260 | 6 | I15550 Sequence 4 |
| 22 | 1227.2 | 79.3 | 1260 | 6 | I83779 Sequence 4 |
| 23 | 1227.2 | 79.3 | 1260 | 6 | AR308031 Sequence |
| 24 | 1227.2 | 79.3 | 1260 | 6 | AR350343 Sequence |
| 25 | 1194.8 | 77.2 | 1215 | 6 | BD124160 Treatment |
| 26 | 1085.2 | 70.1 | 2148 | 4 | AF041421 Oryctolag |
| 27 | 1045.2 | 67.6 | 1314 | 6 | BD003258 P-Selecti |
| 28 | 1042.4 | 67.4 | 2540 | 9 | BC100344 Mus muscu |
| 29 | 970.8 | 62.8 | 1275 | 9 | RNBMP2 |
| 30 | 964.6 | 62.4 | 1258 | 9 | RAYMORPH2A |
| 31 | 896.6 | 58.0 | 1233 | 6 | I62380 |
| 32 | 896.6 | 58.0 | 1233 | 6 | AR492773 Sequence |
| 33 | 880 | 56.9 | 14759 | 6 | CQ876148 Sequence |
| 34 | 880 | 56.9 | 14759 | 6 | CQ877130 Sequence |
| 35 | 880 | 56.9 | 14759 | 6 | CQ880078 Sequence |
| 36 | 880 | 56.9 | 14759 | 6 | AR405119 Sequence |
| 37 | 880 | 56.9 | 16133 | 8 | AF040249 |
| 38 | 880 | 56.9 | 173308 | 8 | HS859D4 |
| 39 | 876.8 | 56.7 | 157000 | 14 | AC026511 |
| 40 | 876.8 | 50.9 | 856 | 10 | BV166038 BMP2_294 |
| 41 | 764.6 | 49.4 | 1179 | 5 | AY237249 Gallus ga |
| 42 | 694.2 | 44.9 | 1120 | 5 | GBBMP2A |
| 43 | 681.2 | 44.0 | 11605 | 9 | MUSBMP2A |
| 44 | 681.2 | 44.0 | 15144 | 6 | ARI00888 Sequence |
| 45 | 681.2 | 44.0 | 180573 | 9 | AL831753 Mouse DNA |

ALIGNMENTS

| | | | | | | |
|------------|---|---------------------------------------|---------|-----|--------|-----------------|
| RESULT 1 | CQ875282 | Sequence 25 from Patent WO2004076613. | 1547 bp | DNA | linear | PAT 27-SEP-2004 |
| LOCUS | CQ875282 | Sequence 25 from Patent WO2004076613. | 1547 bp | DNA | linear | PAT 27-SEP-2004 |
| DEFINITION | CQ875282 | Sequence 25 from Patent WO2004076613. | 1547 bp | DNA | linear | PAT 27-SEP-2004 |
| ACCESSION | CQ875282 | Sequence 25 from Patent WO2004076613. | 1547 bp | DNA | linear | PAT 27-SEP-2004 |
| VERSION | CQ875282.1 | GI:52748370 | 1547 bp | DNA | linear | PAT 27-SEP-2004 |
| KEYWORDS | | | | | | |
| SOURCE | Homo sapiens | (human) | | | | |
| ORGANISM | Homo sapiens | | | | | |
| | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | | | |
| | Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; | | | | | |
| | Hominidae; Homo. | | | | | |
| REFERENCE | 1 | | | | | |
| AUTHORS | Herr, A., Hinzmann, B., Dahl, E., Staub, E., Pillarsky, C. and Specht, T. | | | | | |
| TITLE | Human nucleic acid sequences from carcinomas of the bladder | | | | | |
| JOURNAL | Patent: WO 2004076613-A 25 10-SEP-2004; | | | | | |
| | Herr, Alexander (DE); Hinzmann, Bernd (DE); Dahl, Edgar (DE); | | | | | |
| | Staub, Eike (DE); Pillarsky, Christian (DE); Specht, Thomas (DE) | | | | | |
| FEATURES | Location/Qualifiers | | | | | |
| source | 1..1547 | | | | | |
| | /organism="Homo sapiens" | | | | | |
| | /mol_type="unassigned DNA" | | | | | |
| | /db_xref="taxon:9606" | | | | | |

| | | |
|----------------------------|---------|---|
| ORIGIN | 1 | GGGAGCTCTTGAACCTTGCAGGAGAGATAAATCTTGGCGACCCACCTTTGGCGCGGTGCCTT 60 |
| Query Match | 100.0% | Score 1547; DB 6; Length 1547; |
| Best Local Similarity | 100.0%; | Pred. No. 0; |
| Matches 1547; Conservative | 0; | Mismatches 0; Indels 0; Gaps 0; |
| Qy | 1 | GGGAGCTCTTGAACCTTGCAGGAGAGATAAATCTTGGCGACCCACCTTTGGCGCGGTGCCTT 60 |
| Db | 1 | GGGAGCTCTTGAACCTTGCAGGAGAGATAAATCTTGGCGACCCACCTTTGGCGCGGTGCCTT 60 |
| Qy | 61 | TGCCCCAGCGAGCTGTCTTCCGAGCCCGACCGCCCTTCCACTCTCTGGGCTT 120 |
| Db | 61 | TGCCCCAGCGAGCTGTCTTCCGAGCCCGACCGCCCTTCCACTCTCTGGGCTT 120 |
| Qy | 121 | TGCCCCGACACTGAGAGCGCTGTTCAGCGTGAAGAGAGAGACTGCGCGCGCCGCCCGG 180 |
| Db | 121 | TGCCCCGACACTGAGAGCGCTGTTCAGCGTGAAGAGAGAGACTGCGCGCGCCGCCCGG 180 |

181 GAGAAGGAGGAGGCAAGAAAGAAAGCAATTCGGTCCCTTGGCCAGAGTCCCTTTGACC 240
181 GAGAAGGAGGAGGCAAGAAAGAAAGCAATTCGGTCCCTTGGCCAGAGTCCCTTTGACC 240
241 AGAGTTTTTCCATGTGACGCTCTTTCAATGGAACGTGTCCCGGTGCTTCTTAGACGGA 300
241 AGAGTTTTTCCATGTGACGCTCTTTCAATGGAACGTGTCCCGGTGCTTCTTAGACGGA 300
301 CTGGGTTCTCTAAAGGTGACACATGTGTGGCGGGAGACCCGCTGTCTTAGGTTGCTGC 360
301 CTGGGTTCTCTAAAGGTGACACATGTGTGGCGGGAGACCCGCTGTCTTAGGTTGCTGC 360
361 TTCCCAAGTCTCTCCGCGCGCGCTGTGCTGCTTCCGAGCTGGCGCGCAGGAGT 420
361 TTCCCAAGTCTCTCCGCGCGCGCTGTGCTGCTTCCGAGCTGGCGCGCAGGAGT 420
421 TCGGCGGCGGCTGTGCGGCGCGCCCTCATCCAGCCCTCTGAGAGGCTCTGAGCGAGT 480
421 TCGGCGGCGGCTGTGCGGCGCGCCCTCATCCAGCCCTCTGAGAGGCTCTGAGCGAGT 480
481 TCGAGTTTCGGCTGTGAGAGGCTGTGCGGCTGTGAGAGGCTGTGAGAGGCTGTGAGAGG 540
481 TCGAGTTTCGGCTGTGAGAGGCTGTGCGGCTGTGAGAGGCTGTGAGAGGCTGTGAGAGG 540
541 CCGTGTGCGGCTGTGAGAGGCTGTGAGAGGCTGTGAGAGGCTGTGAGAGGCTGTGAGAGG 600
541 CCGTGTGCGGCTGTGAGAGGCTGTGAGAGGCTGTGAGAGGCTGTGAGAGGCTGTGAGAGG 600
601 CCGGCGGCGGCTGTGAGAGGCTGTGAGAGGCTGTGAGAGGCTGTGAGAGGCTGTGAGAGG 660
601 CCGGCGGCGGCTGTGAGAGGCTGTGAGAGGCTGTGAGAGGCTGTGAGAGGCTGTGAGAGG 660
661 ACCATGAAGATCTTTGGAAGAACTACAGAGGCTGTGAGAGGCTGTGAGAGGCTGTGAGAGG 720
661 ACCATGAAGATCTTTGGAAGAACTACAGAGGCTGTGAGAGGCTGTGAGAGGCTGTGAGAGG 720
721 TCTTTAATTTAAGTTCTATCCCGAGGAGGTTTATCAGGAGGTTTATCAGGAGGTTTATCAGG 780
721 TCTTTAATTTAAGTTCTATCCCGAGGAGGTTTATCAGGAGGTTTATCAGGAGGTTTATCAGG 780
781 TCCGAGAAACAGATGCAAGATGCTTTAGGAAACAAATAGCAGTTTCCATCAGGAAATTAATA 840
781 TCCGAGAAACAGATGCAAGATGCTTTAGGAAACAAATAGCAGTTTCCATCAGGAAATTAATA 840
841 TTTATGAATCATAAACCTGCAACAGGAACTGAAATTCCTGCTGACGAGCTTTTGG 900
841 TTTATGAATCATAAACCTGCAACAGGAACTGAAATTCCTGCTGACGAGCTTTTGG 900
901 ACACAGGTTGCTGATCAGAAATGCAAGAGTGGGAAAGTTTGTATGTCACCCCGCTG 960
901 ACACAGGTTGCTGATCAGAAATGCAAGAGTGGGAAAGTTTGTATGTCACCCCGCTG 960
961 TGATGCGGTGAGTGTGCAAGGAGACGCAACCACTGATGCTGCTGGAAGTGGCCCACT 1020
961 TGATGCGGTGAGTGTGCAAGGAGACGCAACCACTGATGCTGCTGGAAGTGGCCCACT 1020
1021 TGGAGGAAACAGAGTGTCTTCAAGAGACATGTTAGGATAGCAGGTTTGTGACCAAG 1080
1021 TGGAGGAAACAGAGTGTCTTCAAGAGACATGTTAGGATAGCAGGTTTGTGACCAAG 1080
1081 ATGAACAGCTGCTGACAGATAGGCTTGTAGTAACTTTTGGCCATGATGGAAG 1140
1081 ATGAACAGCTGCTGACAGATAGGCTTGTAGTAACTTTTGGCCATGATGGAAG 1140
1141 GGCACTCTCTCCAAAGAGAGAAACGTCAGGCAACCAACAGCGGAAACGCTTTA 1200
1141 GGCACTCTCTCCAAAGAGAGAAACGTCAGGCAACCAACAGCGGAAACGCTTTA 1200
1201 AGTCAGCTGTAGAGACACCTTTTGTAGTGGACTTCAGTGACGTGGGGTGAATGACT 1260
1201 AGTCAGCTGTAGAGACACCTTTTGTAGTGGACTTCAGTGACGTGGGGTGAATGACT 1260
1261 GGATTTGGCTCCCCGGGGTATCAGGCTTTTACTGCGCAGGAGAAATGCCCCCTTTTCTC 1320

Db 1261 GGATTTGGCTCCCCGGGGTATCAGGCTTTTACTGCGCAGGAGAAATGCCCCCTTTTCTC 1320
Qy 1321 TGGCTGATCATCTGAACCTCCACTAATCATGTCATTTGTTGACAGCTTTGTTCAACTCTGTTA 1380
Db 1321 TGGCTGATCATCTGAACCTCCACTAATCATGTCATTTGTTGACAGCTTTGTTCAACTCTGTTA 1380
Qy 1381 ACTCTAAGATTTCTTAAGGCTGCTGTGTCGCGACAGAACTCAGTGCTATCTCGATGCTGT 1440
Db 1381 ACTCTAAGATTTCTTAAGGCTGCTGTGTCGCGACAGAACTCAGTGCTATCTCGATGCTGT 1440
Qy 1441 ACCTTTGACGAGATGAAAGCTTGTATTAAGAACTATCAGGACATGTTGTTGAGGGTT 1500
Db 1441 ACCTTTGACGAGATGAAAGCTTGTATTAAGAACTATCAGGACATGTTGTTGAGGGTT 1500
Qy 1501 GTGGGTGCTGCTAGTACAGCAAAATTAATAACATAAATATATATA 1547
Db 1501 GTGGGTGCTGCTAGTACAGCAAAATTAATAACATAAATATATATA 1547

RESULT 2
CS031823 1547 bp DNA linear PAT 10-MAR-2005
LOCUS
DEFINITION Sequence 1329 from Patent WO2005016962.
ACCESSION CS031823
VERSION CS031823.1 GI:60731673
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1
Abbas, A.; Clark, H.; Ouyang, W.; Williams, M.P.; Wood, W.I. and Wu, T.D.
Compositions and methods for the treatment of immune related diseases
Patent: WO 2005016962-A 1329 24-FEB-2005;
Genentech, Inc. (US)

JOURNAL
FEATURES
Location/Qualifiers
1..1547
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 100.0%; Score 1547; DB 6; Length 1547;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1547; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGACTTCTTGAACCTTGCAGGGAGAAATACTTGGCACCACCCCACTTTGGCGGGTGCCTT 60
Db 1 GGGGACTTCTTGAACCTTGCAGGGAGAAATACTTGGCACCACCCCACTTTGGCGGGTGCCTT 60
Qy 61 TGCCCCAGCGAGCTGCTTCCCATCTCCGAGCCCAACCGCCCTCCACATCTCCGCGCT 120
Db 61 TGCCCCAGCGAGCTGCTTCCCATCTCCGAGCCCAACCGCCCTCCACATCTCCGCGCT 120
Qy 121 TGCCCCGACCTGAGACGCTGTTCCAGCGTGAAAGAGAGACTGCGCGCGCGCACCGG 180
Db 121 TGCCCCGACCTGAGACGCTGTTCCAGCGTGAAAGAGAGACTGCGCGCGCGCACCGG 180
Qy 181 GAGAAGGAGGCGAAAGAAAGAAAGGACGGAATTCGGTCTTGGCCAGGTCCTTTGACC 240
Db 181 GAGAAGGAGGCGAAAGAAAGAAAGGACGGAATTCGGTCTTGGCCAGGTCCTTTGACC 240
Qy 241 AGAGTTTTTTCATGTGACGCTCTTTCAATGGAACGTGTCCCGGTGCTTCTTAGACGGA 300
Db 241 AGAGTTTTTTCATGTGACGCTCTTTCAATGGAACGTGTCCCGGTGCTTCTTAGACGGA 300
Qy 301 CTGGGCTGTCTTAAGGTGACACATGTTGGCGGGAGACCCGCTGTCTTAGGTTGCTGC 360
Db 301 CTGGGCTGTCTTAAGGTGACACATGTTGGCGGGAGACCCGCTGTCTTAGGTTGCTGC 360

| | | | |
|----|------|--|------|
| Qy | 361 | TTCCCCAGGTCCTCTCGGCGGCGCGGCTGGCTCGTTCCGGAGCTTGGGCGCGAGAGT | 420 |
| Db | 361 | TTCCCCAGGTCCTCTCGGCGGCGCGGCTGGCTCGTTCCGGAGCTTGGGCGCGAGAGT | 420 |
| Qy | 421 | TCGGGCGGGTCTGTCGGGCGGCGCCCTCATCCAGCCCTCTGACGAGTCTCTCAGCGAGT | 480 |
| Db | 421 | TCGGGCGGGTCTGTCGGGCGGCGCCCTCATCCAGCCCTCTGACGAGTCTCTCAGCGAGT | 480 |
| Qy | 481 | TCGAGTTGCGGCTGCTCAGCATGTTTGGCCCTTGAAACAGAGACCCACCCCGAGCGGACG | 540 |
| Db | 481 | TCGAGTTGCGGCTGCTCAGCATGTTTGGCCCTTGAAACAGAGACCCACCCCGAGCGGACG | 540 |
| Qy | 541 | CCGTGTTGCCCCCTACATGCTAGACCTGTATGCGAGCCCTCAGTCACTCGCGGCTCAC | 600 |
| Db | 541 | CCGTGTTGCCCCCTACATGCTAGACCTGTATGCGAGCCCTCAGTCACTCGCGGCTCAC | 600 |
| Qy | 601 | CCGCCCCAGACACCGGTTGGAGAGGCGCAGCCGCGAGCCAAACACTGTGCGCAGCTTCC | 660 |
| Db | 601 | CCGCCCCAGACACCGGTTGGAGAGGCGCAGCCGCGAGCCAAACACTGTGCGCAGCTTCC | 660 |
| Qy | 661 | ACCATGAAGAATCTTTGGAGAACTACCCAGAAACGAGTGGGAAACAAACCCGAGATTCT | 720 |
| Db | 661 | ACCATGAAGAATCTTTGGAGAACTACCCAGAAACGAGTGGGAAACAAACCCGAGATTCT | 720 |
| Qy | 721 | TCCTTAATTAAGTCTTATCCCGAGGAGGTTTATCACTCAGCAGAGCTTCAGGTTT | 780 |
| Db | 721 | TCCTTAATTAAGTCTTATCCCGAGGAGGTTTATCACTCAGCAGAGCTTCAGGTTT | 780 |
| Qy | 781 | TCCGAGACAGATCAGATGCTTTTAGBAACATAGCAGTTCATCCATCCCGAATTAATA | 840 |
| Db | 781 | TCCGAGACAGATCAGATGCTTTTAGBAACATAGCAGTTCATCCATCCCGAATTAATA | 840 |
| Qy | 841 | TTTATGAAATCATAAAACTGCAACAGCCAACCTCGAAATTCGCCGTGACCACTTTGG | 900 |
| Db | 841 | TTTATGAAATCATAAAACTGCAACAGCCAACCTCGAAATTCGCCGTGACCACTTTGG | 900 |
| Qy | 901 | ACACGAGTTGGTGAATCAGATGCAAGTGGGAAAGTTTGTGATGTCACCCCGCTG | 960 |
| Db | 901 | ACACGAGTTGGTGAATCAGATGCAAGTGGGAAAGTTTGTGATGTCACCCCGCTG | 960 |
| Qy | 961 | TGATGCGGTGGACTGCAAGGACACGCCAACATGATTCGTTGGTGGAGTGGCCACT | 1020 |
| Db | 961 | TGATGCGGTGGACTGCAAGGACACGCCAACATGATTCGTTGGTGGAGTGGCCACT | 1020 |
| Qy | 1021 | TGGAGGAGAAACAAGGTGTCTCCAGAGACATGTTAGGATAAGCAGGTCTTTGCACCAAG | 1080 |
| Db | 1021 | TGGAGGAGAAACAAGGTGTCTCCAGAGACATGTTAGGATAAGCAGGTCTTTGCACCAAG | 1080 |
| Qy | 1081 | ATGAACACAGCTGTGTACAGATAAGGCAATGCTAGTAACTTTTGGCCATGATGGAAAAG | 1140 |
| Db | 1081 | ATGAACACAGCTGTGTACAGATAAGGCAATGCTAGTAACTTTTGGCCATGATGGAAAAG | 1140 |
| Qy | 1141 | GGCATCTCTCCACAAAGAGAAAAGTCAAGCCAAACAAACAGCGGGAACGCTTA | 1200 |
| Db | 1141 | GGCATCTCTCCACAAAGAGAAAAGTCAAGCCAAACAAACAGCGGGAACGCTTA | 1200 |
| Qy | 1201 | AGTCCAGCTGTAAAGAGACACCTTTGTACGTGGACTTCAGTGAGTGGGGTGGAAAGTCACT | 1260 |
| Db | 1201 | AGTCCAGCTGTAAAGAGACACCTTTGTACGTGGACTTCAGTGAGTGGGGTGGAAAGTCACT | 1260 |
| Qy | 1261 | GGATTGTGGTCCCCCGGGGTATCAGCCTTTTATCTGCCACGGAGAAATGCCCTTTTCCCTC | 1320 |
| Db | 1261 | GGATTGTGGTCCCCCGGGGTATCAGCCTTTTATCTGCCACGGAGAAATGCCCTTTTCCCTC | 1320 |
| Qy | 1321 | TGGCTGATCATCTGAACTTCGACTAATCATGTCATTTGTTTCAAGTGGTCAACTCTGTTTA | 1380 |
| Db | 1321 | TGGCTGATCATCTGAACTTCGACTAATCATGTCATTTGTTTCAAGTGGTGGTCAACTCTGTTTA | 1380 |
| Qy | 1381 | ACTCTTAAGATTCTTAAGGCACTGCTGTGTCGCGACAGAACTCAGTGTCTATCTCGATGCTGT | 1440 |
| Db | 1381 | ACTCTTAAGATTCTTAAGGCACTGCTGTGTCGCGACAGAACTCAGTGTCTATCTCGATGCTGT | 1440 |
| Qy | 1441 | ACCTTGAAGAAATGAAAGGTTGTTATTAAGAACTATCAGGACATCGGTTGTGGAGGTT | 1500 |

| | | | |
|---|------------|--|------|
| Db | 1441 | ACCTTTCAGCAAGATGAAAGGTTGTATTAAAGAACATATCAGGACATGTTGTGGAGGTT | 1500 |
| Qy | 1501 | GTGGGTCTCGCTAGTACAGCAAAATTAAATACATAAATATATATATA | 1547 |
| Db | 1501 | GTGGGTCTCGCTAGTACAGCAAAATTAAATACATAAATATATATATA | 1547 |
| RESULT 3 | | | |
| CS040775 | | | |
| LOCUS | CS040775 | Sequence 1329 from Patent WO2005019258. | |
| ACCESSION | CS040775 | | |
| VERSION | CS040775.1 | GI:61848432 | |
| KEYWORDS | | | |
| SOURCE | | | |
| ORGANISM | | Homo sapiens (human) | |
| REFERENCE | | | |
| AUTHORS | | Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; | |
| TITLE | | Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; | |
| JOURNAL | | Hominidae; Homo. | |
| FEATURES | | | |
| source | | 1. 1547 | |
| | | /organism="Homo sapiens" | |
| | | /mol_type="unassigned DNA" | |
| | | /db_xref="taxon:9606" | |
| ORIGIN | | | |
| Query Match | | 100.0%; Score 1547; DB 6; Length 1547; | |
| Best Local Similarity | | 100.0%; Pred. No. 0; | |
| Matches 1547; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | | | |
| Qy | 1 | GGGACATCTTGAACTTCGAGGAGATAACTTGGCACCCCACTTTGGCCGGTGCCCT | 60 |
| Db | 1 | GGGACATCTTGAACTTCGAGGAGATAACTTGGCACCCCACTTTGGCCGGTGCCCT | 60 |
| Qy | 61 | TGCCCCAGCGAGCGCTCTTCGCCCATCTCCGAGGCCACCGCCCTCCACTCTCGGCCCT | 120 |
| Db | 61 | TGCCCCAGCGAGCGCTCTTCGCCCATCTCCGAGGCCACCGCCCTCCACTCTCGGCCCT | 120 |
| Qy | 121 | TGCCCGACATGAGACGCTGTTCCACGCTGAAAAGAGAGACTGCGCGGCGGACCCGG | 180 |
| Db | 121 | TGCCCGACATGAGACGCTGTTCCACGCTGAAAAGAGAGACTGCGCGGCGGACCCGG | 180 |
| Qy | 181 | GAGAAGGAGGAGGCAAGAAAGAAAGGACGATTCGGTCTCTGGCGCAGAGTCCTTTGACC | 240 |
| Db | 181 | GAGAAGGAGGAGGCAAGAAAGAAAGGACGATTCGGTCTCTGGCGCAGAGTCCTTTGACC | 240 |
| Qy | 241 | AGAGTTTTTCAATGGAACGCTTTTCAATGGACGTTCCCGCGTCTCTTTAGACGGA | 300 |
| Db | 241 | AGAGTTTTTCCATGTGACGCTCTTTCAATGGACGTTCCCGCGTCTCTTTAGACGGA | 300 |
| Qy | 301 | CTGGGTCTCTCTAAAGTTCGACCAATGTGGCCGGGACCCGCTCTCTTAGCGTTGCTGC | 360 |
| Db | 301 | CTGGGTCTCTCTAAAGTTCGACCAATGTGGCCGGGACCCGCTCTCTTAGCGTTGCTGC | 360 |
| Qy | 361 | TTCCCCAGGTCTCTCTGGGGGGCGGCTGGCCCTCGTTCCGGAGCTGGGCGGACGGAAGT | 420 |
| Db | 361 | TTCCCCAGGTCTCTCTGGGGGGCGGCTGGCCCTCGTTCCGGAGCTGGGCGGACGGAAGT | 420 |
| Qy | 421 | TCGGGGGGGCGTCTCGGGGGCGCCCTCATCCACGCCCTCTGACGAGTCTCTGACGAGT | 480 |
| Db | 421 | TCGGGGGGGCGTCTCGGGGGCGCCCTCATCCACGCCCTCTGACGAGTCTCTGACGAGT | 480 |
| Qy | 481 | TCGAGTTTCGGCTCTCTCAGCATGTTTCGGCTTGAACGAGNACCCACCCCGACGAGGACG | 540 |
| Db | 481 | TCGAGTTTCGGCTCTCTCAGCATGTTTCGGCTTGAACGAGNACCCACCCCGACGAGGACG | 540 |

Qy 541 CCGTGGTCCGCCCTACATCTAGACCTGTATCGCAGGCACTCAGGTGAGCCGGCTCAC 600
Db 541 CCGTGGTCCGCCCTACATCTAGACCTGTATCGCAGGCACTCAGGTGAGCCGGCTCAC 600
Qy 601 CCGCCCCAGACCAACCGGTTGAGAGGGCAGCCAGCCGAGCCAACTGTGTGCGAGCTTCC 660
Db 601 CCGCCCCAGACCAACCGGTTGAGAGGGCAGCCAGCCGAGCCAACTGTGTGCGAGCTTCC 660
Qy 661 ACCATGAAGATCTTTGGAAGAACTTACAGAAACGAGTGGGAAACACACCCGGAGATTCT 720
Db 661 ACCATGAAGATCTTTGGAAGAACTTACAGAAACGAGTGGGAAACACACCCGGAGATTCT 720
Qy 721 TCTTTAAATTTAAGTTCTATCCCGCAGGAGGTTTATCACTCAGCAGAGCTTCAGGTTT 780
Db 721 TCTTTAAATTTAAGTTCTATCCCGCAGGAGGTTTATCACTCAGCAGAGCTTCAGGTTT 780
Qy 781 TCCGAGAACAGATGCAAGATCTTTAGGAAACAATAGCAGTTTCCATCACCAGAAATTAATA 840
Db 781 TCCGAGAACAGATGCAAGATCTTTAGGAAACAATAGCAGTTTCCATCACCAGAAATTAATA 840
Qy 841 TTTATGAATCATATAAACCTGCAACAGCCAACTCGAAATTCGCCGTGACAGACTTTTGG 900
Db 841 TTTATGAATCATATAAACCTGCAACAGCCAACTCGAAATTCGCCGTGACAGACTTTTGG 900
Qy 901 ACACAGGTTGGTGAATCAGAAATGCAAGCAGGTGGGAAAGTTTGTATGTCAACCCCGCTG 960
Db 901 ACACAGGTTGGTGAATCAGAAATGCAAGCAGGTGGGAAAGTTTGTATGTCAACCCCGCTG 960
Qy 961 TGATCGGTGAGTGCACAGGAGACCGCCAAACCAATGGATTGTTGGTGGAAATGCCCCACT 1020
Db 961 TGATCGGTGAGTGCACAGGAGACCGCCAAACCAATGGATTGTTGGTGGAAATGCCCCACT 1020
Qy 1021 TGGAGGAGAAACAAGTGTCTCCAGAGACATGTTAGGATAAGCAGGTCTTTGACCCAG 1080
Db 1021 TGGAGGAGAAACAAGTGTCTCCAGAGACATGTTAGGATAAGCAGGTCTTTGACCCAG 1080
Qy 1081 ATGAACACAGCTGGTCAAGATAGGCAATTTAGTAACTTTTGGCCATCATGCGAAAG 1140
Db 1081 ATGAACACAGCTGGTCAAGATAGGCAATTTAGTAACTTTTGGCCATCATGCGAAAG 1140
Qy 1141 GGCAATCTCTCCACAAAGAGAAACCGTCAAGCCAAACACAAACAGCGGAAACGCTTTA 1200
Db 1141 GGCAATCTCTCCACAAAGAGAAACCGTCAAGCCAAACACAAACAGCGGAAACGCTTTA 1200
Qy 1201 AGTCCAGCTGAAGAGACACCCCTTTGTACGTGGGATTCAGTCAAGTGGGATGACT 1260
Db 1201 AGTCCAGCTGAAGAGACACCCCTTTGTACGTGGGATTCAGTCAAGTGGGATGACT 1260
Qy 1261 GGATTTGGCTCCCCCGGGTATCAGCGCTTTTACTGCGCAGGAGAAATGCCCTTTTCTC 1320
Db 1261 GGATTTGGCTCCCCCGGGTATCAGCGCTTTTACTGCGCAGGAGAAATGCCCTTTTCTC 1320
Qy 1321 TGGCTGATCATCTGAATCCCACTAATCATGCCATTTGTTGACAGCTTGGTCAACTCTGTTA 1380
Db 1321 TGGCTGATCATCTGAATCCCACTAATCATGCCATTTGTTGACAGCTTGGTCAACTCTGTTA 1380
Qy 1381 ACTCTAAGATCTTAAGCATCTGTGTCCGACAGAACTCAGTCTCATCTCGATGCTGT 1440
Db 1381 ACTCTAAGATCTTAAGCATCTGTGTCCGACAGAACTCAGTCTCATCTCGATGCTGT 1440
Qy 1441 ACCTTGACGAGATGAAAAGTTGTATTAAGAACTATCAGACATGTTGTGGAGGGTT 1500
Db 1441 ACCTTGACGAGATGAAAAGTTGTATTAAGAACTATCAGACATGTTGTGGAGGGTT 1500
Qy 1501 GTGGGTGTCTAGTACAGCAAAATTAATAATATATATATA 1547
Db 1501 GTGGGTGTCTAGTACAGCAAAATTAATAATATATATATA 1547

RESULT 4
I78455 1547 bp DNA linear PAT 03-APR-1998
LOCUS I78455
DEFINITION Sequence 2 from patent US 5693615.

ACCESSION I78455
VERSION I78455.1 GI:3014609
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 1547)
AUTHORS Stone, R. Lee.
TITLE Therapeutic compositions for osteoinduction
JOURNAL Patent: US 5693615-A 2 02-DEC-1997;
FEATURES Location/Qualifiers
source 1..1547
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
Query Match 100.0%; Score 1547; DB 6; Length 1547;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1547; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GGGGACTTCTTGAACCTTGACGGGAGAAATACTTGGCAGCAACCCCACTTTGGCGCGGTGCTT 60
Db 1 GGGGACTTCTTGAACCTTGACGGGAGAAATACTTGGCAGCAACCCCACTTTGGCGCGGTGCTT 60
Qy 61 TGCCCCAGCGAGGCTCTTCCGCACTCTCGAGCCCAACCGCCCTCCACTTCTCGGCT 120
Db 61 TGCCCCAGCGAGGCTCTTCCGCACTCTCGAGCCCAACCGCCCTCCACTTCTCGGCT 120
Qy 121 TGCCCCAGCACTTGAGACGCTGTTCACGCTGAAAGAGAGACTGCGGCGCGGCAACCCGG 180
Db 121 TGCCCCAGCACTTGAGACGCTGTTCACGCTGAAAGAGAGACTGCGGCGCGGCAACCCGG 180
Qy 181 GAGAGAGAGAGGCAAAAGAAAGAGACGAGACATTCGGTCTTGGCGCAGGTCTTTGACC 240
Db 181 GAGAGAGAGAGGCAAAAGAAAGAGACGAGACATTCGGTCTTGGCGCAGGTCTTTGACC 240
Qy 241 AGAGTTTTTCATGTGACGCTCTTCAATGAGAGTGTCCCGGCTGCTTCTTAGACGGA 300
Db 241 AGAGTTTTTCATGTGACGCTCTTCAATGAGAGTGTCCCGGCTGCTTCTTAGACGGA 300
Qy 301 CTGCGGTCTCTAAGGTGACCAATGTGTGCGCGGACCCCGCTGTCTTCTAGCTGTCTGC 360
Db 301 CTGCGGTCTCTAAGGTGACCAATGTGTGCGCGGACCCCGCTGTCTTCTAGCTGTCTGC 360
Qy 361 TTCCCCAGGTCTCTTGGGCGGCGGCTGGCTGGCTTCCGAGCTGGCGCGCAGGAGT 420
Db 361 TTCCCCAGGTCTCTTGGGCGGCGGCTGGCTGGCTTCCGAGCTGGCGCGCAGGAGT 420
Qy 421 TCGGCGGCGGCTCGTGGGCGGCGCCCTCATCCAGCCCTCTGACGAGGTCTGAGCGAGT 480
Db 421 TCGGCGGCGGCTCGTGGGCGGCGCCCTCATCCAGCCCTCTGACGAGGTCTGAGCGAGT 480
Qy 481 TCGAGTTGCGGCTGCTCAGCATGTTTGGCCCTTGAAACAGAGACCCACCCCGCAGGAGCG 540
Db 481 TCGAGTTGCGGCTGCTCAGCATGTTTGGCCCTTGAAACAGAGACCCACCCCGCAGGAGCG 540
Qy 541 CCGTGGTCCCGCTCATATGTAGACTGTATCGCAGGCACTCAGGTGAGCGCGGCTCAC 600
Db 541 CCGTGGTCCCGCTCATATGTAGACTGTATCGCAGGCACTCAGGTGAGCGCGGCTCAC 600
Qy 601 CCGCCCCAGACCAACCGGTTGAGAGGGCAGCCAGCCGAGCCAACTGTGTGCGAGCTTCC 660
Db 601 CCGCCCCAGACCAACCGGTTGAGAGGGCAGCCAGCCGAGCCAACTGTGTGCGAGCTTCC 660
Qy 661 ACCATGAAGATCTTTTGGAGAACTACAGAAACGAGTGGGAAACAAACCCGGAGATTCT 720
Db 661 ACCATGAAGATCTTTTGGAGAACTACAGAAACGAGTGGGAAACAAACCCGGAGATTCT 720
Qy 721 TCTTTAAATTTAAGTTCTATCCCGCAGGAGGTTTATCACTCAGCAGAGCTTCAGGTTT 780
Db 721 TCTTTAAATTTAAGTTCTATCCCGCAGGAGGTTTATCACTCAGCAGAGCTTCAGGTTT 780
Qy 781 TCCGAGAACAGATGCAAGATGCTTTAGGAAACAATAGCAGTTTCCATCACCAGAAATTAATA 840

[illegible]

```

RESULT 5
AX775087
LOCUS          1547 bp      DNA      linear
DEFINITION    Sequence 403 from Patent WO03038129.
ACCESSION     AX775087
VERSION       AX775087.1  GI:32486603
KEYWORDS      .
SOURCE        Homo sapiens (human)
ORGANISM      Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
               Hominidae; Homo.
REFERENCE     1
AUTHORS      Raponi, M.
TITLE        Methods for assessing and treating leukemia
JOURNAL      Patent: WO 03038129-A 403 08-MAY-2003;
              Ortho-Clinical diagnostics, Inc. (US)
FEATURES     Location/Qualifiers
               1..1547
               /organism="Homo sapiens"
               /mol_type="unassigned DNA"
SOURCE

```

```

Db      961  TGATGCGGTGAGCTGTCACAGGACACGCCAACCATGATGCTGCTGGTGGAAAGTGCCTCACT 1020
Qy      1021  TGGAGGAGAAACAAGGTGTCTCCAAAGAGACATGTTAGGATAAGCAGGTCTTTTGACCAAG 1080
Db      1021  TGGAGGAGAAACAAGGTGTCTCCAAAGAGACATGTTAGGATAAGCAGGTCTTTTGACCAAG 1080
Qy      1081  ATGAACACAGCTGCTGTCACAGATAAGGCCATCTGCTAGTAACCTTTTGGCCATGATGGAAGAAG 1140
Db      1081  ATGAACACAGCTGCTGTCACAGATAAGGCCATCTGCTAGTAACCTTTTGGCCATGATGGAAGAAG 1140
Qy      1141  GGCATCTCTCCACAAAGAGAAAAAGCTCAAGCAAAACACAAACAGCGGAAACGCTTTA 1200
Db      1141  GGCATCTCTCCACAAAGAGAAAAAGCTCAAGCAAAACACAAACAGCGGAAACGCTTTA 1200
Qy      1201  AGTCAGCTGTAAGAGACACCCCTTTGTACGTGGAGCTTTCAGTGACGTGGGGTGAATGACT 1260
Db      1201  AGTCAGCTGTAAGAGACACCCCTTTGTACGTGGAGCTTTCAGTGACGTGGGGTGAATGACT 1260
Qy      1261  GGATTTGTGGTCCCGCGGGTATCACGCTTTTACTGCGCAGGAGAAATGCCCTTTTCTC 1320
Db      1261  GGATTTGTGGTCCCGCGGGTATCACGCTTTTACTGCGCAGGAGAAATGCCCTTTTCTC 1320
Qy      1321  TGGCTGATCATCTGAATCCCACTCAATCATGCCATGTTTCAGACGTTGGTCAACTCTGTTA 1380
Db      1321  TGGCTGATCATCTGAATCCCACTCAATCATGCCATGTTTCAGACGTTGGTCAACTCTGTTA 1380
Qy      1381  ACTCTAAGATTCCTTAAGCATGCTGTGTCGCGACAGAACTCAGTGCTATCTCGATGCTGT 1440
Db      1381  ACTCTAAGATTCCTTAAGCATGCTGTGTCGCGACAGAACTCAGTGCTATCTCGATGCTGT 1440
Qy      1441  ACCTTGACGAGAAATGAAGAAGTTGTATTAAAGAACTATCAGGACATGGTTGTGAGGGTT 1500
Db      1441  ACCTTGACGAGAAATGAAGAAGTTGTATTAAAGAACTATCAGGACATGGTTGTGAGGGTT 1500
Qy      1501  GTGGGTGCTGCTAGTACAGCAAAATTAATACATAATATATATATA 1547
Db      1501  GTGGGTGCTGCTAGTACAGCAAAATTAATACATAATATATATATA 1547

```

```

RESULT 6
HUMBMP2A      HUMBMP2A      1547 bp      mRNA      linear      PRI 31-OCT-1994
LOCUS      Human bone morphogenetic protein 2A (BMP-2A) mRNA.
DEFINITION      M22489
ACCESSION      M22489
VERSION      1 GI:179501
KEYWORDS      bone morphogenetic protein.
SOURCE      Homo sapiens
ORGANISM      Homo sapiens
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE      1 (sites)
AUTHORS      Wozney,J.M., Rosen,V., Celeste,A.J., Mitsock,L.M., Whitters,M.J.,
Kriz,R.W., Hewick,R.M. and Wang,E.A.
TITLE      Novel regulators of bone formation: molecular clones and activities
JOURNAL      Science 242 (4885), 1528-1534 (1988)
PUBMED      3201241
REFERENCE      2 (bases 1 to 1547)
AUTHORS      Wozney,J.M., Rosen,V., Celeste,A.J., Mitsock,L.M., Whitters,M.J.,
Kriz,R.W., Hewick,R.M. and Wang,E.A.
JOURNAL      Unpublished (1989)
COMMENT      Original source text: Human osteosarcoma cell line U-2 OS, cDNA to
mRNA, clone hBMP-2A.
[1] sites.
Draft entry and computer readable copy of sequence [1] kindly
submitted by R.W. Kriz 10-FEB-1989.
FEATURES
source      Location/Qualifiers
1. .1547
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/map="20"
1. .1547
gene

```

```

CDS
/gene="BMP2"
324. .1514
/gene="BMP2"
/notes="bone morphogenetic protein 2A"
/codon_start=1
/protein_id="AAA51834.1"
/db_xref="GI:179502"
/db_xref="GDB:G00-125-204"
/translation="MVAGTRCLALLPVLGGAGLVPELGRKFAAASSSGRPSSQ
PSDEVSEPELRLLSMGLKORPTPSRDAVVPVMDLXYRHSGQSGSPADHRLERA
ASRANTVSRFHHEESLEELPETSCKTRRFFNLSSITPEFTISAELOVREQMDA
LGNSSPHHRIINIEYIIKPATANSKFPVRLDRLVQNQASRWESFDVTPAVNRWTA
QGHANFGFVVEVAHLEEKQSVSRHVRISRLQDEHSWSQIRLLPTVFGHDGHPL
KHKEKQAKHKQRKLKSSCKRHPLVYDFSDGVNDWIVAPPGYHAYFCHGECFFPLA
HLNSTNHAIVQTLVNSVNSKI PKACCVPTSELSAISMLYLDENEKVKVLKNYQDMVVEG
CGCR"
ORIGIN
Query Match      100.0%; Score 1547; DB 8; Length 1547;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1547; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      1      GGGGACTTCTTGAACCTTGCAAGGAGAAATACTTGGCAGCCCACTTTGGCGCGGTGCTT 60
Db      1      GGGGACTTCTTGAACCTTGCAAGGAGAAATACTTGGCAGCCCACTTTGGCGCGGTGCTT 60
Qy      61      TGCCCGACGCGAGGCTCTCTTCCGCTCTCCGAGCCCAACCGCCCTCCACTTCCTCGGCCT 120
Db      61      TGCCCGACGCGAGGCTCTCTTCCGCTCTCCGAGCCCAACCGCCCTCCACTTCCTCGGCCT 120
Qy      121      TGCCCGACACTGAGACGCTGTTCACGCTGTAAGAGAGACTCGCGCGCGCGCACCGG 180
Db      121      TGCCCGACACTGAGACGCTGTTCACGCTGTAAGAGAGACTCGCGCGCGCGCACCGG 180
Qy      181      GAGAGGAGGAGGCAAGAAAGAAAGGAACTTGGCTCTTGGCCAGGTCTCTTTGACC 240
Db      181      GAGAGGAGGAGGCAAGAAAGAAAGGAACTTGGCTCTTGGCCAGGTCTCTTTGACC 240
Qy      241      AGAGTTTTTCATGTGACGCTCTTTCAATGGAGCTGTCCCGCGGTGCTCTTAGACGGA 300
Db      241      AGAGTTTTTCATGTGACGCTCTTTCAATGGAGCTGTCCCGCGGTGCTCTTAGACGGA 300
Qy      301      CTGCGGTCTCTCTAAAGTTCGACCAATGTTGGCGCGGACCCGCTGTCTTTAGCTGTGCTG 360
Db      301      CTGCGGTCTCTCTAAAGTTCGACCAATGTTGGCGCGGACCCGCTGTCTTTAGCTGTGCTG 360
Qy      361      TTCCCGAGGTCTCTCTGGCGCGCGCTGCTGCTGTTCCGAGCTGGCGCGGAGAGT 420
Db      361      TTCCCGAGGTCTCTCTGGCGCGCGCTGCTGCTGTTCCGAGCTGGCGCGGAGAGT 420
Qy      421      TCGCGCGCGGTCTGCTGCGCGCGCCCTCATCCAGCCCTCTGACGAGGTCTGAGCGAGT 480
Db      421      TCGCGCGCGGTCTGCTGCGCGCGCCCTCATCCAGCCCTCTGACGAGGTCTGAGCGAGT 480
Qy      481      TCGAGTTGCGGTCTCTCAGCATGTTTCGCGCTGAAACAGAGACCCACCCAGCAGGAGACG 540
Db      481      TCGAGTTGCGGTCTCTCAGCATGTTTCGCGCTGAAACAGAGACCCACCCAGCAGGAGACG 540
Qy      541      CCGTGTGCGCGCGGTCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 600
Db      541      CCGTGTGCGCGCGGTCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 600
Qy      601      CCGCGCGCAGACCCCGGTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 660
Db      601      CCGCGCGCAGACCCCGGTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 660
Qy      661      ACCATGAAGAATCTTTTGAAGAACTACCAAGAAACGAGTGGGAAACAAACCCCGAGATTCT 720
Db      661      ACCATGAAGAATCTTTTGAAGAACTACCAAGAAACGAGTGGGAAACAAACCCCGAGATTCT 720
Qy      721      TCTTTAATTTAAGTTCTATCCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 780
Db      721      TCTTTAATTTAAGTTCTATCCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 780

```

| | | | |
|----|------|---|------|
| QY | 781 | TCCGAGAACAGATGCAAGATGCTTTAGGAAACAAATAGCAGTTTCCATCACCGAATTAATA | 840 |
| Db | 781 | TCCGAGAACAGATGCAAGATGCTTTAGGAAACAAATAGCAGTTTCCATCACCGAATTAATA | 840 |
| QY | 841 | TTTATGAATCATATAAACTCGAACAGCCAACTCGAAATTCCTCCGTGACGACACTTTTGG | 900 |
| Db | 841 | TTTATGAATCATATAAACTCGAACAGCCAACTCGAAATTCCTCCGTGACGACACTTTTGG | 900 |
| QY | 901 | ACACCAAGTTGGTGAATCAGATGCAAGCAGGTGCGAAAGTTTTCATGTCACCCCGGTG | 960 |
| Db | 901 | ACACCAAGTTGGTGAATCAGATGCAAGCAGGTGCGAAAGTTTTCATGTCACCCCGGTG | 960 |
| QY | 961 | TGATCGGTGGAATGCAAGGACACGCCAACCATGGAATTCGTGTGGAAGTGGCCCACT | 1020 |
| Db | 961 | TGATCGGTGGAATGCAAGGACACGCCAACCATGGAATTCGTGTGGAAGTGGCCCACT | 1020 |
| QY | 1021 | TGGAGGAGAAACAAGGTGTCTCAAGAGACATGTTAGGATAGAGAGTCTTTGCAACCAAG | 1080 |
| Db | 1021 | TGGAGGAGAAACAAGGTGTCTCAAGAGACATGTTAGGATAGAGAGTCTTTGCAACCAAG | 1080 |
| QY | 1081 | ATGACACAGCTGCTCAGATGAAGCCATTGCTAGTAACCTTTTGGCCATGATGAAAG | 1140 |
| Db | 1081 | ATGACACAGCTGCTCAGATGAAGCCATTGCTAGTAACCTTTTGGCCATGATGAAAG | 1140 |
| QY | 1141 | GGCATCTCTCCCAAAAGAGAAAAACGTCAGGCCAAACACAAACAGCGGAAACGCCCTTA | 1200 |
| Db | 1141 | GGCATCTCTCCCAAAAGAGAAAAACGTCAGGCCAAACACAAACAGCGGAAACGCCCTTA | 1200 |
| QY | 1201 | AGTCAGCTGTAAGAGACACCTTTTGTAGCTGACCTTCAGTGACGCGGGTGGAAATGACT | 1260 |
| Db | 1201 | AGTCAGCTGTAAGAGACACCTTTTGTAGCTGACCTTCAGTGACGCGGGTGGAAATGACT | 1260 |
| QY | 1261 | GGATTTGGTCTCCCGGGGTATCAGCCTTTTACTGCCACGAGAAATGCCCTTTTCCTC | 1320 |
| Db | 1261 | GGATTTGGTCTCCCGGGGTATCAGCCTTTTACTGCCACGAGAAATGCCCTTTTCCTC | 1320 |
| QY | 1321 | TGGCTGATCATCTGAATCCCAATCATGCTGATGTTTACAGACGTTGGTCAACTCTGTTA | 1380 |
| Db | 1321 | TGGCTGATCATCTGAATCCCAATCATGCTGATGTTTACAGACGTTGGTCAACTCTGTTA | 1380 |
| QY | 1381 | ACTCTAAGATTCCTAAGGATGCTGTCCTGACGAACTCAGTGCTATCTCGATGCTGT | 1440 |
| Db | 1381 | ACTCTAAGATTCCTAAGGATGCTGTCCTGACGAACTCAGTGCTATCTCGATGCTGT | 1440 |
| QY | 1441 | ACCTTGACGAGATGAAAGTTGTTAAGAACTATCAGACATGTTTGGAGGTT | 1500 |
| Db | 1441 | ACCTTGACGAGATGAAAGTTGTTAAGAACTATCAGACATGTTTGGAGGTT | 1500 |
| QY | 1501 | GTGGGTGTCGCTAGTACAGCAAAATTAATACATAAATATATATA | 1547 |
| Db | 1501 | GTGGGTGTCGCTAGTACAGCAAAATTAATACATAAATATATATA | 1547 |

RESULT 7
CS038212
LOCUS CS038212 1581 bp DNA linear PAT 10-MAR-2005
DEFINITION Sequence 10 from Patent WO2005016368.
ACCESSION CS038212
VERSION CS038212.1 GI:60734760
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1
AUTHORS Sfeir, C., Campbell, P., Jadowiec, J.A. and Kumta, P.
TITLE Method of inducing biomineralization, method of inducing bone regeneration and methods related thereof
JOURNAL Patent: WO 2005016368-A 10 24-FEB-2005;
University of Pittsburgh of the Commonwealth System of Hi gher Education (US); Carnegie Mellon University (US)

| FEATURES | | Location/Qualifiers | |
|----------------------------|-----|---|-----|
| source | | 1..1581 | |
| | | /organism="Homo sapiens" | |
| | | /mol_type="unassigned DNA" | |
| | | /db_xref="taxon:9606" | |
| ORIGIN | | | |
| Query Match | | 100.0%; Score 1547; DB 6; Length 1581; | |
| Best Local Similarity | | 100.0%; Pred. No. 0; | |
| Matches 1547; Conservative | | 0; Mismatches 0; Indels 0; Gaps 0; | |
| QY | 1 | GGGGACTTCTTGAACCTTCAGGAGAAATAACTTGGGCAACCCACCTTTGGCCCGGTCCTT | 60 |
| Db | 1 | GGGGACTTCTTGAACCTTCAGGAGAAATAACTTGGGCAACCCACCTTTGGCCCGGTCCTT | 60 |
| QY | 61 | TGCCCCACGGAGCCTGCTTCGCCATCTCCAGAGCCCAACCGCCCTCCACCTCTCGGCT | 120 |
| Db | 61 | TGCCCCACGGAGCCTGCTTCGCCATCTCCAGAGCCCAACCGCCCTCCACCTCTCGGCT | 120 |
| QY | 121 | TGCCCGACACTGAGACGCTGTTCCAGCGTGAAGAGAGAGACTGCGCGCCGCGCACCCGG | 180 |
| Db | 121 | TGCCCGACACTGAGACGCTGTTCCAGCGTGAAGAGAGAGACTGCGCGCCGCGCACCCGG | 180 |
| QY | 181 | GAGAGGAGGAGGCAAGAAAGGAAACGGAATTCGGTCTTTCGCCAGGTCCTTTGACC | 240 |
| Db | 181 | GAGAGGAGGAGGCAAGAAAGGAAACGGAATTCGGTCTTTCGCCAGGTCCTTTGACC | 240 |
| QY | 241 | AGAGTTTTCATGAGACGCTCTTCAATGAGAGCTGTCGCCGCTGCTCTTAGACGGA | 300 |
| Db | 241 | AGAGTTTTCATGAGACGCTCTTCAATGAGAGCTGTCGCCGCTGCTCTTAGACGGA | 300 |
| QY | 301 | CTGCGGCTCTCTAAAGGTTCGACATGTTGGCGGAGACCCGCTGCTCTTAGCGTTGCTGC | 360 |
| Db | 301 | CTGCGGCTCTCTAAAGGTTCGACATGTTGGCGGAGACCCGCTGCTCTTAGCGTTGCTGC | 360 |
| QY | 361 | TTCCCCAGGTCTCTCGGGCGGCGGCTGCGTTCGGAGCTGCGGCGCGAGAAAT | 420 |
| Db | 361 | TTCCCCAGGTCTCTCGGGCGGCGGCTGCGTTCGGAGCTGCGGCGCGAGAAAT | 420 |
| QY | 421 | TGCGGGCGGCTGCTGCGGGCGGCGGCTCATCCAGCGCTCTGACGAGTCTGAGCGAGT | 480 |
| Db | 421 | TGCGGGCGGCTGCTGCGGGCGGCGGCTCATCCAGCGCTCTGACGAGTCTGAGCGAGT | 480 |
| QY | 481 | TCGAGTTCGGCTGCTCAGCATGTTTCGGCTGAAACAGAGACCCACCCAGCAGGAGC | 540 |
| Db | 481 | TCGAGTTCGGCTGCTCAGCATGTTTCGGCTGAAACAGAGACCCACCCAGCAGGAGC | 540 |
| QY | 541 | CGTGGTCCCGCTTACATGCTAGACCTGATCGAGGCACTCAGGTCAAGCGGCTCAC | 600 |
| Db | 541 | CGTGGTCCCGCTTACATGCTAGACCTGATCGAGGCACTCAGGTCAAGCGGCTCAC | 600 |
| QY | 601 | CGGCCCCAGACCAACCGGTTGGAGAGGCGAGCCGAGCCCACTGTGCGCAGTTCC | 660 |
| Db | 601 | CGGCCCCAGACCAACCGGTTGGAGAGGCGAGCCGAGCCCACTGTGCGCAGTTCC | 660 |
| QY | 661 | ACCTGAAGAAATCTTTGGAAGAACTACAGAAACGAGTGGGAAAAACAACCCGAGATTCT | 720 |
| Db | 661 | ACCTGAAGAAATCTTTGGAAGAACTACAGAAACGAGTGGGAAAAACAACCCGAGATTCT | 720 |
| QY | 721 | TCTTTAAATTTAAGTTCTATCCCGCAGGAGGTTTATCACTCAGCAGAGCTTCAGGTTT | 780 |
| Db | 721 | TCTTTAAATTTAAGTTCTATCCCGCAGGAGGTTTATCACTCAGCAGAGCTTCAGGTTT | 780 |
| QY | 781 | TCCGAGAACAGATGCAAGATGCTTTAGGAAACAAATAGCAGTTTCCATCACCGAATTAATA | 840 |
| Db | 781 | TCCGAGAACAGATGCAAGATGCTTTAGGAAACAAATAGCAGTTTCCATCACCGAATTAATA | 840 |
| QY | 841 | TTTATGAATCATATAAACTCGAACAGCCAACTCGAAATTCCTCCGTGACGACACTTTTGG | 900 |
| Db | 841 | TTTATGAATCATATAAACTCGAACAGCCAACTCGAAATTCCTCCGTGACGACACTTTTGG | 900 |
| QY | 901 | ACACCAAGTTGGTGAATCAGATGCAAGCAGGTGCGAAAGTTTTCATGTCACCCCGGTG | 960 |
| Db | 901 | ACACCAAGTTGGTGAATCAGATGCAAGCAGGTGCGAAAGTTTTCATGTCACCCCGGTG | 960 |

Db 901 ACACAGGTTGGTGAATCAGAATCAGAGCGTGGGAAAGTTTTGATGTCACCCCCGCTG 960

Qy 961 TGATGCGGTGACCTGCACAGGGACACGCCAACCAATGATTCGTGGTGAAGTGCCTCACT 1020

Db 961 TGATGCGGTGACCTGCACAGGGACACGCCAACCAATGATTCGTGGTGAAGTGCCTCACT 1020

Qy 1021 TGGAGGAGAACAAAGGTGTCTCCTCAAGAGACATGTTAGGATAAGCAGGTCTTTTGACCAAG 1080

Db 1021 TGGAGGAGAACAAAGGTGTCTCCTCAAGAGACATGTTAGGATAAGCAGGTCTTTTGACCAAG 1080

Qy 1081 ATGAACACAGCTGGTGCACAGATAAGGCCATCTGTAGTAACCTTTTGGCCATGATGAAAG 1140

Db 1081 ATGAACACAGCTGGTGCACAGATAAGGCCATCTGTAGTAACCTTTTGGCCATGATGAAAG 1140

Qy 1141 GGCATCTCTCCACAAAGAGAAAAACGTCAAGCCAAACACAAACAGCGGAAACGCCTTA 1200

Db 1141 GGCATCTCTCCACAAAGAGAAAAACGTCAAGCCAAACACAAACAGCGGAAACGCCTTA 1200

Qy 1201 AGTCAGCTGTAAAGAGACACCTTTTGTACGTGGACTTCAGTGACGTGGGTGGAAATGACT 1260

Db 1201 AGTCAGCTGTAAAGAGACACCTTTTGTACGTGGACTTCAGTGACGTGGGTGGAAATGACT 1260

Qy 1261 GGATTTGGTCTCCCGGGGTATCACGCTTTTACTGCCACGGAGAAATGCCCTTTTCTC 1320

Db 1261 GGATTTGGTCTCCCGGGGTATCACGCTTTTACTGCCACGGAGAAATGCCCTTTTCTC 1320

Qy 1321 TGGCTGATCATCTGAATCCTCACTAATCATGTCATGTTTCAGACGTTGGTCACTCTGTTA 1380

Db 1321 TGGCTGATCATCTGAATCCTCACTAATCATGTCATGTTTCAGACGTTGGTCACTCTGTTA 1380

Qy 1381 ACTCTAGATCTCTAAAGCATGCTGTGTCGCGACAGAACTCAGTGCTATCTCGATGCTGT 1440

Db 1381 ACTCTAGATCTCTAAAGCATGCTGTGTCGCGACAGAACTCAGTGCTATCTCGATGCTGT 1440

Qy 1441 ACCTTGACGAGATGAAAGGTTGTATTAAGAACTATCAGGACATGTTGTGGAGGTT 1500

Db 1441 ACCTTGACGAGATGAAAGGTTGTATTAAGAACTATCAGGACATGTTGTGGAGGTT 1500

Qy 1501 GTGGGTGCTGTAGTACGAAATTAATTAATACATAATATATATA 1547

Db 1501 GTGGGTGCTGTAGTACGAAATTAATTAATACATAATATATATA 1547

RESULT 8

AR157708

LOCUS AR157708 1607 bp DNA linear PAT 17-OCT-2001

DEFINITION Sequence 3 from patent US 6245889.

ACCESSION AR157708

VERSION AR157708.1 GI:16218701

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 1607)

Unclassified.

AUTHORS Wang, E. A., Wozney, J. M. and Rosen, V. A.

TITLE BMP-4 products

JOURNAL Patent: US 6245889-A 3 12-JUN-2001;

FEATURES

Location/Qualifiers

1..1607

/organism="unknown"

/mol_type="unassigned DNA"

ORIGIN

Query Match 100.0%; Score 1547; DB 6; Length 1607;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1547; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGACTCTTGAATTCGAGGGAGATAACTTGGCACCCCACTTTTGGCGGGTGCCTT 60

Db 33 GGGGACTCTTGAATTCGAGGGAGATAACTTGGCACCCCACTTTTGGCGGGTGCCTT 92

Qy 61 TGGCCCGGAGGAGGCTGTTCGCCATCTCCGAGGCCACCGCCCTTCACATCTCTCGGCT 120

Db 93 TGGCCCGGAGGAGCTGCTTTGGCCATCTCGAGCCCCACCGCCCTTCACTCTCTCGGCT 152

Qy 121 TGGCCCGACACTGAGACGCTGTTCCAGCGTGAAGAGAGACTGCGGCGCGGACCCGG 180

Db 153 TGGCCCGACACTGAGACGCTGTTCCAGCGTGAAGAGAGACTGCGGCGCGGACCCGG 212

Qy 181 GAGAAGCAGGAGGCAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240

Db 213 GAGAAGCAGGAGGCAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 272

Qy 241 AGAGTTTTTCCATGTGAGCGCTCTTTCAATGGAGCTGTCCCAGCTGCTTTCTTAGACGA 300

Db 273 AGAGTTTTTCCATGTGAGCGCTCTTTCAATGGAGCTGTCCCAGCTGCTTTCTTAGACGA 332

Qy 301 CTGGCGTCTCTTAAGGTGACACATGTTGGCGGGGACCCGCTGCTTTCTAGCGTTGCTGC 360

Db 333 CTGGCGTCTCTTAAGGTGACACATGTTGGCGGGGACCCGCTGCTTTCTTAGCGTTGCTGC 392

Qy 361 TTCCCGCAGGTCTCTCTGGCGGGCGGCTGCGCTCTGTTTCGGAGCTGCGGCGCAGGAAGT 420

Db 393 TTCCCGCAGGTCTCTCTGGCGGGCGGCTGCGCTCTGTTTCGGAGCTGCGGCGCAGGAAGT 452

Qy 421 TCGCGCGGGCTGCTGGCGGGCGGCTCTATCCAGCCCTCTGACGAGCTCTGAGCGAGT 480

Db 453 TCGCGCGGGCTGCTGGCGGGCGGCTCTATCCAGCCCTCTGACGAGCTCTGAGCGAGT 512

Qy 481 TCGAGTTGCGGCTGCTCAGCATGTTTGGGCTTGAAGAGAGAGAGAGAGAGAGAGAGAG 540

Db 513 TCGAGTTGCGGCTGCTCAGCATGTTTGGGCTTGAAGAGAGAGAGAGAGAGAGAGAGAG 572

Qy 541 CCGTGGTGGCCCCCTACATGCTAGACCTGTATGCGAGGCTCAGAGTTCAGCGCGGCTCAC 600

Db 573 CCGTGGTGGCCCCCTACATGCTAGACCTGTATGCGAGGCTCAGAGTTCAGCGCGGCTCAC 632

Qy 601 CCGCCCCAGACACACCGGTTGGAGGGGAGCGAGCGAGGCCAACATCTGTGCGCAGCTTCC 660

Db 633 CCGCCCCAGACACACCGGTTGGAGGGGAGCGAGCGAGGCCAACATCTGTGCGCAGCTTCC 692

Qy 661 ACCATGAAGATCTTTTGGAGAGACTACAGAAACGAGTGGGAAACAAACCCGGAGATCT 720

Db 693 ACCATGAAGATCTTTTGGAGAGACTACAGAAACGAGTGGGAAACAAACCCGGAGATCT 752

Qy 721 TCTTTAATTTAAGTTCTATCCCGAGGAGGTTTATCCTCCTCAGCAGAGCTTCAGGTTT 780

Db 753 TCTTTAATTTAAGTTCTATCCCGAGGAGGTTTATCCTCCTCAGCAGAGCTTCAGGTTT 812

Qy 781 TCCGAGAACAGATGCAAGATGCTTTTAGGAAACAAATAGCAGTTTCATCACCAGATTAATA 840

Db 813 TCCGAGAACAGATGCAAGATGCTTTTAGGAAACAAATAGCAGTTTCATCACCAGATTAATA 872

Qy 841 TTTATGAATCATAAACCTTGCAACAGCCAACTCGAAATTTCCCGCTGACGAGACTTTTGG 900

Db 873 TTTATGAATCATAAACCTTGCAACAGCCAACTCGAAATTTCCCGCTGACGAGACTTTTGG 932

Qy 901 ACACGAGTTGGTGAATCAGAAATGCAAGAGAGTGGGAAAGTTTGTATGTACCCCGCTG 960

Db 933 ACACGAGTTGGTGAATCAGAAATGCAAGAGAGTGGGAAAGTTTGTATGTACCCCGCTG 992

Qy 961 TGATGCGGTGACTGTCACAGGGACACGCCAACCATGGAATTCGTGGTGGAGAGTGCCTCACT 1020

Db 993 TGATGCGGTGACTGTCACAGGGACACGCCAACCATGGAATTCGTGGTGGAGAGTGCCTCACT 1052

Qy 1021 TGGAGGAGAAACAAAGGTGCTCAGAGACATGTTAGGATAAGCAGGTCTTTTGACCCAG 1080

Db 1053 TGGAGGAGAAACAAAGGTGCTCAGAGAGACATGTTAGGATAAGCAGGTCTTTTGACCCAG 1112

Qy 1081 ATGAACACAGCTGTTCACAGATAAGGCCATTTGTAGTAACTTTTGGCCATCATGAGAAAG 1140

Db 1113 ATGAACACAGCTGTTCACAGATAAGGCCATTTGTAGTAACTTTTGGCCATCATGAGAAAG 1172

Qy 1141 GGCACTCTCTCCACAAAGAGAGAAACAGTCAAGCCAAACACAAACAGCGGAAACGCCTTA 1200

Db 1173 GGCACTCTCTCCACAAAGAGAGAAACAGTCAAGCCAAACACAAACAGCGGAAACGCCTTA 1232


```
QY 1201 AGTCAGCTGTAAAGAGACACCCCTTTGTACGTGGAACTTCAGTGACCTGGGGTGGAAATGACT 1260
Db 1233 AGTCAGCTGTAAAGAGACACCCCTTTGTACGTGGAACTTCAGTGACCTGGGGTGGAAATGACT 1292
QY 1261 GGAATGTGGCTCCCGCGGGGTATACCGCTTTTATCGCCACGGAGAAATGCCCTTTTTCCTC 1320
Db 1293 GGAATGTGGCTCCCGCGGGGTATACCGCTTTTATCGCCACGGAGAAATGCCCTTTTTCCTC 1352
QY 1321 TGGCTGATCACTGAACCTCCATAATCATGCAATGTCATTTGTCAGACGTGGTCAACTCTGTTA 1380
Db 1353 TGGCTGATCACTGAACCTCCATAATCATGCAATGTCATTTGTCAGACGTGGTCAACTCTGTTA 1412
QY 1381 ACTCTAAGATTCCTAAGCGATGCTGTGTCGCCGACGAACTCAGTGCTATCTCGATGCTGT 1440
Db 1413 ACTCTAAGATTCCTAAGCGATGCTGTGTCGCCGACGAACTCAGTGCTATCTCGATGCTGT 1472
QY 1441 ACCTTGACGAGATGAAGAGTTGTATTAAAGAACTATCAGACATGCTGTTGTGGAGGTT 1500
Db 1473 ACCTTGACGAGATGAAGAGTTGTATTAAAGAACTATCAGGACATGCTGTTGTGGAGGTT 1532
QY 1501 GTGGGTGCTGTAGTACAGCAAAATTAATACATAAATATATATATA 1547
Db 1533 GTGGGTGCTGTAGTACAGCAAAATTAATACATAAATATATATATA 1579

RESULT 9
LOCUS AR447458 3526 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 11 from patent US 6673549.
ACCESSION AR447458
VERSION AR447458.1 GI:42675782
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 3526)
AUTHORS Furness,L.M. and Buchbinder,J.L.
TITLE Genes expressed in C3A liver cell cultures treated with steroids
JOURNAL Patent: US 6673549-A 11 06-JAN-2004;
Incyte Corporation; Palo Alto, CA
FEATURES
source
1..3526
/mol_type="genomic DNA"

ORIGIN
Query Match 100.0%; Score 1547; DB 6; Length 3526;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1547; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGGACTTCTTGAACCTTGAGGGAGAAATACTTGGCGACCCCACTTTGGCGGGTGCCTT 60
Db 857 GGGGACTTCTTGAACCTTGAGGGAGAAATACTTGGCGACCCCACTTTGGCGGGTGCCTT 916
QY 61 TGCCCCAGCGAGCTGCTTGGCCATCTCCGAGCCCAACCGCCCTCCACTCTCGGCT 120
Db 917 TGCCCCAGCGAGCTGCTTGGCCATCTCCGAGCCCAACCGCCCTCCACTCTCGGCT 976
QY 121 TGCCCCGACACTGAGACGCTGTTCCAGCGTGAAGAGAGACTGCGCGGCGGCAACCGG 180
Db 977 TGCCCCGACACTGAGACGCTGTTCCAGCGTGAAGAGAGACTGCGCGGCGGCAACCGG 1036
QY 181 GAGAGGAGGAGGCAAGAAAGGAAACGACATTCGGTCTTGGCGCAGGCTCTTTGACC 240
Db 1037 GAGAGGAGGAGGCAAGAAAGGAAACGACATTCGGTCTTGGCGCAGGCTCTTTGACC 1096
QY 241 ACAGATTTTCCATGTGGACGCTCTTCAATGACGTGTCGCCGCGTCTTTAGACGA 300
Db 1097 ACAGATTTTCCATGTGGACGCTCTTCAATGACGTGTCGCCGCGTCTTTAGACGA 1156
QY 301 CTGCGGTCTCTTAAAGAGTGCACCATGTTGGCGCGGACCCGCTGTCTTTAGCGTTGCTGC 360
```

```
Db 1157 CTGCGGTCTCTTAAAGGTGCAACATGTGTGGCGGGACCCGCTGTCTTCTAGCGTTGCTGC 1216
QY 361 TTCCCCAGGTCTCTCTGGGCGGCGGCTGCGCTGCTTCCGAGCTGGGCGCAGAGAGT 420
Db 1217 TTCCCCAGGTCTCTCTGGGCGGCGGCTGCGCTGCTTCCGAGCTGGGCGCAGAGAGT 1276
QY 421 TCGCGGCGGCGTCTGTGGGCGGCGGCTCATCCGACCCCTCTTGAAGAGTCTTGAAGCGAGT 480
Db 1277 TCGCGGCGGCGTCTGTGGGCGGCGGCTCATCCGACCCCTCTTGAAGAGTCTTGAAGCGAGT 1336
QY 481 TCGAGTTGGGCTGCTCAGCATGTTCGGCTCTGAAGACAGAGACCCACCCAGCAGGAGG 540
Db 1337 TCGAGTTGGGCTGCTCAGCATGTTCGGCTCTGAAGACAGAGACCCACCCAGCAGGAGG 1396
QY 541 CCGTGGTCCCGCTTACATGCTAGACCTGTATCGCAGGCACTCAGGTCAAGCGGGCTCAC 600
Db 1397 CCGTGGTCCCGCTTACATGCTAGACCTGTATCGCAGGCACTCAGGTCAAGCGGGCTCAC 1456
QY 601 CCGCCCCAGACCAACCGGTTGGAGAGGCGAGCCAGCCGACCAACTGTGGCAGCTTCC 660
Db 1457 CCGCCCCAGACCAACCGGTTGGAGAGGCGAGCCAGCCGACCAACTGTGGCAGCTTCC 1516
QY 661 ACCATGAAGATCTTTGGAAGAACTACCAAGAAACGAGTGGGAAACCAACCCGAGATCT 720
Db 1517 ACCATGAAGATCTTTGGAAGAACTACCAAGAAACGAGTGGGAAACCAACCCGAGATCT 1576
QY 721 TCTTTAATTTAAGTTCTATCCCGAGGAGTTTATCACTCAGCAGAGCTTCAGGTTT 780
Db 1577 TCTTTAATTTAAGTTCTATCCCGAGGAGTTTATCACTCAGCAGAGCTTCAGGTTT 1636
QY 781 TCCGAGAACAGATGCAAGATGCTTTTAGGAAACAATAGCAGTTTCCATCACCGAATTAATA 840
Db 1637 TCCGAGAACAGATGCAAGATGCTTTTAGGAAACAATAGCAGTTTCCATCACCGAATTAATA 1696
QY 841 TTTATGAATCATTAACCTGCAACAGCAACTCGAAATTCCTCGGTACACAGACTTTGG 900
Db 1697 TTTATGAATCATTAACCTGCAACAGCAACTCGAAATTCCTCGGTACACAGACTTTGG 1756
QY 901 ACACAGGTGCTGTAATCAGATGCAAGCAAGTGGGAAAGTTTTCATGTACCCCGCTG 960
Db 1757 ACACAGGTGCTGTAATCAGATGCAAGCAAGTGGGAAAGTTTTCATGTACCCCGCTG 1816
QY 961 TGATCGGTGGAAGTGCACAGGAGACGCAACCACTGATGATTCGTGTGGAAGTGGCCACT 1020
Db 1817 TGATCGGTGGAAGTGCACAGGAGACGCAACCACTGATGATTCGTGTGGAAGTGGCCACT 1876
QY 1021 TGGAGGAGAAACAAGGTGCTCCAAAGACACATGTTAGGATAGCAGGCTTTTGACCAAG 1080
Db 1877 TGGAGGAGAAACAAGGTGCTCCAAAGACACATGTTAGGATAGCAGGCTTTTGACCAAG 1936
QY 1081 ATGAACACAGCTGGTTCAGATAGGCGCATTTGCTAGTAACCTTTTCGCCATGATGGAAG 1140
Db 1937 ATGAACACAGCTGGTTCAGATAGGCGCATTTGCTAGTAACCTTTTCGCCATGATGGAAG 1996
QY 1141 GGCATCTCTCCACAAAAGAGAGAAAACGTCAGGCCAAAACACAAAACAGCGGAAACGCTTTA 1200
Db 1997 GGCATCTCTCCACAAAAGAGAGAAAACGTCAGGCCAAAACACAAAACAGCGGAAACGCTTTA 2056
QY 1201 AGTCAGCTGTAAAGAGACACCCCTTTGTAGTGGACTTCAGTGACCTGGGGTGGAAATGACT 1260
Db 2057 AGTCAGCTGTAAAGAGACACCCCTTTGTAGTGGACTTCAGTGACCTGGGGTGGAAATGACT 2116
QY 1261 GGATTTGGCTCCCGCGGGGTATACGCTTTTACTGCCAGGAGAAAGTCCCTTTTCCCTC 1320
Db 2117 GGATTTGGCTCCCGCGGGGTATACGCTTTTACTGCCAGGAGAAAGTCCCTTTTCCCTC 2176
QY 1321 TGGCTGATCATCTGAATCTCACTATCATGCAATGTTTTCAGACGTTGGTCAACTCTGTGTA 1380
Db 2177 TGGCTGATCATCTGAATCTCACTATCATGCAATGTTTTCAGACGTTGGTCAACTCTGTGTA 2236
QY 1381 ACTCTAAGATTCCTAAGGCACTGCTGTGTCGAGCAAACTCAGTGTCTATCTCGATGCTGT 1440
Db 2237 ACTCTAAGATTCCTAAGGCACTGCTGTGTCGAGCAAACTCAGTGTCTATCTCGATGCTGT 2296
```


| | | | | | |
|-----------------------|------|---|---------------|------------|--------------|
| Query Match | | 99.9%; | Score 1545.4; | DB 6; | Length 1607; |
| Best Local Similarity | | 99.9%; | Pred. No. 0; | | |
| Matches 1546; | | Conservative | 0; | Mismatches | 1; |
| | | | | Indels | 0; |
| | | | | Gaps | 0; |
| Qy | 1 | GGGACATCTTTGAATTTGACGGAGATAAATCTTGCGCACCCCACTTTTGCGCGCGTGGCTT | 60 | | |
| Db | 33 | GGGACATCTTTGAATTTGACGGAGATAAATCTTGCGCACCCCACTTTTGCGCGCGTGGCTT | 92 | | |
| Qy | 61 | TGCCCCAGCGAGCGCTGCTTCCGCAATCTCCAGAGCCCAACCGCCCTCCATCTCTCGGCT | 120 | | |
| Db | 93 | TGCCCCAGCGAGCGCTGCTTCCGCAATCTCCAGAGCCCAACCGCCCTCCATCTCTCGGCT | 152 | | |
| Qy | 121 | TGCCCCGACATGACAGCGCTGCTTCCAGCGTCAAGAGAGACTCGCGCGCGGACCCGG | 180 | | |
| Db | 153 | TGCCCCGACATGACAGCGCTGCTTCCAGCGTCAAGAGAGACTCGCGCGCGGACCCGG | 212 | | |
| Qy | 181 | GAGAAGGAGGAGGCAAGAAAGGAAACGGAATTTGGTCTTGGCGCAGGTCTTTTGACC | 240 | | |
| Db | 213 | GAGAAGGAGGAGGCAAGAAAGGAAACGGAATTTGGTCTTGGCGCAGGTCTTTTGACC | 272 | | |
| Qy | 241 | AGAGTTTTCATGTGACGCTCTTTCAATGGAAGTGTCCCGCGTCTTCTTAGACGA | 300 | | |
| Db | 273 | AGAGTTTTCATGTGACGCTCTTTCAATGGAAGTGTCCCGCGTCTTCTTAGACGA | 332 | | |
| Qy | 301 | CTGCGGTCTCTAAAGGTTCGACCATGTGTGGCGGAGCCCGCTGCTCTAGCGTTGCTGC | 360 | | |
| Db | 333 | CTGCGGTCTCTAAAGGTTCGACCATGTGTGGCGGAGCCCGCTGCTCTAGCGTTGCTGC | 392 | | |
| Qy | 361 | TTCCCCAGGTCTCTTGGCGGCGCGGTGGCTCTGTTCCGAGCTTGCGCGCAGGAGT | 420 | | |
| Db | 393 | TTCCCCAGGTCTCTTGGCGGCGCGGTGGCTCTGTTCCGAGCTTGCGCGCAGGAGT | 452 | | |
| Qy | 421 | TCGCGGCGCGCTGCTGCGGCGCGCCCTCATCCAGCCCTCTGAAGAGTCTGAGCGAGT | 480 | | |
| Db | 453 | TCGCGGCGCGCTGCTGCGGCGCGCCCTCATCCAGCCCTCTGAGAGTCTGAGCGAGT | 512 | | |
| Qy | 481 | TCGAGTTTCGCGCTCTCAGCATGTTCCGCTGGAACAGAGACCCACCCAGCAGGACG | 540 | | |
| Db | 513 | TCGAGTTTCGCGCTCTCAGCATGTTCCGCTGGAACAGAGACCCACCCAGCAGGACG | 572 | | |
| Qy | 541 | CCGTGCTGCCCTTACATGCTAGACCTGTATCGCAGGCACTCAGGTCAGCGCGGCTCAC | 600 | | |
| Db | 573 | CCGTGCTGCCCTTACATGCTAGACCTGTATCGCAGGCACTCAGGTCAGCGCGGCTCAC | 632 | | |
| Qy | 601 | CCGCCACAGACACCGTTGAGAGGAGGAGCCAGCCAGGACCAACACTGTGCGAGCTTCC | 660 | | |
| Db | 633 | CCGCCACAGACACCGTTGAGAGGAGGAGCCAGCCAGGACCAACACTGTGCGAGCTTCC | 692 | | |
| Qy | 661 | ACCATGAAGATCTTTGGAAGAACTACCAGAAACGAGTGGGAAACCAACCCGAGATTCT | 720 | | |
| Db | 693 | ACCATGAAGATCTTTGGAAGAACTACCAGAAACGAGTGGGAAACCAACCCGAGATTCT | 752 | | |
| Qy | 721 | TCCTTAATTTAAGTTCTATCCCAACGAGGAGTTTATCACCTCAGCAGAGCTTCAGGTTT | 780 | | |
| Db | 753 | TCCTTAATTTAAGTTCTATCCCAACGAGGAGTTTATCACCTCAGCAGAGCTTCAGGTTT | 812 | | |
| Qy | 781 | TCCGAGAACAGATGCAAGATGCTTTAGGAACAATAGCAGTTTCCATCAGCAATTAATA | 840 | | |
| Db | 813 | TCCGAGAACAGATGCAAGATGCTTTAGGAACAATAGCAGTTTCCATCAGCAATTAATA | 872 | | |
| Qy | 841 | TTTATGAATCATATAAACCTGCAACAGCCTGCAATTCCTGCAACAGACTTTTGG | 900 | | |
| Db | 873 | TTTATGAATCATATAAACCTGCAACAGCCTGCAATTCCTGCAACAGACTTTTGG | 932 | | |
| Qy | 901 | ACACAGGTTGGTGAATCAGAAATGCAAGCAGGTGGGAAAGTTTGTATGTCAACCCCGCTG | 960 | | |
| Db | 933 | ACACAGGTTGGTGAATCAGAAATGCAAGCAGGTGGGAAAGTTTGTATGTCAACCCCGCTG | 992 | | |
| Qy | 961 | TGATGCGGTGACATGCAACAGGACACGCCAACATAGATTTGCTGCTGGAAGTGGCCCACT | 1020 | | |
| Db | 993 | TGATGCGGTGACATGCAACAGGACACGCCAACATAGATTTGCTGCTGGAAGTGGCCCACT | 1052 | | |
| Qy | 1021 | TGGAGGAGAAACAAGGTGTCTCCAAGAGACATGTTAGGATAAGCAGGTCTTTTGACCAAG | 1080 | | |

| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|----|------|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|
| Db | 1053 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|----|------|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|

| | | | | |
|----|------|--|--|-----|
| Db | 213 | | GAGAAAGGAGGAGGCAAAAGAAAGGAAACGGACATTCGTGCTCTGCGCCAGAGTCTTTGACC | 272 |
| Qy | 241 | AGAGTTTTTTCATGTGACAGCTCTTTTCAATGGAGTGCTCCCGCGTGCTTTCTTTAGACGGA | 300 | |
| Db | 273 | AGAGTTTTTTCATGTGACAGCTCTTTTCAATGGAGTGCTCCCGCGTGCTTTCTTTAGACGGA | 332 | |
| Qy | 301 | CTGCGGTCTCTTAAAGGTGCGACCAATGFTGGCCGGGACCCGCTGTCTTTCTTAGCGTTGCTGC | 360 | |
| Db | 333 | CTGCGGTCTCTTAAAGGTGCGACCAATGFTGGCCGGGACCCGCTGTCTTTCTTAGCGTTGCTGC | 392 | |
| Qy | 361 | TTCCCCAGGTCTCTGCGGCGCGCGGTGCGCTCTGTTCCGGAGCTGGGCGCAGGAGT | 420 | |
| Db | 393 | TTCCCCAGGTCTCTGCGGCGCGCGGTGCGCTCTGTTCCGGAGCTGGGCGCAGGAGT | 452 | |
| Qy | 421 | TGCGGCGCGGTGCTGCGGCGCGCCCTCATCCAGCCCTCTGACGAGTCTCTGACGAGT | 480 | |
| Db | 453 | TGCGGCGCGGTGCTGCGGCGCGCCCTCATCCAGCCCTCTGACGAGTCTCTGACGAGT | 512 | |
| Qy | 481 | TCGAGTTGCGGTGCTCAGCATGTTGCGCTTGAAACAGAGACCCACCCCCAGCAGGGAAG | 540 | |
| Db | 513 | TCGAGTTGCGGTGCTCAGCATGTTGCGCTTGAAACAGAGACCCACCCCCAGCAGGGAAG | 572 | |
| Qy | 541 | CGTGCTGCGCCCTACATGCTAGACCTGTATCGCAGGCACCTCAGTTCAGCCGGGCTCAC | 600 | |
| Db | 573 | CGTGCTGCGCCCTACATGCTAGACCTGTATCGCAGGCACCTCAGTTCAGCCGGGCTCAC | 632 | |
| Qy | 601 | CGGCCCCAGACACCCGGTTGAGAGGGGAGCCAGCCGAGCCAAACACTGTGCGCAGCTTCC | 660 | |
| Db | 633 | CGGCCCCAGACACCCGGTTGAGAGGGGAGCCAGCCGAGCCAAACACTGTGCGCAGCTTCC | 692 | |
| Qy | 661 | ACCATGAAGAATCTTTTGAAGAACTTACCAGAAACGAGTGGGAAACCAACCCGAGAGTTCT | 720 | |
| Db | 693 | ACCATGAAGAATCTTTTGAAGAACTTACCAGAAACGAGTGGGAAACCAACCCGAGAGTTCT | 752 | |
| Qy | 721 | TCTTTAAATTAAGTTCTATCCCGCAGGAGGATTTATCACTCAGCAGAGGTTTCAGGTTT | 780 | |
| Db | 753 | TCTTTAAATTAAGTTCTATCCCGCAGGAGGATTTATCACTCAGCAGAGGTTTCAGGTTT | 812 | |
| Qy | 781 | TCCGAGAACAGATCAAGATGCTTTTAGGAAACAATAGCAGTTCCTCATCCGGAATTAATA | 840 | |
| Db | 813 | TCCGAGAACAGATCAAGATGCTTTTAGGAAACAATAGCAGTTCCTCATCCGGAATTAATA | 872 | |
| Qy | 841 | TTTATGAATCATAAAACTGCAACAGCCAACTCGAAATTTCCCGTGACACAGACTTTTGG | 900 | |
| Db | 873 | TTTATGAATCATAAAACTGCAACAGCCAACTCGAAATTTCCCGTGACACAGACTTTTGG | 932 | |
| Qy | 901 | ACACAGGTGGTGAATCAGAAATGCAAGCAGGTGGGAAAGTTTGTATGTCACCCCGCTG | 960 | |
| Db | 933 | ACACAGGTGGTGAATCAGAAATGCAAGCAGGTGGGAAAGTTTGTATGTCACCCCGCTG | 992 | |
| Qy | 961 | TGATCGGTGGACTGCCAGGGACACGCCAACCATGGATTCGTGCTGGAAAGTGCCCACT | 1020 | |
| Db | 993 | TGATCGGTGGACTGCCAGGGACACGCCAACCATGGATTCGTGCTGGAAAGTGCCCACT | 1052 | |
| Qy | 1021 | TGGAGGAGAAACAAGTGTCTCCAGAGACATGTTAGGATTAAGCAGAGTCTTTTGACCAAG | 1080 | |
| Db | 1053 | TGGAGGAGAAACAAGTGTCTCCAGAGACATGTTAGGATTAAGCAGAGTCTTTTGACCAAG | 1112 | |
| Qy | 1081 | ATGAACACAGCTGGTCAAGATTAAGGCCATTGCTAGTAACTTTTGGCCATGATGGAAG | 1140 | |
| Db | 1113 | ATGAACACAGCTGGTCAAGATTAAGGCCATTGCTAGTAACTTTTGGCCATGATGGAAG | 1172 | |
| Qy | 1141 | GGCATCTCTCAAAAAGAGAAAACGTCAAGCCAAACAAACAGCGGGAAGCCCTTA | 1200 | |
| Db | 1173 | GGCATCTCTCTCAAAAAGAGAAAACGTCAAGCCAAACAAACAGCGGGAAGCCCTTA | 1232 | |
| Qy | 1201 | AGTTCAGCTGTAAGAGACACCCCTTTGTACGTGGACTTCAGTGAAGTGGGGTGAATGACT | 1260 | |
| Db | 1233 | AGTTCAGCTGTAAGAGACACCCCTTTGTACGTGGACTTCAGTGAAGTGGGGTGAATGACT | 1292 | |
| Qy | 1261 | GGATTGTGCTCCCCCGGGTATCACGCTTTTATCTGCCAGGAGAAATGCCCTTTTCTCTC | 1320 | |

| | | | |
|------------|------------|--|------|
| Db | 1293 | GGATTGTGGCTCCCGGGGTATCAGCGCTTTTACTGCCAGGAAATGCGCTTTTCCTC | 1355 |
| Qy | 1321 | TGGCTGATCATCTGAATCCCACTAATCATGCCATTTGTTCAGAGCTTGGTCAACTCTGTTA | 1380 |
| Db | 1353 | TGGCTGATCATCTGAATCCCACTAATCATGCCATTTGTTCAGAGCTTGGTCAACTCTGTTA | 1412 |
| Qy | 1381 | ACTCTAAGATTCTTAAGCATGCTGTGTCGCCAGAGAACTCAGTGCCTATCTCGATGCTGT | 1440 |
| Db | 1413 | ACTCTAAGATTCTTAAGCATGCTGTGTCGCCAGAGAACTCAGTGCCTATCTCGATGCTGT | 1472 |
| Qy | 1441 | ACCTTGACGAGAATGAAAGGTTCTATTAAAGAACTATCAGGACATGTTGTGTGAGGGTT | 1500 |
| Db | 1473 | ACCTTGACGAGAATGAAAGGTTCTATTAAAGAACTATCAGGACATGTTGTGTGAGGGTT | 1532 |
| Qy | 1501 | GTGGGTGTGCTAGTACAGCAAAAATTAATAATACATAAATATATATATA | 1547 |
| Db | 1533 | GTGGGTGTGCTAGTACAGCAAAAATTAATAATACATAAATATATATATA | 1579 |
| RESULT 14 | | | |
| BC069214 | | | |
| LOCUS | | | |
| DEFINITION | BC069214 | 2041 bp mRNA linear PRI 25-JUN-2004 | |
| ACCESSION | | Homo sapiens bone morphogenetic protein 2, mRNA (cdna clone | |
| VERSION | BC069214 | IMAGE:6303163), partial cds. | |
| KEYWORDS | | | |
| SOURCE | BC069214.1 | GI:46812656 | |
| ORGANISM | | Homo sapiens (human) | |
| REFERENCE | | | |
| AUTHORS | | | |
| | | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | |
| | | Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; | |
| | | Hominidae; Homo. | |
| | | 1 (bases 1 to 2041) | |
| | | Straussberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., | |
| | | Klausner, R.D., Collins, P.S., Wagner, L., Shenmen, C.M., Schuler, G.D., | |
| | | Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., | |
| | | Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Heieh, P., | |
| | | Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., | |
| | | Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., | |
| | | Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., | |
| | | Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., | |
| | | Abramson, R.D., Mullahy, S.D., Bosak, S.A., McEwan, P.J., | |
| | | McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., | |
| | | Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., | |
| | | Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., | |
| | | Fahy, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S., | |
| | | Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., | |
| | | Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., | |
| | | Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., | |
| | | Butterfield, A.S., Krzywicki, M.I., Skalska, U., Smaluk, D.E., | |
| | | Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A. | |
| | | Generation and initial analysis of more than 15,000 full-length | |
| | | human and mouse cDNA sequences | |
| | | Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002) | |
| JOURNAL | | 12477932 | |
| PUBMED | | 2 (bases 1 to 2041) | |
| REFERENCE | | Straussberg, R. | |
| AUTHORS | | Direct Submission | |
| TITLE | | Submitted (26-APR-2004) National Institutes of Health, Mammalian | |
| JOURNAL | | Gene Collection (MGC), Cancer Genomics Office, National Cancer | |
| | | Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, | |
| | | USA | |
| REMARK | | NIH-MGC Project URL: http://mgc.nci.nih.gov | |
| COMMENT | | Contact: MGC help desk | |
| | | Email: cgapbs-remail.nih.gov | |
| | | Tissue Procurement: Dr. Mark Watson | |
| | | cDNA Library Preparation: Rubin Laboratory | |
| | | cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILLNL) | |
| | | DNA Sequencing by: Genome Sequence Centre, | |
| | | BC Cancer Agency, Vancouver, BC, Canada | |
| | | info@bcsc.bc.ca | |
| | | Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield, | |
| | | Andy Chan, Steve S. Chand, William Chow, Alison Cloutier, Ruth | |

REFERENCE 1
AUTHORS Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W.
TITLE Kites, such as nucleic acid arrays, comprising a majority of
humanexons or transcripts, for detecting expression and other uses
thereof
JOURNAL Patent: WO 02068579-A 14342 06-SEP-2002;
PE Corporation (NY) (US)
FEATURES Location/Qualifiers
source : 1..1547
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"
ORIGIN
Query Match : 99.7%; Score 1542.2; DB 6; Length 1547;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1544; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 GGGGACTTCTTGAACCTTGAGGAGAAATAACTTGGCACCCCACTTTGGCGCGGTGCCTT 60
Db 1 GGGGACTTCTTGAACCTTGAGGAGAAATAACTTGGCGACCCCACTTTGGCGCGGTGCCTT 60
QY 61 TGCCCCAGGGAGCTGCTTGGCCATCTCCGAGCCCCACCGCCCTTCCACTCTCGGCCT 120
Db 61 TGCCCCAGGGAGCTGCTTGGCCATCTCCGAGCCCCACCGCCCTTCCACTCTCGGCCT 120
QY 121 TGCCCGACACTGAGACGCTGTTCCAGCGTGAAGAGAGAGACTGCGCGCGCGCACCCGG 180
Db 121 TGCCCGACACTGAGACGCTGTTCCAGCGTGAAGAGAGAGACTGCGCGCGCGCACCCGG 180
QY 181 GAGAGAGGAGGCGAAGAAAGAAAGGACATTCGGTCTTTGCGCCAGGTCCTTTGACC 240
Db 181 GAGAGAGGAGGCGAAGAAAGAAAGGACATTCGGTCTTTGCGCCAGGTCCTTTGACC 240
QY 241 AGAGTTTTCATGTGAGAGCTCTTTCAATGAGAGCTGTCGCCGCTGCTTTAGACGA 300
Db 241 AGAGTTTTCATGTGAGAGCTCTTTCAATGAGAGCTGTCGCCGCTGCTTTAGACGA 300
QY 301 CTGCGGTCTCTTAAAGTTCGACATGTGGCGCGGACCCGCTGCTCTTAGGTTGCTGC 360
Db 301 CTGCGGTCTCTTAAAGTTCGACATGTGGCGCGGACCCGCTGCTCTTAGGTTGCTGC 360
QY 361 TTCCCCAGGTCTCTCTGCGCGCGGCTGCTGCTTCCGAGCTGGGCGCGCAGGAAAT 420
Db 361 TTCCCCAGGTCTCTCTGCGCGCGGCTGCTGCTTCCGAGCTGGGCGCGCAGGAAAT 420
QY 421 TCGCGCGCGCTGCTGCGCGCGCCCTCATCCAGCCCTCTGACGAGTCTCTGAGCGAGT 480
Db 421 TCGCGCGCGCTGCTGCGCGCGCCCTCATCCAGCCCTCTGACGAGTCTCTGAGCGAGT 480
QY 481 TCGAGTTGCGGTCTCAGCATGTTTCGGCTGAAGACAGAGACCCACCCCGAGCGAGCG 540
Db 481 TCGAGTTGCGGTCTCAGCATGTTTCGGCTGAAGACAGAGACCCACCCCGAGCGAGCG 540
QY 541 CCGTGGTGCCTCCCTACATGCTAGACCTGTATCGAGGCACTCAGGTTCAGCGCGGCTCAC 600
Db 541 CCGTGGTGCCTCCCTACATGCTAGACCTGTATCGAGGCACTCAGGTTCAGCGCGGCTCAC 600
QY 601 CGCGCCCGACACCAACCGGTTGGAGAGGCGCAGCGAGCCCAACCACTGTGCGCAGCTTCC 660
Db 601 CGCGCCCGACACCAACCGGTTGGAGAGGCGCAGCGAGCCCAACCACTGTGCGCAGCTTCC 660
QY 661 ACCATGAGAAATCTTTGGAGAACTACACAGAAACAGGTGGGAAACCAACCCCGAGATCT 720
Db 661 ACCATGAGAAATCTTTGGAGAACTACACAGAAACAGGTGGGAAACCAACCCCGAGATCT 720
QY 721 TCTTTAAATTAAGTTCTATCCCAACCGAGAGTTTATCACCTCAGCAGAGCTTCAGGTTT 780
Db 721 TCTTTAAATTAAGTTCTATCCCAACCGAGAGTTTATCACCTCAGCAGAGCTTCAGGTTT 780
QY 781 TCCGAGAACAGATGCAAGATGCTTTTAGGAAAACAATAGCAGTTTCCATCAACCGAAATTAATA 840
Db 781 TCCGAGAACAGATGCAAGATGCTTTTAGGAAAACAATAGCAGTTTCCATCAACCGAAATTAATA 840

QY 841 TTTATGAATCATAAACCTGCACAGCCAACTCGAAATTCGCCGTGACCAGACTTTTGG 900
Db 841 TTTATGAATCATAAACCTGCACAGCCAACTCGAAATTCGCCGTGACCAGACTTTTGG 900
QY 901 ACACCAAGTTGGTGAATCAGATGCAAGCAGGTGGGAAAGTTTTCATGTCAACCCCGCTG 960
Db 901 ACACCAAGTTGGTGAATCAGATGCAAGCAGGTGGGAAAGTTTTCATGTCAACCCCGCTG 960
QY 961 TGATGCGGTGGAAGTGCACAGGAGACACGCAACCATGGATTTCGTGTGGAAGTGGCCACT 1020
Db 961 TGATGCGGTGGAAGTGCACAGGAGACACGCAACCATGGATTTCGTGTGGAAGTGGCCACT 1020
QY 1021 TGGAGGAGAAACAAGTGTCTCCAGAGACATGTTAGGATAGCAGGCTCTTTCACCAAG 1080
Db 1021 TGGAGGAGAAACAAGTGTCTCCAGAGACATGTTAGGATAGCAGGCTCTTTCACCAAG 1080
QY 1081 ATGAACAACAGCTGCTCAGATAGAGCCATTCGTAGTAACCTTTTGGCCATGATGGAAG 1140
Db 1081 ATGAACAACAGCTGCTCAGATAGAGCCATTCGTAGTAACCTTTTGGCCATGATGGAAG 1140
QY 1141 GGCATCTCTCCACAAAAGAGAAACCTCAAGCCAAACACAAACAGCGGAAACGCTTTA 1200
Db 1141 GGCATCTCTCTCCACAAAAGAGAAACCTCAAGCCAAACACAAACAGCGGAAACGCTTTA 1200
QY 1201 AGTCCAGCTGTAAGAGACACCCCTTTGTACGTGGAATTCAGTGACGTGGGGTGAATGACT 1260
Db 1201 AGTCCAGCTGTAAGAGACACCCCTTTGTACGTGGAATTCAGTGACGTGGGGTGAATGACT 1260
QY 1261 GGAATGTGGTCCCGCGGGGTATACGCGCTTTTACTGCGACGGAATGCGCTTTTCTC 1320
Db 1261 GGAATGTGGTCCCGCGGGGTATACGCGCTTTTACTGCGACGGAATGCGCTTTTCTC 1320
QY 1321 TGGCTGATCATCTGAACCTCCACTAATCATGCCAATGTTTCAGACGTTGGTCAACTCTGTTA 1380
Db 1321 TGGCTGATCATCTGAACCTCCACTAATCATGCCAATGTTTCAGACGTTGGTCAACTCTGTTA 1380
QY 1381 ACTCTAAGATTCCTAAGGCATGCTGTCTCCGACAGAACTCAGTGTCTATCTCGATGCTGT 1440
Db 1381 ACTCTAAGATTCCTAAGGCATGCTGTCTCCGACAGAACTCAGTGTCTATCTCGATGCTGT 1440
QY 1441 ACCTTGAAGAGATGAAAAGTTGTAATAAGAACTATCAGGACATGTTGTGAGGGTT 1500
Db 1441 ACCTTGAAGAGATGAAAAGTTGTAATAAGAACTATCAGGACATGTTGTGAGGGTT 1500
QY 1501 GTGGGTGCTGCTAGTACAGCAAAATTAATACATAAATATATATA 1547
Db 1501 GTGGGTGCTGCTAGTACAGCAAAATTAATACATAAATATATATA 1547

Search completed: January 10, 2006, 22:09:17

Job time : 5444 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 10, 2006, 16:30:58 ; Search time 679 Seconds
(without alignments)

15184.506 Million cell updates/sec

Title: US-10-801-648-1

Perfect score: 1547

Sequence: 1 ggggactcttggaacttgca.....aatacataaatatatata 1547

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N_Geneseq_21.*

1: geneseqn1980s.*

2: geneseqn1990s.*

3: geneseqn2000s.*

4: geneseqn2001as.*

5: geneseqn2001bs.*

6: geneseqn2002as.*

7: geneseqn2002bs.*

8: geneseqn2003as.*

9: geneseqn2003bs.*

10: geneseqn2003cs.*

11: geneseqn2003ds.*

12: geneseqn2004as.*

13: geneseqn2004bs.*

14: geneseqn2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|---------------------|
| 1 | 1547 | 100.0 | 1547 | 2 | AaQ32851 BMP2. 3/2 |
| 2 | 1547 | 100.0 | 1547 | 2 | AaV01679 Bone morph |
| 3 | 1547 | 100.0 | 1547 | 6 | AbX90308 DNA encod |
| 4 | 1547 | 100.0 | 1547 | 8 | Abx76358 Lung canc |
| 5 | 1547 | 100.0 | 1547 | 8 | AcF34481 Gene enco |
| 6 | 1547 | 100.0 | 1547 | 10 | AcF05920 Human bon |
| 7 | 1547 | 100.0 | 1547 | 10 | AdD14609 Human src |
| 8 | 1547 | 100.0 | 1547 | 10 | AdE85186 Farnesyl |
| 9 | 1547 | 100.0 | 1547 | 10 | AdE63420 Human bon |
| 10 | 1547 | 100.0 | 1547 | 10 | AdT17041 Human MP2 |
| 11 | 1547 | 100.0 | 1547 | 10 | AdL13510 Osteoarth |
| 12 | 1547 | 100.0 | 1547 | 11 | AdN38841 Cancer/an |
| 13 | 1547 | 100.0 | 1547 | 12 | AdH11558 Human bon |
| 14 | 1547 | 100.0 | 1547 | 12 | AdK90635 Human CBM |
| 15 | 1547 | 100.0 | 1547 | 12 | AdO49064 Human ded |
| 16 | 1547 | 100.0 | 1547 | 13 | AdQ80231 Bone morph |
| 17 | 1547 | 100.0 | 1547 | 13 | AdR67125 Human bla |
| 18 | 1547 | 100.0 | 1547 | 13 | AdS73742 Human bon |
| 19 | 1547 | 100.0 | 1547 | 14 | AdW15055 Bone morph |

| | | | | | | |
|----|--------|-------|------|----|-----------|--------------------|
| 20 | 1547 | 100.0 | 1547 | 14 | ADY15523 | Ady15523 DNA encod |
| 21 | 1547 | 100.0 | 1547 | 14 | ADX39020 | Adx39020 Human bon |
| 22 | 1547 | 100.0 | 1547 | 14 | ADY81389 | Ady81389 Human bon |
| 23 | 1547 | 100.0 | 1547 | 14 | AEA01570 | Aea01570 Human bon |
| 24 | 1547 | 100.0 | 1581 | 14 | ADY28715 | Ady28715 Human bon |
| 25 | 1547 | 100.0 | 1607 | 2 | AAQ31869 | AaQ31869 Human BMP |
| 26 | 1547 | 100.0 | 1607 | 2 | AAT64523 | Aat64523 Human BMP |
| 27 | 1547 | 100.0 | 1607 | 2 | AAT78941 | Aat78941 Human bon |
| 28 | 1547 | 100.0 | 1607 | 4 | AAAD16012 | AaA16012 Human bon |
| 29 | 1547 | 100.0 | 1607 | 4 | AAC90497 | Aac90497 Human BMP |
| 30 | 1547 | 100.0 | 1607 | 12 | ADO40078 | Ado40078 Human BMP |
| 31 | 1547 | 100.0 | 3526 | 12 | ADL12282 | AdL12282 Human ste |
| 32 | 1546 | 99.9 | 1607 | 2 | AAQ14036 | AaQ14036 Human BMP |
| 33 | 1545.4 | 99.9 | 1607 | 2 | AAQ41291 | AaQ41291 Human BMP |
| 34 | 1542.2 | 99.7 | 1606 | 1 | AAAN80632 | AaA80632 Human Bon |
| 35 | 1520.2 | 98.3 | 3557 | 12 | ADK70405 | AdK70405 Respirato |
| 36 | 1511.8 | 97.7 | 1547 | 10 | ADL13514 | AdL13514 Osteoarth |
| 37 | 1314.8 | 85.0 | 2154 | 6 | ABK40276 | ABK40276 CDNA enco |
| 38 | 1314.8 | 85.0 | 2154 | 10 | ADJ37326 | AdJ37326 Human tum |
| 39 | 1314.8 | 85.0 | 2154 | 12 | ADG68250 | AdG68250 Human PRO |
| 40 | 1314.8 | 85.0 | 2154 | 14 | ADY15521 | Ady15521 DNA encod |
| 41 | 1227.2 | 79.3 | 1258 | 12 | ADM80488 | Adm80488 Human ost |
| 42 | 1227.2 | 79.3 | 1258 | 13 | ADO03610 | Ado03610 CDNA enco |
| 43 | 1227.2 | 79.3 | 1260 | 2 | AAQ53143 | AaQ53143 Sequence |
| 44 | 1227.2 | 79.3 | 1260 | 2 | AAT02602 | Aat02602 Human CBM |
| 45 | 1227.2 | 79.3 | 1260 | 2 | AAV15206 | Aav15206 Human ost |

ALIGNMENTS

RESULT 1

AAQ32851

ID AAQ32851 standard; CDNA; 1547 BP.

XX

AC AAQ32851;

XX

DT 25-MAR-2003 (revised)

DT 05-MAY-1993 (first entry)

XX

DE BMP2.

XX

KW Bone; morphogenetic; protein; BMP; growth; vitamin D; systemic;

KW treatment; dimer; ss.

XX

OS Rattus rattus.

XX

PN WO9221365-A1.

XX

PD 10-DEC-1992.

XX

PF 26-MAY-1992; 92WO-US004356.

XX

PR 05-JUN-1991; 91US-00709621.

PR 27-MAR-1992; 92US-00856110.

XX

(PROC) PROCTER & GAMBLE CO.

PI Stone RL;

XX

DR WPI; 1992-433371/52.

XX

PT Synergistic compan. for generating mammalian bone growth - comprises

PT vitamin=D cpd. and bone morphogenetic protein.

XX

PS Disclosure; Page 27-29; 44pp; English.

XX

CC The sequences given in AAQ32850-56 encode bone morphogenetic proteins (BMP). BMP's increase bone growth and when used in conjunction with vitamin D the level of new bone growth is greater than when a BMP or vitamin D are used alone. The BMP's are administered for systemic treatment at a dose range of 1pg to 100 microg. BMP are active as dimers. (Updated on 25-MAR-2003 to correct PN field.)

PT Generation of new bone growth - by co-administering bone morphogenetic
XX protein and vitamin D.
PS Claim 1; Col 19-22; 18pp; English.
XX
CC A new method has been developed for generating new bone growth in a
CC mammal. The method comprises administering a bone morphogenetic protein
CC in combination with a vitamin D compound, where: (a) the bone
CC morphogenetic protein is BMP-2 and is administered in an amount of 500-
CC 1000 ng in combination with about 6 ng vitamin D compound; or (b) the
CC bone morphogenetic protein is BMP-4 and is administered in an amount of
CC about 62.5 ng in combination with about 6 ng vitamin D compound. The
CC present sequence encodes BMP-2. The method is used for treating bone
CC defects or disorders, e.g. fractures, surgical lesions, periodontal
CC disease, osteoporosis, arthritis and rickets. (Updated on 25-MAR-2003 to
CC correct PP field.)
XX
SQ Sequence 1547 BP; 377 A; 423 C; 410 G; 337 T; 0 U; 0 Other;
Query Match 100.0%; Score 1547; DB 2; Length 1547;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1547; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGGACTTCTTGAACCTTGAGGAGAAATACTTGGCACCACCTTTGGCGGCTT 60
DB 1 GGGGACTTCTTGAACCTTGAGGAGAAATACTTGGCACCACCTTTGGCGGCTT 60
QY 61 TGCCCCAGGGAGCTTGGCCATCTCCGAGCCCAACCGCCCTCCACTCTCGGCT 120
DB 61 TGCCCCAGGGAGCTTGGCCATCTCCGAGCCCAACCGCCCTCCACTCTCGGCT 120
QY 121 TGCCCGACACTGAGACGCTTGTCCAGCGTGAAGAGAGAGACTGCGCGGACCCGG 180
DB 121 TGCCCGACACTGAGACGCTTGTCCAGCGTGAAGAGAGAGACTGCGCGGACCCGG 180
QY 181 GAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 240
DB 181 GAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 240
QY 241 AGAGTTTTTCCATGTGAGCGCTTTTCAATGAGCGTGTCCCGCGGCTCTTTAGACGA 300
DB 241 AGAGTTTTTCCATGTGAGCGCTTTTCAATGAGCGTGTCCCGCGGCTCTTTAGACGA 300
QY 301 CTGCGGCTCTCTTAAAGGTGACCATGTGGCGGACCGCTGTCTTCTAGGCTTGTGC 360
DB 301 CTGCGGCTCTCTTAAAGGTGACCATGTGGCGGACCGCTGTCTTCTAGGCTTGTGC 360
QY 361 TTCCCCAGGTCCTCTGCGGCGGCGGCTTGGCTCTGTTCCGAGCTGGGCGGAGGAGT 420
DB 361 TTCCCCAGGTCCTCTGCGGCGGCGGCTTGGCTCTGTTCCGAGCTGGGCGGAGGAGT 420
QY 421 TCGCGGCGGCTGCTGCGGCGGCGGCTCTATCCAGCGCTCTGACGAGTCTGAGCGAGT 480
DB 421 TCGCGGCGGCTGCTGCGGCGGCGGCTCTATCCAGCGCTCTGACGAGTCTGAGCGAGT 480
QY 481 TCGAGTTGCGGCTGCTCAGCATGTTCCGCTGAAACAGAGACCCACCCCGGAGGAG 540
DB 481 TCGAGTTGCGGCTGCTCAGCATGTTCCGCTGAAACAGAGACCCACCCCGGAGGAG 540
QY 541 CCGTGGTGGCCCCCTACATGCTAGACCTGTATCGCAGGCACTCAGGTGAGCGGCTCAC 600
DB 541 CCGTGGTGGCCCCCTACATGCTAGACCTGTATCGCAGGCACTCAGGTGAGCGGCTCAC 600
QY 601 CCGCCCCAGACCAACCGGTTGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 660
DB 601 CCGCCCCAGACCAACCGGTTGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 660
QY 661 ACCATGAGAAATCTTTGGAGAACTACACAGAAACGAGTGGGAAACAAACCGGAGATCT 720
DB 661 ACCATGAGAAATCTTTGGAGAACTACACAGAAACGAGTGGGAAACAAACCGGAGATCT 720
QY 721 TCTTTAAATTAAGTTCTATCCCGCAGGAGGAGTTTATCACCTCAGCAGAGCTTCAGGTTT 780

DB 721 TCTTTAAATTAAGTTCTATCCCGCAGGAGGAGTTTATCACCTCAGCAGAGCTTCAGGTTT 780
QY 781 TCCGAGAACAGATCAAGATGCTTTAGGAAACAATAGCAGTTTCCATCACCGAATTAATA 840
DB 781 TCCGAGAACAGATCAAGATGCTTTAGGAAACAATAGCAGTTTCCATCACCGAATTAATA 840
QY 841 TTTATGAATCATATAAACCTGCAACAGCAACTCGAATATCCCGTGACAGACTTTTGG 900
DB 841 TTTATGAATCATATAAACCTGCAACAGCAACTCGAATATCCCGTGACAGACTTTTGG 900
QY 901 ACACAGGTTGGTGAATCAGATGCAAGCAGGTTGGGAAAGTTTTCATGTCAACCCCGCTG 960
DB 901 ACACAGGTTGGTGAATCAGATGCAAGCAGGTTGGGAAAGTTTTCATGTCAACCCCGCTG 960
QY 961 TGATGCGTGGACTGCAAGGAGACAGCCAAACCATGGATTCGTGTGGAAGTGGCCACT 1020
DB 961 TGATGCGTGGACTGCAAGGAGACAGCCAAACCATGGATTCGTGTGGAAGTGGCCACT 1020
QY 1021 TGGAGGAGAAACAAGGTGTCTCCAAGAGACATGTTAGGATAAGCAGGTCCTTTGCAACCAAG 1080
DB 1021 TGGAGGAGAAACAAGGTGTCTCCAAGAGACATGTTAGGATAAGCAGGTCCTTTGCAACCAAG 1080
QY 1081 ATGAACAACAGCTGTGTCAAGATAGGCGCATTTGCTAGTAACTTTGGCCATGATGGAAG 1140
DB 1081 ATGAACAACAGCTGTGTCAAGATAGGCGCATTTGCTAGTAACTTTGGCCATGATGGAAG 1140
QY 1141 GGCATCTCTCCACAAAAGAGAAAACGTCAGGCCAAACACAAACAGCGGAAACGCTTTA 1200
DB 1141 GGCATCTCTCCACAAAAGAGAAAACGTCAGGCCAAACACAAACAGCGGAAACGCTTTA 1200
QY 1201 AGTCAGCTGTGAAGAGACACCTTTTGTACGTGGACTTCAGTGACGTGGGGTGGAAATGACT 1260
DB 1201 AGTCAGCTGTGAAGAGACACCTTTTGTACGTGGACTTCAGTGACGTGGGGTGGAAATGACT 1260
QY 1261 GGATTTGGCTCCCGCGGGGTATCACGCTTTTACTGCGACAGGAGAAATGCCCTTTTCCCTC 1320
DB 1261 GGATTTGGCTCCCGCGGGGTATCACGCTTTTACTGCGACAGGAGAAATGCCCTTTTCCCTC 1320
QY 1321 TGGCTGATCATCTGAATCCCACTAATCATGCAATGTTTGGTTCAGACGTTGGTCAACTCTGTTA 1380
DB 1321 TGGCTGATCATCTGAATCCCACTAATCATGCAATGTTTGGTTCAGACGTTGGTCAACTCTGTTA 1380
QY 1381 ACTCTAAGATTTCTAAGGATGCTGTGTCCCGACAGAACTCAGTGCTATCTCGATGCTGT 1440
DB 1381 ACTCTAAGATTTCTAAGGATGCTGTGTCCCGACAGAACTCAGTGCTATCTCGATGCTGT 1440
QY 1441 ACCTTGACGAGAAAGAAAGGTTGTTAAAGAACTATCAGGACATGTTGTGGAGGGTT 1500
DB 1441 ACCTTGACGAGAAAGAAAGGTTGTTAAAGAACTATCAGGACATGTTGTGGAGGGTT 1500
QY 1501 GTGGGTGCTGCTAGTACAGCAAAATTAATATACATAAATATATATATA 1547
DB 1501 GTGGGTGCTGCTAGTACAGCAAAATTAATATACATAAATATATATATA 1547
RESULT 3
ABK90308
ID ABK90308 standard; DNA; 1547 BP.
XX
AC ABK90308;
XX
DT 21-OCT-2002 (first entry)
XX
DE DNA encoding human bone morphogenetic protein 2 (BMP2).
XX
KW Bone morphogenetic protein 2; BMP2; cancer; breast cancer; lung cancer;
XX gene; ss; human.
XX
OS Homo sapiens.
XX
FH Key
CDS 324..1514
FT /*tag= a

```
FT misc_feature /product= "BMP2 protein"
FT FT 429..1127
FT FT /*tag= b
FT FT /note= "TGF-beta propeptide"
FT variation replace(432,G)
FT FT /*tag= c
FT FT /standard_name= "Single nucleotide polymorphism"
FT FT replace(584,G)
FT FT /*tag= d
FT FT /standard_name= "Single nucleotide polymorphism"
FT FT replace(893,A)
FT FT /*tag= e
FT FT /standard_name= "Single nucleotide polymorphism"
FT FT 1209..1511
FT FT /*tag= f
FT FT /note= "TGF-beta-like domain"
XX FT
XX PN WO200254940-A2.
XX XX
XX PD 18-JUL-2002.
XX XX
XX PF 11-JAN-2002; 2002WO-US0000610.
XX XX
XX PR 12-JAN-2001; 2001US-0261252P.
XX XX
XX PA (UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.
XX XX
XX PI Langenfeld J;
XX XX
XX DR WPI; 2002-575416/61.
XX XX
XX PT Treating cancer, e.g. lung cancer, comprises administering a bone
XX PT morphogenic protein-2 (BMP-2) activity inhibitor, or a vector encoding
XX PT the inhibitor or an antisense oligonucleotide that binds to a BMP-2
XX PT nucleic acid sequence.
XX PS Disclosure; Page 37-40; 162pp; English.
XX XX
XX CC This invention relates to a novel method for treating cancer comprising
XX CC administering to a patient a bone morphogenic protein-2 (BMP-2) activity
XX CC inhibitor or an expression vector which has a nucleic acid sequence
XX CC encoding the BMP-2 activity inhibitor or which encodes an antisense
XX CC oligonucleotide that binds to a BMP-2 nucleic acid sequence. Inhibitors
XX CC of BMP-2 activity encompassed in the invention are the proteins noggin,
XX CC chordin, gremlin, cerberus 1 homologue and DAN. The method of the
XX CC invention which utilises a BMP-2 activity inhibitor or an expression
XX CC vector, is useful in diagnosing or treating cancers such as breast cancer
XX CC or lung cancer. A kit is useful in the administration of the BMP-2
XX CC activity inhibitor in the treatment of cancers. The present sequence
XX CC represents the DNA encoding the human bone morphogenetic protein (BMP2)
XX CC protein used in the method of the invention
XX SQ Sequence 1547 BP; 377 A; 423 C; 410 G; 337 T; 0 U; 0 Other;
Query Match 100.0%; Score 1547; DB 6; Length 1547;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1547; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GGGGACTTCTTGAATTCGAGGGAGAATACTTCGCGACCCCACTTTGGCCGGTGCCTT 60
Db 1 GGGGACTTCTTGAATTCGAGGGAGAATACTTCGCGACCCCACTTTGGCCGGTGCCTT 60
Qy 61 TGCCCGGAGGAGCTGCTCGCCATCTCCAGGCCCAACCGCCCTCCACTCTCCGGCCT 120
Db 61 TGCCCGGAGGAGGAGCTGCTCGCCATCTCCAGGCCCAACCGCCCTCCACTCTCCGGCCT 120
Qy 121 TGCCCGGACACTGAGACGCTGTTCCAGCGTGAAGAAGAGAGACTGCGGGCGCGCACCCGG 180
Db 121 TGCCCGGACACTGAGACGCTGTTCCAGCGTGAAGAAGAGAGACTGCGGGCGCGCACCCGG 180
Qy 181 GAGAAGGAGGAGGCAAGAAAGAAACGACATTCGGTCTTTGGCCGACGATTCCTTGACC 240
Db 181 GAGAAGGAGGAGGCAAGAAAGAAACGACATTCGGTCTTTGGCCGACGATTCCTTGACC 240
Qy 241 AGAGTTTTTCCATGTGAGCGCTCTTTCAATGAGCGTGTCCCGCGTCTTCTTTAGACGGA 300
Db 241 AGAGTTTTTCCATGTGAGCGCTCTTTCAATGAGCGTGTCCCGCGTCTTCTTTAGACGGA 300
Qy 301 CTGCGGTCTCTCTAAAGTTCGACCATGTGTGGCCGGGACCCCGCTGTCTTTCTATGACGTGCTGC 360
Db 301 CTGCGGTCTCTCTAAAGTTCGACCATGTGTGGCCGGGACCCCGCTGTCTTTCTATGACGTGCTGC 360
Qy 361 TTCCCAAGTCTCTCTGCGGCGCGGCTGCGCTCGTTTCGAGAGCTGGGCGCGCAGGAAGT 420
Db 361 TTCCCAAGTCTCTCTGCGGCGCGGCTGCGCTCGTTTCGAGAGCTGGGCGCGCAGGAAGT 420
Qy 421 TCGCGGCGGCGTGTGCGGCGCGCCCTCATCCAGACCTCTGAGAGGTCCTCTGACCGAGT 480
Db 421 TCGCGGCGGCGTGTGCGGCGCGCCCTCATCCAGACCTCTGAGAGGTCCTCTGACCGAGT 480
Qy 481 TCGAGTTGCGGCTGCTCAGCATGTTTCGGCTCTGAAAACAGAGACCCACCCAGCAGGAGCG 540
Db 481 TCGAGTTGCGGCTGCTCAGCATGTTTCGGCTCTGAAAACAGAGACCCACCCAGCAGGAGCG 540
Qy 541 CGGTGTCGCCCTCATGCTAGACCTGTATCGAGGCACTCAGGTCAGCCGGGCTCAC 600
Db 541 CGGTGTCGCCCTCATGCTAGACCTGTATCGAGGCACTCAGGTCAGCCGGGCTCAC 600
Qy 601 CCGCCCGAGACCAACCGGTTGGAGAGGCGCAGCCGAGCCCAACACTGTGCGCAGCTTCC 660
Db 601 CCGCCCGAGACCAACCGGTTGGAGAGGCGCAGCCGAGCCCAACACTGTGCGCAGCTTCC 660
Qy 661 ACCATGAAGAATCTTTTGGAAAGAACTACAGAAACGAGTGGGAAAACAAACCCGGAGATTCT 720
Db 661 ACCATGAAGAATCTTTTGGAAAGAACTACAGAAACGAGTGGGAAAACAAACCCGGAGATTCT 720
Qy 721 TCTTTAATTAAGTTCTATCCCAAGGAGGTTTATCAGCTCAGAGAGCTTCAGGTTT 780
Db 721 TCTTTAATTAAGTTCTATCCCAAGGAGGTTTATCAGCTCAGAGAGCTTCAGGTTT 780
Qy 781 TCCGAGAACAGATGCAAGATGCTTTAGGAAACAATAGCAGTTTCCATCCCGAATTATA 840
Db 781 TCCGAGAACAGATGCAAGATGCTTTAGGAAACAATAGCAGTTTCCATCCCGAATTATA 840
Qy 841 TTTATGAAATCATAAAAACCTGCAACAGCCAACTCGAAATTTCCCGTGACACAGACTTTGG 900
Db 841 TTTATGAAATCATAAAAACCTGCAACAGCCAACTCGAAATTTCCCGTGACACAGACTTTGG 900
Qy 901 ACACAGGTTGTTGAATCAGATGCAAGAGGTTGGGAAAAGTTTGTATGTCAACCCCGCTG 960
Db 901 ACACAGGTTGTTGAATCAGATGCAAGAGGTTGGGAAAAGTTTGTATGTCAACCCCGCTG 960
Qy 961 TGATGCGGTGAGCTGTCACAGGAGCACGCCAACCATGATTCGTGTTGGAAGTGGCCCACT 1020
Db 961 TGATGCGGTGAGCTGTCACAGGAGCACGCCAACCATGATTCGTGTTGGAAGTGGCCCACT 1020
Qy 1021 TGGAGGAGAAAACAAGGTGTCTCCAAGAGACATGTTAGGATAAGCAGGTCTTTTGACCAAG 1080
Db 1021 TGGAGGAGAAAACAAGGTGTCTCCAAGAGACATGTTAGGATAAGCAGGTCTTTTGACCAAG 1080
Qy 1081 ATGAAACACAGCTGGTCAAGATGAGGCAATGCTAGTAACTTTTGGCCATGATGGAAGAAG 1140
Db 1081 ATGAAACACAGCTGGTCAAGATGAGGCAATGCTAGTAACTTTTGGCCATGATGGAAGAAG 1140
Qy 1141 GGCATCTCTCCACAAAAGAGAAAACGTCAGCCAAACACAAACAGCGGAAACGCTTAA 1200
Db 1141 GGCATCTCTCCACAAAAGAGAAAACGTCAGCCAAACACAAACAGCGGAAACGCTTAA 1200
Qy 1201 AGTCAGCTGTAAAGAGACACCTTTTGTACGTGGACTTCAGTGACGTGGGTGGGAATGACT 1260
Db 1201 AGTCAGCTGTAAAGAGACACCTTTTGTACGTGGACTTCAGTGACGTGGGTGGGAATGACT 1260
Qy 1261 GGATGTGGCTCCCCCGGGGTATCACGCCCTTTTACTGCCAGGAGATGCCCTTTTCTC 1320
Db 1261 GGATGTGGCTCCCCCGGGGTATCACGCCCTTTTACTGCCAGGAGATGCCCTTTTCTC 1320
```

QY 1321 TGGCTGATCATCTGAACCTCCACTAATCATGCCATTTGTTGAGACGTTGGTCAACTCTGTTA 1380
Db 1321 TGGCTGATCATCTGAACCTCCACTAATCATGCCATTTGTTGAGACGTTGGTCAACTCTGTTA 1380
QY 1381 ACTCTAAGATTCCTAAGGATGCTGTGTCGCCGACAGAACTCAGTGTCTATCTCGATGCTGT 1440
Db 1381 ACTCTAAGATTCCTAAGGATGCTGTGTCGCCGACAGAACTCAGTGTCTATCTCGATGCTGT 1440
QY 1441 ACCTTGACGAGAAATGAAAAGGTTGTATTAAAGAACTATCAGGACATGTTGTGGAGGCTT 1500
Db 1441 ACCTTGACGAGAAATGAAAAGGTTGTATTAAAGAACTATCAGGACATGTTGTGGAGGCTT 1500
QY 1501 GTGGGTGTCGCTAGTACAGCAAAATTAATAATACATAAATATATATA 1547
Db 1501 GTGGGTGTCGCTAGTACAGCAAAATTAATAATACATAAATATATATA 1547

RESULT 4

ABX76358
ID ABX76358 standard; DNA; 1547 BP.

XX AC ABX76358;

XX DT 02-APR-2003 (first entry)

XX DE Lung cancer-associated polynucleotide #222.

XX KW Lung cancer-associated polynucleotide; gene; ds; cytostatic; emphysema;
XX KW antiinflammatory; antiasthmatic; non-small cell lung cancer; atelectasis;
XX KW small cell lung cancer; benign lesion; precancerous lesion; bronchitis;
XX KW chronic obstructive pulmonary disease; hypersensitivity pneumonitis;
XX KW interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.

XX OS Unidentified.

XX PN WO200286443-A2.

XX PD 31-OCT-2002.

XX PF 18-APR-2002; 2002WO-US012476.

XX PR 18-APR-2001; 2001US-0284770P.

XX PR 10-MAY-2001; 2001US-0290492P.

XX PR 09-NOV-2001; 2001US-0339245P.

XX PR 13-NOV-2001; 2001US-0350668P.

XX PR 29-NOV-2001; 2001US-0334370P.

XX PR 12-APR-2002; 2002US-0372246P.

XX PA (EOSB-) EOS BIOTECHNOLOGY INC.

XX PI Aziz N, Murray R;

XX DR WPI; 2003-093161/08.

XX PT P-PSDB; ABUS6629.

XX PS Claim 22; Page 357; 453pp; English.

XX CC The invention relates to a method for detecting a lung cancer-associated
XX CC transcript in a cell from a patient, comprising contacting a biological
XX CC sample from the patient with a polynucleotide that selectively hybridizes
XX CC to a sequence that is at least 80 % identical to a gene that exhibits
XX CC increased or decreased expression in lung cancer samples. Lung cancer-
XX CC associated polynucleotides and polypeptides are used for identifying a
XX CC compound that modulates a lung cancer-associated polypeptide, for
XX CC inhibiting proliferation of a lung cancer-associated cell to treat lung
XX CC cancer in a patient and for treating a mammal having lung cancer by
XX CC administering a modulatory compound identified. The methods are useful
XX CC for treating lung cancer, such as small cell lung cancer, non-small cell

CC lung cancer or other benign or precancerous lesions, e.g. atelectasis,
CC emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis,
CC hypersensitivity pneumonitis, interstitial pulmonary fibrosis, asthma and
CC bronchiectasis. The genes, polynucleotides and polypeptides are useful
CC for diagnostic purposes and as targets for screening for therapeutic
CC compounds that modulate lung cancer, such as antibodies. Sequences
CC ABX76124-ABX76474 represent lung cancer-associated polynucleotides of the
CC invention

XX Sequence 1547 BP; 377 A; 423 C; 410 G; 337 T; 0 U; 0 Other;

SQ Query Match 100.0%; Score 1547; DB 8; Length 1547;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1547; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGACTTCTTGAACCTTCAGGAGAAATACTTGGGACCCACATTTGGCGCGGTTCCTT 60

Db 1 GGGGACTTCTTGAACCTTCAGGAGAAATACTTGGGACCCACATTTGGCGCGGTTCCTT 60

QY 61 TGCCCCAGCGAGCTGCTTCGCCATCTCCAGAGCCACCGCCCTCCACTCTCGGCT 120

Db 61 TGCCCCAGCGAGCTGCTTCGCCATCTCCAGAGCCACCGCCCTCCACTCTCGGCT 120

QY 121 TGCCCCGACACTGAGACGCTGTTCCAGCGTGAAAGAGAGACTGCGCGCGGACCCGG 180

Db 121 TGCCCCGACACTGAGACGCTGTTCCAGCGTGAAAGAGAGACTGCGCGCGGACCCGG 180

QY 181 GAGAGAGAGAGGCAAGAAAGGAAACGGAATTCGGTCTTGGCCAGGTCCTTTGACC 240

Db 181 GAGAGAGAGAGGCAAGAAAGGAAACGGAATTCGGTCTTGGCCAGGTCCTTTGACC 240

QY 241 AGAGTTTTTCATGTGGACGCTCTTCAATGAGAGCTGTCGCCGCGTCTTCTAGACGGA 300

Db 241 AGAGTTTTTCATGTGGACGCTCTTCAATGAGAGCTGTCGCCGCGTCTTCTAGACGGA 300

QY 301 CTGCGGCTCTCTAAAGGTGACACCTGTTGGCGGAGACCCGCTGTCTTCTAGCGTTGCTGC 360

Db 301 CTGCGGCTCTCTAAAGGTGACACCTGTTGGCGGAGACCCGCTGTCTTCTAGCGTTGCTGC 360

QY 361 TTCCCGAGGTCCTCTGCGCGCGGCTGCGCTGTTCCGAGTCTGGCCGCGCAGGAAGT 420

Db 361 TTCCCGAGGTCCTCTGCGCGCGGCTGCGCTGTTCCGAGTCTGGCCGCGCAGGAAGT 420

QY 421 TCGCGGCGGCTGCTGCGGCGCGCCCTCATCCAGCCCTCTGACGAGTCTCTGACGAGT 480

Db 421 TCGCGGCGGCTGCTGCGGCGCGCCCTCATCCAGCCCTCTGACGAGTCTCTGACGAGT 480

QY 481 TCGAGTTGCGGCTGCTCAGCATGTTTGGGCTTGAAACAGAGACCCACCCCGCAGCGGAG 540

Db 481 TCGAGTTGCGGCTGCTCAGCATGTTTGGGCTTGAAACAGAGACCCACCCCGCAGCGGAG 540

QY 541 CCGTGGTGCCTTACATGCTAGACCTGTTATCGAGGCACTCAGGTGAGCCGGGCTCAC 600

Db 541 CCGTGGTGCCTTACATGCTAGACCTGTTATCGAGGCACTCAGGTGAGCCGGGCTCAC 600

QY 601 CGGCCCCAGACCGGTTGGAGGGGCGAGCCGAGCCGCAACACTGTGCGCAGCTCC 660

Db 601 CGGCCCCAGACCGGTTGGAGGGGCGAGCCGAGCCGCAACACTGTGCGCAGCTCC 660

QY 661 ACCATGAAGAAATCTTTGGAAGAACTTACCAAGAAACAGTGGGAAAAACAACCCGAGATTCT 720

Db 661 ACCATGAAGAAATCTTTGGAAGAACTTACCAAGAAACAGTGGGAAAAACAACCCGAGATTCT 720

QY 721 TCTTTAATTTAAGTTCTATCCCGAGGAGTTTATCACTCAGCAGAGCTTCAGGTTT 780

Db 721 TCTTTAATTTAAGTTCTATCCCGAGGAGTTTATCACTCAGCAGAGCTTCAGGTTT 780

QY 781 TCCGAGACAGATGACAGATCTTTAGGAAACAATAGCAGTTTCCATCACCGAATTAATA 840

Db 781 TCCGAGACAGATGACAGATCTTTAGGAAACAATAGCAGTTTCCATCACCGAATTAATA 840

QY 841 TTTTGAATCATATAAACCTGCAACAGGCCAACTCGAAATTCGCCGTGACACAGACTTTTGG 900

Db 841 TTTTGAATCATATAAACCTGCAACAGGCCAACTCGAAATTCGCCGTGACACAGACTTTTGG 900

Db 841 TTTATGAAATCATAAACCTGCAACAGCAACTCGAAATTCCTCCGTCAGCAGACTTTTGG 900
Qy 901 ACACAGGTTGGTCAATCAGATCGAAGCAGGTCGGAAAGTTTGTATGTACCCCGGCTG 960
Db 901 ACACAGGTTGGTCAATCAGATCGAAGCAGGTCGGAAAGTTTGTATGTACCCCGGCTG 960
Qy 961 TGATCGGTCGACTGCAAGGAGCAGCGCAACCACTGATTCGTGTGGAGTGGCCCACT 1020
Db 961 TGATCGGTCGACTGCAAGGAGCAGCGCAACCACTGATTCGTGTGGAGTGGCCCACT 1020
Qy 1021 TGGAGGAGAAACAAGTGTCTTCAAGAGACATGTTAGGATAAGCAGGTCCTTTGACCAAG 1080
Db 1021 TGGAGGAGAAACAAGTGTCTTCAAGAGACATGTTAGGATAAGCAGGTCCTTTGACCAAG 1080
Qy 1081 ATGACACAGCTGTCACAGATAGGCAATGCTAGTAACTTTTGGCCATGATGGAAG 1140
Db 1081 ATGACACAGCTGTCACAGATAGGCAATGCTAGTAACTTTTGGCCATGATGGAAG 1140
Qy 1141 GGCATCTCTCCACAAAGAGAAAAGCGTCAAGCCAAACACAAACAGCGGAAACGCTTAA 1200
Db 1141 GGCATCTCTCCACAAAGAGAAAAGCGTCAAGCCAAACACAAACAGCGGAAACGCTTAA 1200
Qy 1201 AGTCAGCTGTAAGAGACACACCTTTGTACGTGGACTTCAGTGACGTGGGTGGAATGACT 1260
Db 1201 AGTCAGCTGTAAGAGACACACCTTTGTACGTGGACTTCAGTGACGTGGGTGGAATGACT 1260
Qy 1261 GGATGTGGTCCCGGGGTATCAGCGCTTTTACTGCCAGGAGATGCCCTTTTCTC 1320
Db 1261 GGATGTGGTCCCGGGGTATCAGCGCTTTTACTGCCAGGAGATGCCCTTTTCTC 1320
Qy 1321 TGGCTGATCATCTCAACTCCCAATCATGTCATTTGTTTCAAGCTTGTCAACTCTGTAA 1380
Db 1321 TGGCTGATCATCTCAACTCCCAATCATGTCATTTGTTTCAAGCTTGTCAACTCTGTAA 1380
Qy 1381 ACTTAAGATTCCTAAGGCATGCTGTGTCCCGACAGAACTCAGTGCTATCTCGATGCTGT 1440
Db 1381 ACTTAAGATTCCTAAGGCATGCTGTGTCCCGACAGAACTCAGTGCTATCTCGATGCTGT 1440
Qy 1441 ACCTTGACGAGAAATGAAAAGTTGTATTAAGAACTATCAGGACATGTTGTGAGGGTT 1500
Db 1441 ACCTTGACGAGAAATGAAAAGTTGTATTAAGAACTATCAGGACATGTTGTGAGGGTT 1500
Qy 1501 GTGGGTGTCGTAGTACAGCAAAATTAATAACATAATATATATA 1547
Db 1501 GTGGGTGTCGTAGTACAGCAAAATTAATAACATAATATATATA 1547

RESULT 5
ACF34481
ID ACF34481 standard; DNA; 1547 BP.
XX ACF34481;
AC ACF34481;
XX
DT 15-OCT-2003 (first entry)
XX
XX Gene encoding angiogenesis protein BNO99.
DE
XX Cytostatic; antirheumatic; antiarthritic; antidiabetic; ophthalmological;
KW antiproliferative; antiarteriosclerotic; cardiant; vasotropic; angiogenesis;
KW gene therapy; vasculature; cancer; rheumatoid arthritis; psoriasis;
KW diabetic retinopathy; cardiovascular disease; atherosclerosis;
KW ischemic limb disease; coronary artery disease; gene, ds.
XX
OS Homo sapiens.
XX
XX WO2003027285-A1.
XX
XX 03-APR-2003.
XX
XX 19-SEP-2002; 2002WO-AU001282.
XX
XX 27-SEP-2001; 2001AU-00007973.
PR
XX 27-SEP-2001; 2001AU-00007974.

PR 11-OCT-2001; 2001AU-00008210.
PR 29-OCT-2001; 2001AU-00008532.
PR 13-NOV-2001; 2001AU-00008838.
PR 28-AUG-2002; 2002AU-00951032.
XX
PA (BION-) BIONOMICS LTD.
XX
XX Gamble JR, Hahn CN, Vadas MA;
PI WPI; 2003-354655/33.
XX DR P-PSDB; ABR64206.
XX
XX New angiogenic genes and polypeptides, useful for diagnosing,
PT prognosticating or treating an angiogenesis-related disorder, e.g.
PT cancer, rheumatoid arthritis, diabetic retinopathy, psoriasis or
PT cardiovascular diseases.
XX
XX Claim 2; SEQ ID NO 36; 90pp; English.
XX
XX The invention relates to the isolation of novel genes (ACF34446-ACF34559)
CC encoding proteins (ABR64180-ABR64281) involved in the process of
CC angiogenesis. The nucleic acid molecules are useful in identifying and/or
CC obtaining full-length human genes involved in an angiogenic process. The
CC nucleic acid molecule, polypeptides or complexes encoded, cells or
CC genetically modified non-human animals derived from these are useful for
CC the screening of candidate pharmaceutical compounds used in treating
CC angiogenesis-related disorders. They are also useful for diagnosing,
CC prognosticating or treating an angiogenesis-related disorder, which
CC involves uncontrolled or enhanced angiogenesis or is a disorder in which
CC a decreased vasculature is of benefit (e.g. cancer, rheumatoid arthritis,
CC diabetic retinopathy, psoriasis or cardiovascular diseases such as
CC atherosclerosis), or involves inappropriately arrested or decreased
CC angiogenesis or is a disorder in which an expanding vasculature is of
CC benefit (e.g. ischemic limb disease or coronary artery disease). The
CC modulator of expression or activity of the polypeptide encoded by the
CC nucleic acid sequence is useful for manufacturing a medicament for the
CC treatment of an angiogenesis-related disorder. This sequence corresponds
CC to the gene encoding one of the novel angiogenic protein
XX
SQ Sequence 1547 BP; 377 A; 423 C; 410 G; 337 T; 0 U; 0 Other;
Query Match 100.0%; Score 1547; DB 8; Length 1547;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1547; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GGGGACTTCTTGAACCTTGCAGGGAGAAATACTTGGCACCACCTTTTGGCGGTCCTT 60
Db 1 GGGGACTTCTTGAACCTTGCAGGGAGAAATACTTGGCACCACCTTTTGGCGGTCCTT 60
Qy 61 TGCCCCAGCGGAGCTGCTTCCGATCTCCGAGCCGCCACCGCCCTCCACTCCTCGGCT 120
Db 61 TGCCCCAGCGGAGCTGCTTCCGATCTCCGAGCCGCCACCGCCCTCCACTCCTCGGCT 120
Qy 121 TGCCCCAGCTGAGACGCTGTTCCAGCGTGAAGAGAGACTCGCGGCGCGCACCGG 180
Db 121 TGCCCCAGCTGAGACGCTGTTCCAGCGTGAAGAGAGACTCGCGGCGCGCACCGG 180
Qy 181 GAGAAGGAGGAGGCAAGAAAGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGG 240
Db 181 GAGAAGGAGGAGGCAAGAAAGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGG 240
Qy 241 AGAGTTTTCATGTCGACGCTCTTTCAATGAGAGCTGTCCTTCTTAGACCGGA 300
Db 241 AGAGTTTTCATGTCGACGCTCTTTCAATGAGAGCTGTCCTTCTTAGACCGGA 300
Qy 301 CTGCGGTCTCTTAAAGGTTCGACCATGTTGGCCGCGGAGCCCGCTGCTTCTAGCTTGTGTC 360
Db 301 CTGCGGTCTCTTAAAGGTTCGACCATGTTGGCCGCGGAGCCCGCTGCTTCTAGCTTGTGTC 360
Qy 361 TTCCCCAGGTCCTCTCTGCGGCGCGGCTGCGCTGCTTCTCGGAGCTGGGCGCGGAGAGT 420
Db 361 TTCCCCAGGTCCTCTCTGCGGCGCGGCTGCGCTGCTTCTCGGAGCTGGGCGCGGAGAGT 420

QY 421 TCGCGCGCGCTGTCGCGCGCGCCCTCATCCAGCCCTCTGACGAGGTCTTGAGCGAGT 480
Db 421 TCGCGCGCGCTGTCGCGCGCGCCCTCATCCAGCCCTCTGACGAGGTCTTGAGCGAGT 480
QY 481 TCGAGTTTCGGGTGCTCAGCATGTTTCGGCTGTGAACAGAGACCCACCCCGAGCGGACG 540
Db 481 TCGAGTTTCGGGTGCTCAGCATGTTTCGGCTGTGAACAGAGACCCACCCCGAGCGGACG 540
QY 541 CGGTGTCGCCCTTACATGCTAGACCTGTATCGCAGGCACCTCAGGTTCAGCGGCTCAC 600
Db 541 CGGTGTCGCCCTTACATGCTAGACCTGTATCGCAGGCACCTCAGGTTCAGCGGCTCAC 600
QY 601 CGCGCCACAGACACCGTTGGAGAGCGAGCCGAGCCAGCAACACTGTGCGCAGCTTCC 660
Db 601 CGCGCCACAGACACCGTTGGAGAGCGAGCCGAGCCAGCAACACTGTGCGCAGCTTCC 660
QY 661 ACCATGAAGATCTTTTGAAGAACTACACAGAAACGAGTGGGAAACAAACCCGAGATTCT 720
Db 661 ACCATGAAGATCTTTTGAAGAACTACACAGAAACGAGTGGGAAACAAACCCGAGATTCT 720
QY 721 TCTTTAAATTAAGTTCTATCCCGAGGAGGTTTATCACCTCAGCAGACTTCAGGTTT 780
Db 721 TCTTTAAATTAAGTTCTATCCCGAGGAGGTTTATCACCTCAGCAGACTTCAGGTTT 780
QY 781 TCCGAGAACAGATGCAAGATGCTTTAGGAAACAATAGCAGTTTCCATCACCGAATTAATA 840
Db 781 TCCGAGAACAGATGCAAGATGCTTTAGGAAACAATAGCAGTTTCCATCACCGAATTAATA 840
QY 841 TTTATGAATCATAAAACTGCAACAGCAACTCGAANAATCCCGTGACACGACTTTTGG 900
Db 841 TTTATGAATCATAAAACTGCAACAGCAACTCGAANAATCCCGTGACACGACTTTTGG 900
QY 901 ACACCGGTTGGTGAATCAGATGCAAGCAGCGTGGGAAAGTTTGTATGTACCCCGCTG 960
Db 901 ACACCGGTTGGTGAATCAGATGCAAGCAGCGTGGGAAAGTTTGTATGTACCCCGCTG 960
QY 961 TGATGCGTGAATGTCACAGGAGACGCAACCAATGAGTTTGGTGAAGTGGCCACT 1020
Db 961 TGATGCGTGAATGTCACAGGAGACGCAACCAATGAGTTTGGTGAAGTGGCCACT 1020
QY 1021 TGGAGGAAACAAAGGTGCTTCAAGAGACATGTTAGGATAGCAGGTCTTTGACACCAAG 1080
Db 1021 TGGAGGAAACAAAGGTGCTTCAAGAGACATGTTAGGATAGCAGGTCTTTGACACCAAG 1080
QY 1081 ATGACACAGCTGTCACAGATAGGCGCATGCTAGTAATCTTTGGCCATGATGGAAG 1140
Db 1081 ATGACACAGCTGTCACAGATAGGCGCATGCTAGTAATCTTTGGCCATGATGGAAG 1140
QY 1141 GGCATCTCTCCACAAAGAGAAAAACGTCAGCCAAACACAAACAGCGGAAACGCTTTA 1200
Db 1141 GGCATCTCTCCACAAAGAGAAAAACGTCAGCCAAACACAAACAGCGGAAACGCTTTA 1200
QY 1201 AGTCAGCTGTAAGAGACACCTTTGTAGTGAATTCAGTGAACGTTGGGTGGAATGACT 1260
Db 1201 AGTCAGCTGTAAGAGACACCTTTGTAGTGAATTCAGTGAACGTTGGGTGGAATGACT 1260
QY 1261 GGATGTGCTCCCGCGGTATCAGCCTTTTACTGCCACGAGAAATGCCCTTTTCCTC 1320
Db 1261 GGATGTGCTCCCGCGGTATCAGCCTTTTACTGCCACGAGAAATGCCCTTTTCCTC 1320
QY 1321 TGGCTGATCATCTGAACCTCACTAATCATGCTTGTGTCAGACGTTGTCACCTGTTA 1380
Db 1321 TGGCTGATCATCTGAACCTCACTAATCATGCTTGTGTCAGACGTTGTCACCTGTTA 1380
QY 1381 ACTCTAAGATTCCTAAGGATGCTGTGTCGAGACAACTCAGTGTCTATCTGATGCTGT 1440
Db 1381 ACTCTAAGATTCCTAAGGATGCTGTGTCGAGACAACTCAGTGTCTATCTGATGCTGT 1440
QY 1441 ACCTTGAAGAGATGAAGGTTGTATTAAGAACTATCAGGACATGTTGTGGAGGTT 1500
Db 1441 ACCTTGAAGAGATGAAGGTTGTATTAAGAACTATCAGGACATGTTGTGGAGGTT 1500
QY 1501 GTGGGTGTCGTAGTACAGCAAAATTAATACATAATATATATATA 1547

Db 1501 GTGGGTGTCGTAGTACAGCAAAATTAATACATAATATATATATA 1547
RESULT 6
ID ACF05920 standard; cDNA; 1547 BP.
XX ACF05920;
XX AC ACF05920;
XX 04-DEC-2003 (first entry)
XX Human bone morphogenic protein 2A polynucleotide.
XX Bone morphogenic protein 2A; BMP-2A; human; glaucoma; diagnosis; therapy;
XX ophthalmological; gene; ss.
XX Homo sapiens.
XX Key Location/Qualifiers
XX CDS 324..1514
XX FT /*tag= a
XX FT /product= "BMP-2A"
XX PN WO2003055443-A2.
XX PD 10-JUL-2003.
XX PF 31-OCT-2002; 2002WO-US035251.
XX PR 31-OCT-2001; 2001US-0334852P.
XX (ALCO-) ALCON INC.
XX (UTNT-) UNIV NORTH TEXAS HEALTH SCI CENT.
XX Clark AF, Wordinger RJ;
XX WPI; 2003-559253/52.
XX P-PSDB; ABR62824.
XX Diagnosing glaucoma in a sample comprises detecting altered expression of
bone morphogenic proteins in sample from a cell or bodily fluid.
PS Claim 1; Fig 1a-c; 55pp; English.
XX The present sequence is a nucleotide sequence for human bone morphogenic
protein 2A (BMP-2A). RT-PCR showed BMP-2 to be expressed in the human
trabecular meshwork and optic nerve head. A claimed method for diagnosing
glaucoma involves detecting altered expression of a BMP family member
such as BMP-2A by PCR in a sample obtained e.g. from blood or buccal
cells. Primers used in the PCR may comprise contiguous nucleotides of the
present sequence. A claimed method for treating glaucoma comprises
administering an agonist of BMP-2, BMP-4, BMP-5, BMP-7 or Smad 1/5, or an
antagonist of chordin, gremlin or follistatin. A claimed method of
identifying a therapeutic agent for treatment of glaucoma comprises
CC identifying a substance that inhibits or stimulates BMP-induced Smad
CC signalling pathways or BMP-regulated gene expression, using recombinant
CC cells expressing BMP-2A, BMP-4, BMP-5 or BMP-7
XX
SQ Sequence 1547 BP; 377 A; 423 C; 410 G; 337 T; 0 U; 0 Other;
Query Match 100.0%; Score 1547; DB 10; Length 1547;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1547; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGGACTTCTTGAACCTTCAGGAGAACTTGGCAGCCCACTTTGGCGCGGTGCTT 60
Db 1 GGGGACTTCTTGAACCTTCAGGAGAACTTGGCAGCCCACTTTGGCGCGGTGCTT 60
QY 61 TGCCCCAGGAGGAGCTTGTTCGCATCTCCGAGCCCAACCGCCCTCCACTCTCGGCT 120
Db 61 TGCCCCAGGAGGAGCTTGTTCGCATCTCCGAGCCCAACCGCCCTCCACTCTCGGCT 120

121 TGCCCGACATGAGACGCTGTTCCAGCGTGAAGAGAGAGACTCGCGCGCGGCACCCGG 180
121 TGCCCGACATGAGACGCTGTTCCAGCGTGAAGAGAGAGACTCGCGCGCGGCACCCGG 180
181 GAGAGAGGAGGCAAGAAAGGAAACGGAATTCGGTCTTGTGCGCAGAGTCTTTGACC 240
181 GAGAGAGGAGGCAAGAAAGGAAACGGAATTCGGTCTTGTGCGCAGAGTCTTTGACC 240
241 AGAGTTTTCATGTGACGCTCTTTCAATGGACGTGTCCCGCGTCTTCTTAGACGGA 300
241 AGAGTTTTCATGTGACGCTCTTTCAATGGACGTGTCCCGCGTCTTCTTAGACGGA 300
301 CTGCGGTCTCTAAAGGTTCAGCAATGTGTGGCGGAGCCCGCTGTCTTCTAGCGTTGCTGC 360
301 CTGCGGTCTCTAAAGGTTCAGCAATGTGTGGCGGAGCCCGCTGTCTTCTAGCGTTGCTGC 360
361 TTCCCGCAGGTCTCTCTGCGCGCGCGCTGGCCCTCGTTCGGAGCTGGCGCGCAGGAAGT 420
421 TCGCGCGCGGTCTCTGCGCGCGCGCTGGCCCTCGTTCGGAGCTGGCGCGCAGGAAGT 480
421 TCGCGCGCGGTCTCTGCGCGCGCGCTGGCCCTCGTTCGGAGCTGGCGCGCAGGAAGT 480
481 TCGAGTTTGGCGCTCTCAGCATGTTTCGGCTTGAACAGAGACCCACCCAGCAGGAGCG 540
481 TCGAGTTTGGCGCTCTCAGCATGTTTCGGCTTGAACAGAGACCCACCCAGCAGGAGCG 540
541 CCGTGTGTCGCCCTCTACATGCTAGACCTGTATCGCAGCACTCAGGTCAGCGCGGCTCAC 600
541 CCGTGTGTCGCCCTCTACATGCTAGACCTGTATCGCAGCACTCAGGTCAGCGCGGCTCAC 600
601 CCGCGCCAGACACCGGTTGAGAGGGCAGCGCAGCGCCAGCCAACTGTGCGCAGCTTCC 660
601 CCGCGCCAGACACCGGTTGAGAGGGCAGCGCAGCGCCAGCCAACTGTGCGCAGCTTCC 660
661 ACCATGAAGATCTTTTGAAGAACTACCAAGAAACGAGTGGGAAACCAACCGGAGATTCT 720
661 ACCATGAAGATCTTTTGAAGAACTACCAAGAAACGAGTGGGAAACCAACCGGAGATTCT 720
721 TCTTTAAATTTAAGTTCTATCCCGCAGGAGGTTTATCACCCTCAGCAGAGCTTCAGGTTT 780
721 TCTTTAAATTTAAGTTCTATCCCGCAGGAGGTTTATCACCCTCAGCAGAGCTTCAGGTTT 780
781 TCCGAGACAGATCGAAGATCTTTAGAAACAAATAGCAGTTTCCATCACCAGATTAAATA 840
781 TCCGAGACAGATCGAAGATCTTTAGAAACAAATAGCAGTTTCCATCACCAGATTAAATA 840
841 TTTATGAATCATAAACCTTCAACAGCCTTGAATTCGCCGTGACAGACTTTTGG 900
841 TTTATGAATCATAAACCTTCAACAGCCTTGAATTCGCCGTGACAGACTTTTGG 900
901 ACACAGGTTGGTGAATCAGAAATCAAGCAGGTGGGAAAGTTTGTATGTCAACCCCGCTG 960
901 ACACAGGTTGGTGAATCAGAAATCAAGCAGGTGGGAAAGTTTGTATGTCAACCCCGCTG 960
961 TGATCGGTGACTGTCACAGGACACGCAACCAATGAGATTGCGTGGTGAAGTGCACCT 1020
961 TGATCGGTGACTGTCACAGGACACGCAACCAATGAGATTGCGTGGTGAAGTGCACCT 1020
1021 TGGAGGAGAAACAAGGTGTCTTCAAGAGACATGTTAGGATAAGCAGGTCTTTGACCAAG 1080
1021 TGGAGGAGAAACAAGGTGTCTTCAAGAGACATGTTAGGATAAGCAGGTCTTTGACCAAG 1080
1081 ATGAACACAGCTGTTGTCAGATAAGGCAATTCGTAGTAACCTTTTGGCCATGATGAAAG 1140
1081 ATGAACACAGCTGTTGTCAGATAAGGCAATTCGTAGTAACCTTTTGGCCATGATGAAAG 1140
1141 GGCATCTCTTCCAAAGAGAAACAGTCAAGCCAAACACAAACAGCGGAAACGCCTTA 1200
1141 GGCATCTCTTCCAAAGAGAAACAGTCAAGCCAAACACAAACAGCGGAAACGCCTTA 1200
1201 AGTCCAGCTGTAAGAGACACCCCTTTGTACGTGGACTTCAGTGACGTGGGGTGAATGACT 1260

Db 1201 AGTCCAGCTGTAGAGACACCCCTTTGTACCTGGACTTCAGTGAGCTGGGGTGGATGACT 1260
Qy 1261 GGAATTTGGTCTCCCGGGGTATACACGCTTTTATGTGCGCAACGAGAAATGCCCTTTTCCTC 1320
Db 1261 GGAATTTGGTCTCCCGGGGTATACACGCTTTTATGTGCGCAACGAGAAATGCCCTTTTCCTC 1320
Qy 1321 TGGCTGATCATCTGAACCTCCACTAATCATGCCATTGTTTCAGACGTTGGTCAACTCTGTTA 1380
Db 1321 TGGCTGATCATCTGAACCTCCACTAATCATGCCATTGTTTCAGACGTTGGTCAACTCTGTTA 1380
Qy 1381 ACTCTAAGATTTCTTAAGCGCATGCTGTCTCCCGACAGAACTCAGTGCCTATCTCCGATGCTGT 1440
Db 1381 ACTCTAAGATTTCTTAAGCGCATGCTGTCTCCCGACAGAACTCAGTGCCTATCTCCGATGCTGT 1440
Qy 1441 ACCTTGACGAGAAATGAAAAGGTTGTATTAAGAACTATCAGGACATCGTTGTGAGGGTT 1500
Db 1441 ACCTTGACGAGAAATGAAAAGGTTGTATTAAGAACTATCAGGACATCGTTGTGAGGGTT 1500
Qy 1501 GTGGGTCTCGCTAGTACAGCAAAATTAATACATAAATATATATA 1547
Db 1501 GTGGGTCTCGCTAGTACAGCAAAATTAATACATAAATATATATA 1547

RESULT 7
ADD14609
ID ADD14609 standard; cDNA; 1547 BP.
XX
AC ADD14609;
XX AC
DT 01-JAN-2004 (first entry)
XX
DE Human src biomarker polynucleotide SEQ ID NO:3.
XX
KW predictor set; protein tyrosine kinase activity modulator;
KW protein tyrosine kinase pathway; protein tyrosine kinase; cytostatic;
KW gene therapy; drug sensitivity; genetic profile; cancer; human; gene; ss.
XX Homo sapiens.
XX
FN WO2003062395-A2.
XX
PD 31-JUL-2003.
XX
PF 17-JAN-2003; 2003WO-US001981.
XX
PR 18-JAN-2002; 2002US-0350061P.
XX
XX (BRIM) BRISTOL-MYERS SQUIBB CO.
XX
XX Huang F, Fairchild CR, Lee FY, Shaw P;
XX
XX WPI; 2003-636735/60.
XX
XX P-PSDB; ADD14015.
XX
XX New polynucleotides and polypeptides for predicting the activity of
XX compounds that interact with protein tyrosine kinases and/or protein
XX tyrosine kinase pathways.
XX
XX Claim 2; SEQ ID NO 3; 139pp; English.
XX
XX The present invention describes a predictor set comprising a plurality of
XX polynucleotides or polypeptides whose expression pattern is predictive of
XX the response of cells to treatment with a compound that modulates protein
XX tyrosine kinase activity or members of the protein tyrosine kinase
XX pathway. Also described: (1) predicting whether a compound is capable of
XX modulating the activity of cells, comprising obtaining a sample of cells,
XX determining whether the cells express a plurality of markers, and
XX correlating the expression of the markers to the compound's ability to
XX modulate the activity of the cells; (2) a plurality of cell lines for
XX identifying polynucleotides and polypeptides whose expression levels
XX correlate with compound sensitivity or resistance of cells associated
XX with a disease state; and (3) identifying polynucleotides and

XX 12-FEB-2004 (first entry)
XX Human bone morphogenetic protein (BMP)-2 DNA.
XX Human; BMP; bone morphogenetic protein; cancer; therapy; gene; ds.
XX Homo sapiens.
XX Key Location/Qualifiers
XX CDS 324..1514
XX /tag= a
XX /product= "Human BMP-2 protein"
XX sig_peptide 324..1169
XX /tag= b
XX /label= Signal_peptide
XX misc_feature 429..1127
XX /tag= d
XX /note= "Transforming growth factor (TGF)-beta propeptide region"
XX allele replace(432,G)
XX /tag= e
XX allele replace(584,G)
XX /tag= f
XX allele replace(893,T)
XX /tag= g
XX mat_peptide 1170..1511
XX /tag= c
XX /product= "Mature human BMP-2 protein"
XX misc_feature 1209..1511
XX /tag= h
XX /note= "Transforming growth factor (TGF)-beta-like domain"
XX
XX US2003134790-A1.
XX 17-JUL-2003.
XX 02-MAY-2002; 2002US-00139814.
XX 11-JAN-2002; 2002US-00044716.
XX (UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.
XX Langenfeld J;
XX WPI; 2003-829645/77.
XX P-PSDB; ABW01849.
XX Treating cancer, e.g. carcinoma of the breast, bladder, colon, kidney, lung, ovary, thyroid, endometrium, omental, testis or liver, comprises administering to the patient a bone morphogenetic protein-4 activity inhibitor.
XX Disclosure; Page 15-17; 64pp; English.
XX The present invention relates to the use of BMP (bone morphogenetic protein)-2 and BMP-4 used in treating cancer. The invention is useful for treating cancer, e.g. carcinoma of the breast, bladder, colon, lung, kidney, ovary, thyroid, endometrium, omental, testis and liver. The present sequence is human bone morphogenetic protein (BMP)-2 DNA
XX Sequence 1547 BP; 377 A; 423 C; 410 G; 337 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 1547; DB 10; Length 1547;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1547; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGGACTTCTTGAACCTTGAGGAGAGATTAACCTTGCGCACCCCACTTTGGCGCGGTGCCTT 60
DB 1 GGGGACTTCTTGAACCTTGAGGAGAGATTAACCTTGCGCACCCCACTTTGGCGCGGTGCCTT 60
QY 61 TGGCCCGAGCGAGCTGCTTGGCCATCTCGAGCCCCACCGCCCTCCACTCTCTGGGCT 120

Db 61 TGGCCCGAGCGAGCTGCTTGGCCATCTCGAGCCCCACCGCCCTCCACTCTCTGGGCT 120
QY 121 TGGCCCGACACTGAGACGCTGTTCCAGCGGTGAAGAGAGAGACTGCGCGCCGCGCACCCCG 180
Db 121 TGGCCCGACACTGAGACGCTGTTCCAGCGGTGAAGAGAGAGACTGCGCGCCGCGCACCCCG 180
QY 181 GAGAGAGGAGGAGCAAGAAAGAAAGGACATTCGGTCTCTTGGCGCAGGTCTCTTGACC 240
Db 181 GAGAGAGGAGGAGCAAGAAAGAAAGGACATTCGGTCTCTTGGCGCAGGTCTCTTGACC 240
QY 241 AGAGTTTTTTCATGTGAGCGCTCTTTCAATGACGTGTCCCGCGGTGCTCTTAGACGGA 300
Db 241 AGAGTTTTTTCATGTGAGCGCTCTTTCAATGACGTGTCCCGCGGTGCTCTTAGACGGA 300
QY 301 CTGCGGTCTCTTAAGAGTGCACCATGTGGCGCGGACCCGCTGTCTTCTAGAGTCTCTGC 360
Db 301 CTGCGGTCTCTTAAGAGTGCACCATGTGGCGCGGACCCGCTGTCTTCTAGAGTCTCTGC 360
QY 361 TTCCCGCAGGTCTCTCTGGCGCGGCTGGGCTCTGTTCCGGAGCTGGGCGCGCAGGAAGT 420
Db 361 TTCCCGCAGGTCTCTCTGGCGCGGCTGGGCTCTGTTCCGGAGCTGGGCGCGCAGGAAGT 420
QY 421 TCGCGCGCGGTCTCTGGCGCGGCTCTCATCCAGCCCTCTGACGAGGTCTCTGAGCGAGT 480
Db 421 TCGCGCGCGGTCTCTGGCGCGGCTCTCATCCAGCCCTCTGACGAGGTCTCTGAGCGAGT 480
QY 481 TCGAGTTGGGCTCTCAGCATGTTGGGCTGAACAGAGAGCCACCCCGCAGCGGAGG 540
Db 481 TCGAGTTGGGCTCTCAGCATGTTGGGCTGAACAGAGAGCCACCCCGCAGCGGAGG 540
QY 541 CGGTGGTGGCCCTTACATGCTAGACCTGTATCGAGGCACTCAGGTCAAGCGGCTCAC 600
Db 541 CGGTGGTGGCCCTTACATGCTAGACCTGTATCGAGGCACTCAGGTCAAGCGGCTCAC 600
QY 601 CCGCCCCAGACCAACCGGTTGGAGAGGCGAGCCAGCGGAGCAACTGTGGCAGCTTCC 660
Db 601 CCGCCCCAGACCAACCGGTTGGAGAGGCGAGCCAGCGGAGCAACTGTGGCAGCTTCC 660
QY 661 ACCATGAAGATCTTTGGAGAGCACTACAGAGAGCGAGTGGGAGAAACAACCGGAGTCT 720
Db 661 ACCATGAAGATCTTTTGGAGAGCACTACAGAGAGCGAGTGGGAGAAACAACCGGAGTCT 720
QY 721 TCTTTAAATTAAGTTCTATCCCGAGGAGGTTTATCACCTCAGCAGAGCTTCAGGTTT 780
Db 721 TCTTTAAATTAAGTTCTATCCCGAGGAGGTTTATCACCTCAGCAGAGCTTCAGGTTT 780
QY 781 TCCGAGAACAGATGCAAGATGCTTTAGGAAACAATAGCAGTTTCCATCACCGAATTAATA 840
Db 781 TCCGAGAACAGATGCAAGATGCTTTAGGAAACAATAGCAGTTTCCATCACCGAATTAATA 840
QY 841 TTTATGAATCATAAACCTGCAACAGCCAACTCGAATTCGCCGAGCAGACTTTTGG 900
Db 841 TTTATGAATCATAAACCTGCAACAGCCAACTCGAATTCGCCGAGCAGACTTTTGG 900
QY 901 ACACAGAGTTGTGAATCAGATGCAAGAGTGGGAAAGTTTGTATGTCACCCCGCTG 960
Db 901 ACACAGAGTTGTGAATCAGATGCAAGAGTGGGAAAGTTTGTATGTCACCCCGCTG 960
QY 961 TGATCGGTGGAGTGCACAGGAGCAGCCCAACCATGGATTCTGTGGTGGAGTGGCCACT 1020
Db 961 TGATCGGTGGAGTGCACAGGAGCAGCCCAACCATGGATTCTGTGGTGGAGTGGCCACT 1020
QY 1021 TGGAGAGAAACAAGGTGTCGAGAGACATGTTAGGATAGCAGGTCTTTGCACCAAG 1080
Db 1021 TGGAGAGAAACAAGGTGTCGAGAGACATGTTAGGATAGCAGGTCTTTGCACCAAG 1080
QY 1081 ATGAACACAGCTGGTGCACAGATAAGGCCATTGCTAGTAATCTTTGSCCATGATGGAAG 1140
Db 1081 ATGAACACAGCTGGTGCACAGATAAGGCCATTGCTAGTAATCTTTGSCCATGATGGAAG 1140
QY 1141 GGCATCTCTCCACAAAAGAGAAAAACGTCAGGCCAAAACAACAGACGCGGAAACGCTTTA 1200

Db 1141 GGCACTCCTCCACAAAGAGAAAAAGTCAAGCCAAACACAAACAGCGGAAACGCCTTA 1200
Qy 1201 AGTCAGCTGTAAGAGACACACCTTTGTACGTGGAGCTTCAGTGACGTGGGGTGGAAAGACT 1260
Db 1201 AGTCAGCTGTAAGAGACACACCTTTGTACGTGGAGCTTCAGTGACGTGGGGTGGAAAGACT 1260
Qy 1261 GGATTGTGGCTCCCGGGGTATCAGCGCTTTTACTGCGACGGAGAAATGCCCTTTTCTC 1320
Db 1261 GGATTGTGGCTCCCGGGGTATCAGCGCTTTTACTGCGACGGAGAAATGCCCTTTTCTC 1320
Qy 1321 TGGCTGATCACTGAACCTCAATCATGATCCATTTGTTGACAGCTTGGTCAACTCTGTTA 1380
Db 1321 TGGCTGATCACTGAACCTCAATCATGATCCATTTGTTGACAGCTTGGTCAACTCTGTTA 1380
Qy 1381 ACTCTAAGATTCCTAAGGCATGCTGTGCCGACAGAACTCAGTGCTATCTCGATGCTGT 1440
Db 1381 ACTCTAAGATTCCTAAGGCATGCTGTGCCGACAGAACTCAGTGCTATCTCGATGCTGT 1440
Qy 1441 ACCTTGACGAGAAATGAAAGGTTGTATTAAAGAACTATCAGGACATGTTGTGGAGGTT 1500
Db 1441 ACCTTGACGAGAAATGAAAGGTTGTATTAAAGAACTATCAGGACATGTTGTGGAGGTT 1500
Qy 1501 GTGGGTGTGCTAGTACAGCAAAATTTAAATACATAAATATATATATA 1547
Db 1501 GTGGGTGTGCTAGTACAGCAAAATTTAAATACATAAATATATATATA 1547

RESULT 10
ID ABT17041
XX ABT17041 standard; DNA; 1547 BP.
XX
AC ABT17041;
XX
DT 03-APR-2003 (first entry)
XX
DE Human MP21 gene BMP2 SEQ ID No 15.
XX
KW Cytostatic; P21 pathway modulating agent; cancer; angiogenic; apoptotic;
KW cell proliferation disorder; MP21; gene; ds.
XX
OS Homo sapiens.
XX
FN WO2003006990-A1.
XX
PD 23-JAN-2003.
XX
PF 10-JUL-2002; 2002WO-US021549.
XX
PR 12-JUL-2001; 2001US-0305017P.
PR 10-OCT-2001; 2001US-0328491P.
PR 15-FEB-2002; 2002US-0357452P.
XX
PA (EXEL-) EXELIXIS INC.
XX
PI Friedman L, Plowman GD, Belvin M, Li D, Funke RP;
XX
DR WPI; 2003-221779/21.
DR P-PSDB; ABJ19767.
XX
PT Identifying candidate p21 pathway modulator, by contacting an assay
PT system having modifiers of p21 polypeptide or gene with a test agent to
PT provide a reference activity in system and detecting test agent-biased
PT activity.
XX
PS Example; Page 86-87; 199pp; English.
XX
CC The invention relates to a novel method for identifying a candidate p21
CC pathway modulating agent. The novel method comprises contacting an assay
CC system, comprising a purified MP21 polypeptide (modifier of p21) or
CC nucleic acid, with a test agent under conditions, so that but for the
CC presence of a test agent, the assay system provides a reference activity
CC and detection of test agent-biased activity of the assay system. The
CC novel method of the invention is useful for identifying a candidate p21

CC pathway modulating agent. The invention also includes a method for
CC modulating the p21 pathway of a cell, and a method for diagnosing a
CC disease e.g. cancer in a patient. The identified modulators are useful in
CC diagnosis, therapy and pharmaceutical development. The modulators are
CC useful in a variety of diagnostic and therapeutic applications including
CC angiogenic, apoptotic and cell proliferation disorders. This
CC polynucleotide sequence represents a gene encoding an MP21 protein of the
XX invention
SQ Sequence 1547 BP; 377 A; 423 C; 410 G; 337 T; 0 U; 0 Other;
Query Match 100.0%; Score 1547; DB 10; Length 1547;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1547; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GGGGACTTCTTGAACCTTGCAGGGGAGAAATACTTGGCACCACCCACTTTTGGCGCGGTGCTT 60
Db 1 GGGGACTTCTTGAACCTTGCAGGGGAGAAATACTTGGCACCACCCACTTTTGGCGCGGTGCTT 60
Qy 61 TGGCCGACGGAGCGCTTCTGCGCATCTCCGAGCCGCCACCGCCCTTCCACTTCTCGGCT 120
Db 61 TGGCCGACGGAGCGCTTCTGCGCATCTCCGAGCCGCCACCGCCCTTCCACTTCTCGGCT 120
Qy 121 TGGCCGACACTGAGACGCTGTTCCAGCGTGAAAAGAGAGACTCGCGGCGCGCACCCGG 180
Db 121 TGGCCGACACTGAGACGCTGTTCCAGCGTGAAAAGAGAGACTCGCGGCGCGCACCCGG 180
Qy 181 GAGAAAGGAGGAGCAAAAGAAACGGAACGCAATTCGGTCTCTTGGCCACAGGTCCTTTGACC 240
Db 181 GAGAAAGGAGGAGCAAAAGAAACGGAACGCAATTCGGTCTCTTGGCCACAGGTCCTTTGACC 240
Qy 241 AGAGTTTTTCATGTGACGCTCTTTCAATGGAGCTGTCCCGCGTGTCTTTAGACGGA 300
Db 241 AGAGTTTTTCATGTGACGCTCTTTCAATGGAGCTGTCCCGCGTGTCTTTAGACGGA 300
Qy 301 CTGGGTCCTCTAAAGGTTCGACCATGTGGCCGCGACCCCGTGTCTTCTAGCGTTGCTGC 360
Db 301 CTGGGTCCTCTAAAGGTTCGACCATGTGGCCGCGACCCCGTGTCTTCTAGCGTTGCTGC 360
Qy 361 TTCCCCAGGTCCTCTCTGGGCGGCGGCTGCGCTCGTTCGGAGCTGCGGCGCGAGAGT 420
Db 361 TTCCCCAGGTCCTCTCTGGGCGGCGGCTGCGCTCGTTCGGAGCTGCGGCGCGAGAGT 420
Qy 421 TCGCGGCGGCTGCTGCGGCGGCGGCTCATCCAGCCCTCTGAGAGCTCTGAGCGGAGT 480
Db 421 TCGCGGCGGCTGCTGCGGCGGCGGCTCATCCAGCCCTCTGAGAGCTCTGAGCGGAGT 480
Qy 481 TCGAGTTGCGGCTGCTCAGCATGTTTCGGGCTGAAAACAGAGACCCACCCAGCAGGAGCG 540
Db 481 TCGAGTTGCGGCTGCTCAGCATGTTTCGGGCTGAAAACAGAGACCCACCCAGCAGGAGCG 540
Qy 541 CCGTGGTGCCCGCTACATGCTAGACCTGTATCGAGGCACTCAGGTGAGCGCGGCTCAC 600
Db 541 CCGTGGTGCCCGCTACATGCTAGACCTGTATCGAGGCACTCAGGTGAGCGCGGCTCAC 600
Qy 601 CCGCCCCAGACACCGGTTGGAGAGGCGAGCCAGCCAGCCAACTGTGCGGAGCTTCC 660
Db 601 CCGCCCCAGACACCGGTTGGAGAGGCGAGCCAGCCAGCCAACTGTGCGGAGCTTCC 660
Qy 661 ACCATGAAGAAATCTTTGGAAGAACTACAGAAACAGAGTGGGAAAACAAACCGAGATTCT 720
Db 661 ACCATGAAGAAATCTTTGGAAGAACTACAGAAACAGAGTGGGAAAACAAACCGAGATTCT 720
Qy 721 TCTTTAAATTTAAGTTCTATCCCCACGGAGGAGTTTATCCTCAGCAGAGCTTCAGGTTT 780
Db 721 TCTTTAAATTTAAGTTCTATCCCCACGGAGGAGTTTATCCTCAGCAGAGCTTCAGGTTT 780
Qy 781 TCCGAGACAGATCAGATGCTTTTAGGAACATAGCAGTTTCCATCACCAGATTATA 840
Db 781 TCCGAGACAGATCAGATGCTTTTAGGAACATAGCAGTTTCCATCACCAGATTATA 840
Qy 841 TTTATGAATCATAAAAACCTGCAACAGCCAACTCGAAATTCGCCGTGACACAGACTTTGG 900
Db 841 TTTATGAATCATAAAAACCTGCAACAGCCAACTCGAAATTCGCCGTGACACAGACTTTGG 900

Db 841 TTTATGAATCATAAACCTGCAACAGCCAACTCGAAATTCCTCCGTGACCACTTTTGG 900
Qy 901 ACACAGGTTGGTGAATCAGATGCAAGCAGGTGGGAAAGTTTTCATGTACACCCCGCTG 960
Db 901 ACACAGGTTGGTGAATCAGATGCAAGCAGGTGGGAAAGTTTTCATGTACACCCCGCTG 960
Qy 961 TGATCGGTGGACTGCACAGGACACGCCAACCATGATGCTGCTGGAAGTGGCCACT 1020
Db 961 TGATCGGTGGACTGCACAGGACACGCCAACCATGATGCTGCTGGAAGTGGCCACT 1020
Qy 1021 TGGAGGAGAAACAAGGTCTCTCAAGAGACATGTTAGGATAGCAGGTCTTTGCAACAG 1080
Db 1021 TGGAGGAGAAACAAGGTCTCTCAAGAGACATGTTAGGATAGCAGGTCTTTGCAACAG 1080
Qy 1081 ATGAACACAGCTGGTGCACAGATAAGGCCATTCTAGTAACTTTTGGCCATGATGAAAG 1140
Db 1081 ATGAACACAGCTGGTGCACAGATAAGGCCATTCTAGTAACTTTTGGCCATGATGAAAG 1140
Qy 1141 GGCATCTCTTCCACAAAGAGAAAAACGTCAGCCAAAACACAAACAGCGGAAACGCTTA 1200
Db 1141 GGCATCTCTTCCACAAAGAGAAAAACGTCAGCCAAAACACAAACAGCGGAAACGCTTA 1200
Qy 1201 AGTCAGCTGTAAGAGACACCTTTGTAGTGGACTTCAGTGACGTGGGTGGAATGACT 1260
Db 1201 AGTCAGCTGTAAGAGACACCTTTGTAGTGGACTTCAGTGACGTGGGTGGAATGACT 1260
Qy 1261 GGATTTGGTCTCCCGGGGTATACGCTTTTACTGCCACGGGAATGCCCTTTTCTC 1320
Db 1261 GGATTTGGTCTCCCGGGGTATACGCTTTTACTGCCACGGGAATGCCCTTTTCTC 1320
Qy 1321 TGGCTGATCATCTGAACCTCACTAATCATGCCATTGTTTCAGACGTTGGTCAACTCTGTTA 1380
Db 1321 TGGCTGATCATCTGAACCTCACTAATCATGCCATTGTTTCAGACGTTGGTCAACTCTGTTA 1380
Qy 1381 ACTCTAAGATTCCTAAGGCATGCTGTGTCGCCAGACAACTAGTCTATCTGATGCTGT 1440
Db 1381 ACTCTAAGATTCCTAAGGCATGCTGTGTCGCCAGACAACTAGTCTATCTGATGCTGT 1440
Qy 1441 ACCTTGACGAGAAATGAAAGGTTGTTAAAGAACTATCAGACATGTTGGAGGGTT 1500
Db 1441 ACCTTGACGAGAAATGAAAGGTTGTTAAAGAACTATCAGACATGTTGGAGGGTT 1500
Qy 1501 GTGGGTGTCGTAGTACAGCAAAATTAATACATAAATATATATATA 1547
Db 1501 GTGGGTGTCGTAGTACAGCAAAATTAATACATAAATATATATATA 1547

RESULT 11
ID ADL13510 standard; DNA; 1547 BP.
XX AC ADL13510;
XX
XX
XX 06-MAY-2004 (first entry)
XX Osteoarthritis-associated polymorphic nucleotide #42.
XX ds; gene; osteopathic; antiinflammatory; antiarthritic; gene therapy;
KW joint space narrowing; osteophyte development; joint pain;
KW osteoarthritis; SNP; single nucleotide polymorphism.
XX Homo sapiens.
XX
XX WO2003054166-A2.
XX
XX 03-JUL-2003.
XX
XX 19-DEC-2002; 2002WO-US041225.
XX
XX 20-DEC-2001; 2001US-0342603P.
XX (INCY-) INCYTE GENOMICS INC.
XX

PI Jones KA, Schafer A;
XX WPI; 2003-559141/52.
XX
XX Determining susceptibility of an individual to joint space narrowing,
PT osteophyte development and/or joint pain comprises identifying whether
PT the individual has at least one polymorphism in a polynucleotide encoding
PT a protein.
XX
XX Disclosure; SEQ ID NO 42; 297pp; English.
XX
XX The invention relates to a method of determining susceptibility of an
CC individual to joint space narrowing and/or osteophyte development and/or
CC joint pain comprising identifying whether the individual has at least one
CC polymorphism in a polynucleotide encoding at least one of the protein
CC listed in the specification. The methods, composition and agent are
CC useful for modulating the susceptibility of an individual to joint space
CC narrowing and/or osteophyte development and/or joint pain that is
CC associated with a disease, preferably osteoarthritis. The cell line and
CC the non-human animal are useful for screening for an agent for diagnosing
CC an individual having susceptibility to joint space narrowing and/or
CC osteophyte development and/or joint pain. This sequence corresponds to
CC the polynucleotide encoding a protein listed in the specification. (Note:
CC The sequence data for this patent did not form part of the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences).
XX
SQ Sequence 1547 BP; 377 A; 423 C; 410 G; 337 T; 0 U; 0 Other;
Query Match 100.0%; Score 1547; DB 10; Length 1547;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1547; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GGGGACTCTTTGAACCTTGCAGGAGAAATACTTGGCACCCCACTTTGGCGGGTGCCTT 60
Db 1 GGGGACTCTTTGAACCTTGCAGGAGAAATACTTGGCACCCCACTTTGGCGGGTGCCTT 60
Qy 61 TGCCCCAGCGAGCTGCTTCCCATCTCCAGAGCCCAACCCCTCCACCTCCCTGGGCT 120
Db 61 TGCCCCAGCGAGCTGCTTCCCATCTCCAGAGCCCAACCCCTCCACCTCCCTGGGCT 120
Qy 121 TGCCCCGACACTGAGACGCTGTTCCAGCGTGAAAGAGAGACTGCGCGCGGACCCGG 180
Db 121 TGCCCCGACACTGAGACGCTGTTCCAGCGTGAAAGAGAGACTGCGCGCGGACCCGG 180
Qy 181 GAGAGGAGGAGGCAAGAAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 240
Db 181 GAGAGGAGGAGGCAAGAAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 240
Qy 241 AGAGTTTTTCCATGTGACGCTCTTTCAATGAGAGTGTCCTCCCGCGTGTCTTAGACCGA 300
Db 241 AGAGTTTTTCCATGTGACGCTCTTTCAATGAGAGTGTCCTCCCGCGTGTCTTAGACCGA 300
Qy 301 CTGCGGTCTCTAAAGGTCGACCATGTGTGGCGGACCCGCTGTCTTAGCGTTGCTGC 360
Db 301 CTGCGGTCTCTAAAGGTCGACCATGTGTGGCGGACCCGCTGTCTTAGCGTTGCTGC 360
Qy 361 TTCCCCAGGTCTCTTGGCGGCGGCTGCGCTGTTCGGAGCTGGGCGGCGCAGAGT 420
Db 361 TTCCCCAGGTCTCTTGGCGGCGGCTGCGCTGTTCGGAGCTGGGCGGCGCAGAGT 420
Qy 421 TCGGGGCGGCTGCTGCGGGCGCCCTCATCTCCAGCCCTCTGACAGAGTCTTAGCGAGT 480
Db 421 TCGGGGCGGCTGCTGCGGGCGCCCTCATCTCCAGCCCTCTGACAGAGTCTTAGCGAGT 480
Qy 481 TCGAGTTGCGGCTGCTCAGCATGTTTGGCCCTGAAACAGAGACCCACCCCGGAGCG 540
Db 481 TCGAGTTGCGGCTGCTCAGCATGTTTGGCCCTGAAACAGAGACCCACCCCGGAGCG 540
Qy 541 CCGTGGTCCCGCTTACATGCTAGACCTGTATCGAGGCACTCAGGTGAGCGGGCTCAC 600
Db 541 CCGTGGTCCCGCTTACATGCTAGACCTGTATCGAGGCACTCAGGTGAGCGGGCTCAC 600

[illegible]

RESULT 12

ADN38841

ADN38841
ID ADN38841 standard; cDNA; 1547 BP.

AC ADN38841;

XX
XX

DT 17-JUN-2004 (first entry)

XX

Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:159.

Human; differential expression; cancer; angiogenic disorder; fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis; inflammatory disease; autoimmune disease; retinal neovascularisation syndrome; scarring; uterine fibroid; detection; diagnosis; prognosis; drug screening; drug targeting; wound healing; contraception; cytostatic; cardiant; immunomodulatory; vulnery; gene therapy; vaccine; gene; ss.

Homo sapiens.

WO2003042661-A2.

22-MAY-2003.

13-NOV-2002; 2002WO-US036810.

13-NOV-2001; 2001US-0350666P.

21-NOV-2001; 2001US-0332464P.

29-NOV-2001; 2001US-0334393P.

03-DEC-2001; 2001US-0335394P.

14-DEC-2001; 2001US-0340376P.

08-JAN-2002; 2002US-0347211P.

10-JAN-2002; 2002US-0347349P.

08-FEB-2002; 2002US-0355250P.

13-FEB-2002; 2002US-0356714P.

20-FEB-2002; 2002US-0359077P.

29-MAR-2002; 2002US-0368809P.

04-APR-2002; 2002US-0370110P.
12-APR-2002; 2002US-0370246P

12-APR-2002; 2002US-0372246P.
05-JUN-2002: 2002US-0386614P

05-JUN-2002; 2002US-0386614P.
16-JUL-2002; 2002US-0396839P

16-JUL-2002; 2002US-0396839P.
22-JUL-2002; 2002US-0397775P.

22-JUL-2002; 2002US-039775P.
22-JUL-2002; 2002US-0397845P.

ZZ-JUL-2002; 2002US-0397845P;
09-SEP-2002; 2002US-0409450P;

09-SEP-2002; 200205-0409450P:

(EOSB-) EOS BIOTECHNOLOGY INC.

Afar D, Aziz N, Ginsburg WM, Gish KC, Glynn R, Hevezi PA;

Mack DH, Murray R, Watson SR, Wilson KE, Zlotnik A; Alai D, Aziz N, Gumburg WM, Giblin RC, Glynn K, H

WPI; 2003-468649/44.

P-PSDB; ADN38842.

Determining the presence or absence of a pathological cell in a patient, useful for diagnosing, prognosing or treating cancer, comprises detecting a nucleic acid in a biological sample.

Claim 8; SEQ ID NO 159; 1385pp; English.

The invention relates to nucleic acids and proteins (ADN39683-ADN40064) whose expression is upregulated or downregulated in specific cancers or other diseases such as angiogenic or fibrotic disorders, and to methods of determining the presence or absence of a pathological cell in a patient by detecting a nucleic acid at least 80% identical to those of the invention or by detecting a polypeptide of the invention. The invention also relates to expression vectors and host cells comprising a nucleic acid of the invention; antibodies which specifically bind a polypeptide of the invention; use of such antibodies for drug targeting; and methods of screening for modulators of activity or expression of the polypeptides and nucleic acids. The nucleic acids, polypeptides, antibodies and methods are useful for diagnosing, prognosing and treating cancer and other conditions such as psoriasis, ischaemia, heart disease, atherosclerosis, inflammatory diseases, autoimmune diseases, retinal neovascularisation syndromes, scarring and uterine fibroids. They may also be useful in wound healing and in contraception. The present sequence represents a nucleic acid sequence of the invention.

Sequence 1547 BP: 377 A; 423 C; 410 G; 337 T; 0 U; 0 Other;

Query Match

| | | | | | | | |
|-----------------------|---------|-------|--------|----|-----|--------|-------|
| Query Match | 100.0%; | Score | 1547; | DB | 11; | Length | 1547; |
| Best Local Similarity | 100.0%; | Pred. | No. 0; | | | | |

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
84

| Matches 1547; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | | | |
|---|------|--|------|
| Qy | 1 | GGGGAATCTTAACTTCAGGAGAAATACTTGGCGCACCCACCTTGGCGGCGGCTT | 60 |
| Db | 1 | GGGGAATCTTAACTTCAGGAGAAATACTTGGCGCACCCACCTTGGCGGCGGCTT | 60 |
| Qy | 61 | TGCCCCCAGCGAGCTGCTTCCCATCTCCAGAGCCCCACCGCCCTCCACCTCTCGGCT | 120 |
| Db | 61 | TGCCCCCAGCGAGCTGCTTCCCATCTCCAGAGCCCCACCGCCCTCCACCTCTCGGCT | 120 |
| Qy | 121 | TGCCCGACACTGAGACGCTGTTCCAGCGTGAAGAGAGAGACTGCGCGCGGCAACCGG | 180 |
| Db | 121 | TGCCCGACACTGAGACGCTGTTCCAGCGTGAAGAGAGAGACTGCGCGCGGCAACCGG | 180 |
| Qy | 181 | GAGAGGAGGCGCAAGAAAGGACGACACTCGCTCTTGCSCCAGGTCCTTTGACC | 240 |
| Db | 181 | GAGAGGAGGCGCAAGAAAGGACGACACTCGCTCTTGCSCCAGGTCCTTTGACC | 240 |
| Qy | 241 | AGAGTTTTTCCATGTGGAGCGCTCTTTCAATGACCGTGTCCCGCGCTGCTTTAGACGGA | 300 |
| Db | 241 | AGAGTTTTTCCATGTGGAGCGCTCTTTCAATGACCGTGTCCCGCGCTGCTTTAGACGGA | 300 |
| Qy | 301 | CTGCGGTCTCTAAAGTTCGACATGTGGCGCGGACCGCTGTCTTAGCGTTGCTGC | 360 |
| Db | 301 | CTGCGGTCTCTAAAGTTCGACATGTGGCGCGGACCGCTGTCTTAGCGTTGCTGC | 360 |
| Qy | 361 | TTCCCCAGGTCTCTTGGCGGCGGCTGGCTGTTCGAGACTGGCGCGCAGGAAGT | 420 |
| Db | 361 | TTCCCCAGGTCTCTTGGCGGCGGCTGGCTGTTCGAGACTGGCGCGCAGGAAGT | 420 |
| Qy | 421 | TCGCGGCGGCTGTTCGCGGCGGCTGTTCGAGACTGGCGCGCAGGAAGT | 480 |
| Db | 421 | TCGCGGCGGCTGTTCGCGGCGGCTGTTCGAGACTGGCGCGCAGGAAGT | 480 |
| Qy | 481 | TCGAGTTGGCGTCTCAGCATGTTGGCTGAAACAGAGACCCACCCAGCAGGAG | 540 |
| Db | 481 | TCGAGTTGGCGTCTCAGCATGTTGGCTGAAACAGAGACCCACCCAGCAGGAG | 540 |
| Qy | 541 | CGGTGTGCGGCTTACATGCTAGACCTGTATCGCAGGCACTCAGGTGAGCGGCTCAC | 600 |
| Db | 541 | CGGTGTGCGGCTTACATGCTAGACCTGTATCGCAGGCACTCAGGTGAGCGGCTCAC | 600 |
| Qy | 601 | CGGCCCCAGACACCGTTGGAGAGGCGCAGCGGCAACACTGTGCGCAGCTTCC | 660 |
| Db | 601 | CGGCCCCAGACACCGTTGGAGAGGCGCAGCGGCAACACTGTGCGCAGCTTCC | 660 |
| Qy | 661 | ACCATGAAGAATCTTTTGAAGAATACTACAGAAACGAGTGGGAAACAAACCCGAGATTCT | 720 |
| Db | 661 | ACCATGAAGAATCTTTTGAAGAATACTACAGAAACGAGTGGGAAACAAACCCGAGATTCT | 720 |
| Qy | 721 | TCCTTTAAATTAAGTTCTATCCCAAGGAGTTTATCCTCAGCAGAGCTTCAGGTTT | 780 |
| Db | 721 | TCCTTTAAATTAAGTTCTATCCCAAGGAGTTTATCCTCAGCAGAGCTTCAGGTTT | 780 |
| Qy | 781 | TCGAGAACAGATGCAAGATGCTTTAGGAAACAATAGCAGTTTCCATACCGAAATTAATA | 840 |
| Db | 781 | TCGAGAACAGATGCAAGATGCTTTAGGAAACAATAGCAGTTTCCATACCGAAATTAATA | 840 |
| Qy | 841 | TTTATGAATCATAAACCTGCAACAGCAACTCGAAATTCGCCGTGACAGACTTTTGG | 900 |
| Db | 841 | TTTATGAATCATAAACCTGCAACAGCAACTCGAAATTCGCCGTGACAGACTTTTGG | 900 |
| Qy | 901 | ACACAGGTGTGTAATCAAGATGCAAGCAGGTGGGAAAGTTTGTATGTACCCCGCTG | 960 |
| Db | 901 | ACACAGGTGTGTAATCAAGATGCAAGCAGGTGGGAAAGTTTGTATGTACCCCGCTG | 960 |
| Qy | 961 | TGATCGGTGGACTGACAGGAGCACGCCAACCATGTATTCGTGTGGAAGTGGCCACT | 1020 |
| Db | 961 | TGATCGGTGGACTGACAGGAGCACGCCAACCATGTATTCGTGTGGAAGTGGCCACT | 1020 |
| Qy | 1021 | TGAGGAGAGAAACAAGGTGTCTCAAGAGACATGTTAGGATAAGCAGGTCTTTGCACCAAG | 1080 |
| Db | 1021 | TGAGGAGAGAAACAAGGTGTCTCAAGAGACATGTTAGGATAAGCAGGTCTTTGCACCAAG | 1080 |

| | | | |
|----|------|---|------|
| Qy | 1081 | ATGAACACAGCTGTGTCAAGATAAGCCATTGTAGTAACCTTTTGGCCATCATATGAAAAG | 1140 |
| Db | 1081 | ATGAACACAGCTGTGTCAAGATAAGCCATTGTAGTAACCTTTTGGCCATCATATGAAAAG | 1140 |
| Qy | 1141 | GGCATCTCTCCACAAAGAGAGAAAACGTCAGGCCAAACACAAACAGCGGAAACGCTTTA | 1200 |
| Db | 1141 | GGCATCTCTCCACAAAGAGAGAAAACGTCAGGCCAAACACAAACAGCGGAAACGCTTTA | 1200 |
| Qy | 1201 | AGTCAGCTGTAAAGAGACACCTTTGTACGTGGACTTCAGTGACGTGGGTGGATGACT | 1260 |
| Db | 1201 | AGTCAGCTGTAAAGAGACACCTTTGTACGTGGACTTCAGTGACGTGGGTGGATGACT | 1260 |
| Qy | 1261 | GGATTTGTGGCTCCCGCGGGTATCAGCGCTTTTACTGCGCAGCGGAAATGCCCTTTTCCTC | 1320 |
| Db | 1261 | GGATTTGTGGCTCCCGCGGGTATCAGCGCTTTTACTGCGCAGCGGAAATGCCCTTTTCCTC | 1320 |
| Qy | 1321 | TGGCTGATCATCTGAATCCACTAATCATGCACTTTGTCAGCGTTGTCGTAATCTCTGTTA | 1380 |
| Db | 1321 | TGGCTGATCATCTGAATCCACTAATCATGCACTTTGTCAGCGTTGTCGTAATCTCTGTTA | 1380 |
| Qy | 1381 | ACTCTAAGATTCCTAAGGCATGCTGTGTCGCGACAGAACTCAGTGCTATCTCGATGCTGT | 1440 |
| Db | 1381 | ACTCTAAGATTCCTAAGGCATGCTGTGTCGCGACAGAACTCAGTGCTATCTCGATGCTGT | 1440 |
| Qy | 1441 | ACCTTTGACGAGAAATGAAAAGGTTGTATTAAGAACTATCAGGACATGTTGTGGAGGTT | 1500 |
| Db | 1441 | ACCTTTGACGAGAAATGAAAAGGTTGTATTAAGAACTATCAGGACATGTTGTGGAGGTT | 1500 |
| Qy | 1501 | GTGGGTGTGCTGTAGTACAGCAAAATTAATACATAAATATATATATA 1547 | |
| Db | 1501 | GTGGGTGTGCTGTAGTACAGCAAAATTAATACATAAATATATATATA 1547 | |

RESULT 13

ADH11558

ID ADH11558 standard; cDNA; 1547 BP.

XX AC ADH11558;

XX DT 11-MAR-2004 (first entry)

XX DE Human bone morphogenic protein (BMP) polynucleotide #7.

XX KW Human; bone morphogenic protein; BMP; gene; ss; weight gain; appetite suppression; fat mass reduction; cell sensitivity; glucose uptake; diabetes; insulin resistance; hyperglycaemia; hypertension; coronary artery disease; renal failure; neuropathy; metabolic disorder; glucose metabolism disorder; endocrine disorder; obesity; weight loss; liver disorder; cartilage growth disorder; bone growth disorder; inflammation; aberrant cell growth; liver cancer.

XX OS Homo sapiens.

XX PN US2003224501-A1.

XX PD 04-DEC-2003.

XX PF 14-FEB-2003; 2003US-00366345.

XX PR 17-MAR-2000; 2000US-0190067P.

XX PR 16-MAR-2001; 2001US-00809269.

XX PR 23-MAR-2001; 2001WO-US009229.

XX PR 17-JAN-2002; 2002US-0348621P.

XX PR 22-JAN-2002; 2002US-0349356P.

XX PR 28-JAN-2002; 2002US-0351520P.

XX PR 06-FEB-2002; 2002US-0354265P.

XX PR 15-FEB-2002; 2002US-0356749P.

XX PR 16-JAN-2003; 2003US-00345236.

XX (YOUNG) YOUNG P E.

XX (RUBEN) RUBEN S M.

PI Young PE, Ruben SM;
XX MPI; 2004-022075/02.
DR P-PSDB; ADH11579.
XX
PT New bone morphogenic protein polypeptides and polynucleotides, useful for
PT diagnosing, preventing, treating or ameliorating a medical condition,
PT e.g. diabetes, dyslipidemia, hypertension, coronary artery disease or
PT neuropathy.
XX
PS Example 1; SEQ ID NO 10; 224pp; English.
XX
CC The invention relates to human bone morphogenic protein (BMP)
CC polypeptides and the polynucleotides encoding them. The invention also
CC relates to a method for limiting weight gain, suppressing appetite or
CC reducing fat mass, comprising administering to a mammalian subject a
CC therapeutic amount of a BMP polypeptide, and a method for increasing the
CC sensitivity of a cell to insulin or increasing glucose uptake by a cell,
CC comprising contacting the cell with a BMP polypeptide. The BMP
CC polypeptides and polynucleotides are useful for diagnosing a pathological
CC condition or a susceptibility to a pathological condition in a subject or
CC for preventing, treating or ameliorating a medical condition, e.g.
CC diabetes, insulin resistance, hyperglycaemia, hypertension, coronary
CC artery disease, renal failure, neuropathy, metabolic disorders, glucose
CC metabolism disorder, endocrine disorders, obesity, weight loss, liver
CC disorders, cartilage and bone growth disorders, inflammation or aberrant
CC cell growth such as liver cancer. The BMP polypeptides and
CC polynucleotides are also useful for regulating nutritional partitioning,
CC limiting weight gain, suppressing appetite, reducing fat mass, increasing
CC the sensitivity of a cell to insulin or increasing glucose uptake by a
CC cell. This sequence represents a human BMP polynucleotide of the
CC invention.
XX
SQ Sequence 1547 BP; 377 A; 423 C; 410 G; 337 T; 0 U; 0 Other;
Query Match 100.0%; Score 1547; DB 12; Length 1547;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1547; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGGACTTCTTGAATTCGAGGAGATAAATCTGGGCAACCCACTTTGGCGCGGTGCCTT 60
DB 1 GGGGACTTCTTGAATTCGAGGAGATAAATCTGGGCAACCCACTTTGGCGCGGTGCCTT 60
QY 61 TGCCCCAGCGAGCTGCTTCGCCATCTCCGAGCCGCCACCGCCCTCCACTCTCTCGGCT 120
DB 61 TGCCCCAGCGAGCTGCTTCGCCATCTCCGAGCCGCCACCGCCCTCCACTCTCTCGGCT 120
QY 121 TGCCCCGACACTGAGACGCTGTTCCAGCGTGAAAGAGAGACTGCGCGCGGCAACCGG 180
DB 121 TGCCCCGACACTGAGACGCTGTTCCAGCGTGAAAGAGAGACTGCGCGCGGCAACCGG 180
QY 181 GAGAGGAGGAGGCAAGAAAGGAAACGGAATTCGGTCTTGGCCGACGTCCTTTGACC 240
DB 181 GAGAGGAGGAGGCAAGAAAGGAAACGGAATTCGGTCTTGGCCGACGTCCTTTGACC 240
QY 241 AGAGTTTTTCCATGTGACGCTCTTCAATCGAGCTGTCGCCGCTGCTCTTAGACGGA 300
DB 241 AGAGTTTTTCCATGTGACGCTCTTCAATCGAGCTGTCGCCGCTGCTCTTAGACGGA 300
QY 301 CTGGGGTCTCCTAAAGGTGCAACATGTGTGGCGGGGACCCCGTCTTCTAGCGTTGCTGC 360
DB 301 CTGGGGTCTCCTAAAGGTGCAACATGTGTGGCGGGGACCCCGTCTTCTAGCGTTGCTGC 360
QY 361 TTCCCGAGGCTCTCTTGGCGCGCGGCTGCGCTGCTGTTCCGAGGTGGCGCGGAGAGT 420
DB 361 TTCCCGAGGCTCTCTTGGCGCGCGGCTGCGCTGCTGTTCCGAGGTGGCGCGGAGAGT 420
QY 421 TCGGGGGGGCTGCTGCGGGCGCCCTCATCCAGCCCTCTGACGAGTCTGACGCGAGT 480
DB 421 TCGGGGGGGCTGCTGCGGGCGCCCTCATCCAGCCCTCTGACGAGTCTGACGCGAGT 480
QY 481 TCGAGTTGCGGCTGCTCAGCATGTTTCGGCTTGAACACAGAGACCCACCCGAGCGGACG 540
DB 481 TCGAGTTGCGGCTGCTCAGCATGTTTCGGCTTGAACACAGAGACCCACCCGAGCGGACG 540

DB 481 TCGAGTTGCGGCTGCTCAGCATGTTTCGGCTTGAACACAGAGACCCACCCGAGCGGACG 540
QY 541 CCGTGGTGGCCCCCTCATAGCTAGACCTGTATCGCAGGCACTCAGGTCAGCCGGGCTCAC 600
DB 541 CCGTGGTGGCCCCCTCATAGCTAGACCTGTATCGCAGGCACTCAGGTCAGCCGGGCTCAC 600
QY 601 CCGCCCCAGACCAACCGGTGTGGAGGGCAGCAGCCGAGCCAAACACATGTGGCAGCTTCC 660
DB 601 CCGCCCCAGACCAACCGGTGTGGAGGGCAGCAGCCGAGCCAAACACATGTGGCAGCTTCC 660
QY 661 ACCATGAAGAATCTTTGGAAAGAACTACCAAGAACGAGTGGGAAAACAAACCGGAGATTCT 720
DB 661 ACCATGAAGAATCTTTGGAAAGAACTACCAAGAACGAGTGGGAAAACAAACCGGAGATTCT 720
QY 721 TCTTTAATTTAAGTTCTATCCCAACGAGGAGTTTATCACTCAGCAGAGCTTCAGGTTT 780
DB 721 TCTTTAATTTAAGTTCTATCCCAACGAGGAGTTTATCACTCAGCAGAGCTTCAGGTTT 780
QY 781 TCCGAGAACAGATGCAAGATGCTTTAGGAAACAAATAGCAGTTTCCATCACCAGAAATTAATA 840
DB 781 TCCGAGAACAGATGCAAGATGCTTTAGGAAACAAATAGCAGTTTCCATCACCAGAAATTAATA 840
QY 841 TTTATGAAATCATAAAACTGCAACAGCCAACTCGAAATTCGCCGTGACCAAGCTTTGG 900
DB 841 TTTATGAAATCATAAAACTGCAACAGCCAACTCGAAATTCGCCGTGACCAAGCTTTGG 900
QY 901 ACACGAGTTGGTGAATCAGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAG 960
DB 901 ACACGAGTTGGTGAATCAGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAG 960
QY 961 TGATCGCGTGCAGCTGCAAGGACACCGCAACCATGATTCGTTGGTGGAGTGGCCCACT 1020
DB 961 TGATCGCGTGCAGCTGCAAGGACACCGCAACCATGATTCGTTGGTGGAGTGGCCCACT 1020
QY 1021 TGGAGGAGAAACAAAGTGTCTCCAAGAGACATGTTAGGTAAGCAGGTCCTTTGACCAAG 1080
DB 1021 TGGAGGAGAAACAAAGTGTCTCCAAGAGACATGTTAGGTAAGCAGGTCCTTTGACCAAG 1080
QY 1081 ATGNAACACAGCTGGTCAAGATTAAGGCCATTTGCTAGTAACTTTTGGCCATGATGGAAG 1140
DB 1081 ATGNAACACAGCTGGTCAAGATTAAGGCCATTTGCTAGTAACTTTTGGCCATGATGGAAG 1140
QY 1141 GGCATCTCTCCCAAAAGAGAAAAAGCTCAAGCCAAACACAAACAGCGGAAACGCCTTA 1200
DB 1141 GGCATCTCTCCCAAAAGAGAAAAAGCTCAAGCCAAACACAAACAGCGGAAACGCCTTA 1200
QY 1201 AGTCCAGCTGTAAAGACACCCCTTTGTATCGTGGACTTCAAGTGGGTTGGAATGACT 1260
DB 1201 AGTCCAGCTGTAAAGACACCCCTTTGTATCGTGGACTTCAAGTGGGTTGGAATGACT 1260
QY 1261 GGATTTGGCTTCCCCCGGGGTATCACGCTTTTACTGCCACGAGAAATGCCCTTTCTCTC 1320
DB 1261 GGATTTGGCTTCCCCCGGGGTATCACGCTTTTACTGCCACGAGAAATGCCCTTTCTCTC 1320
QY 1321 TGGCTGATCATCTGAACTCCACTTAATCATGCTTGTTCAGACGTTGGTCAACTCTGTTA 1380
DB 1321 TGGCTGATCATCTGAACTCCACTTAATCATGCTTGTTCAGACGTTGGTCAACTCTGTTA 1380
QY 1381 ACTTAAGATTCCTTAAGGCAATGTGTGTCCCGACAGAACTCAGTGTATCTCGATGCTGT 1440
DB 1381 ACTTAAGATTCCTTAAGGCAATGTGTGTGTCCCGACAGAACTCAGTGTATCTCGATGCTGT 1440
QY 1441 ACCTTGACGAGATGAAAAGGTTGTATTAAGAACTATCAGGACATGCTTTGTGAGGGTT 1500
DB 1441 ACCTTGACGAGATGAAAAGGTTGTATTAAGAACTATCAGGACATGCTTTGTGAGGGTT 1500
QY 1501 GTGGGTGCTGCTAGTACAGCAAAATTAATAATACATAAATATATATA 1547
DB 1501 GTGGGTGCTGCTAGTACAGCAAAATTAATAATACATAAATATATATA 1547


```
Qy 301 CTGCGGTCTCTTAAGGTCGACCATGGTGGCGGACCCGGTGTCTTCTAGCGTTGCTGC 360
Db 301 CTGCGGTCTCTTAAGGTCGACCATGGTGGCGGACCCGGTGTCTTCTAGCGTTGCTGC 360
Qy 361 TTCCCCAGGTCTCTCGGGCGCGGGCTGGCTGTGTCGGAGCTGGGGCGCGAGGAAGT 420
Db 361 TTCCCCAGGTCTCTCGGGCGCGGGCTGGCTGTGTCGGAGCTGGGGCGCGAGGAAGT 420
Qy 421 TCGGGCGCGGTCGTCGGGCGCGCCCTCATCCAGCCCTCTGACGAGTCTCTGAGCGAGT 480
Db 421 TCGGGCGCGGTCGTCGGGCGCGCCCTCATCCAGCCCTCTGACGAGTCTCTGAGCGAGT 480
Qy 481 TCGAGTTGCGGTCTCAGCATGTTTCGGCTCGAATCAGAGACCCACCCCGGAGGAGC 540
Db 481 TCGAGTTGCGGTCTCAGCATGTTTCGGCTCGAATCAGAGACCCACCCCGGAGGAGC 540
Qy 541 CCGTGGTCCCGCTTACATGCTAGACCTGTATCGCAGGCACTCAGGTCAAGCGGGCTCAC 600
Db 541 CCGTGGTCCCGCTTACATGCTAGACCTGTATCGCAGGCACTCAGGTCAAGCGGGCTCAC 600
Qy 601 CGGCCCCAGACACCGGTTGGAGGGGCGAGCCGAGCCGACCACTGTGCGCAGCTTCC 660
Db 601 CGGCCCCAGACACCGGTTGGAGGGGCGAGCCGAGCCGACCACTGTGCGCAGCTTCC 660
Qy 661 ACCATGAAGAATCTTTTGAAGAACTACAGAAACGAGTGGGAAACAAACCGGAGATTCT 720
Db 661 ACCATGAAGAATCTTTTGAAGAACTACAGAAACGAGTGGGAAACAAACCGGAGATTCT 720
Qy 721 TCTTTAAATTTAAGTTCTATFCCCAACGAGGAGTTTATCACCTCAGCAGAGTTCAAGTTT 780
Db 721 TCTTTAAATTTAAGTTCTATFCCCAACGAGGAGTTTATCACCTCAGCAGAGTTTCAAGTTT 780
Qy 781 TCCGAGACAGATCAAGATGCTTTAGGAAACAATAGCAGTTCCATCACCGAATTAATA 840
Db 781 TCCGAGACAGATCAAGATGCTTTAGGAAACAATAGCAGTTCCATCACCGAATTAATA 840
Qy 841 TTTATGAATCATAAACCTGCAACAGCCAACTCGAAATTCGCCGTGACCCAGACTTTTGG 900
Db 841 TTTATGAATCATAAACCTGCAACAGCCAACTCGAAATTCGCCGTGACCCAGACTTTTGG 900
Qy 901 ACACAGGTTGGTGAATCAGAAATCAAGCAGGTGGGAAAGTTTTCATGTCAACCCCGCTG 960
Db 901 ACACAGGTTGGTGAATCAGAAATCAAGCAGGTGGGAAAGTTTTCATGTCAACCCCGCTG 960
Qy 961 TGATCGGTGGATGCAAGGACACGCCAACCATGGATTGCTGCTGGAGTGGGCCCACT 1020
Db 961 TGATCGGTGGATGCAAGGACACGCCAACCATGGATTGCTGCTGGAGTGGGCCCACT 1020
Qy 1021 TGGAGGAGAAACAAGGTGCTCCAAGAGACATGTTAGGATAAGCAGGTCTTTGCACCAAG 1080
Db 1021 TGGAGGAGAAACAAGGTGCTCCAAGAGACATGTTAGGATAAGCAGGTCTTTGCACCAAG 1080
Qy 1081 ATGAACACAGCTGGTCACAGATAAGGCCATTGCTAGTAACTTTTGGCCCATGATGAAAAG 1140
Db 1081 ATGAACACAGCTGGTCACAGATAAGGCCATTGCTAGTAACTTTTGGCCCATGATGAAAAG 1140
Qy 1141 GGCATCTCTTCCAAAAGAGAAAAAGCTCAAGCCAAACACAAACAGCGGAAACGCCCTTA 1200
Db 1141 GGCATCTCTTCCAAAAGAGAAAAAGCTCAAGCCAAACACAAACAGCGGAAACGCCCTTA 1200
Qy 1201 AGTCAGCTGTAAAGAGACACCTTTTGTACGTGGACTTCAGTCAGCTGGGTGGAAATGACT 1260
Db 1201 AGTCAGCTGTAAAGAGACACCTTTTGTACGTGGACTTCAGTCAGCTGGGTGGAAATGACT 1260
Qy 1261 GGAATGTGGCTCCCGGGGTATCACGCTTTTACTGCCACGGAGAAATGCCCTTTTCCTC 1320
Db 1261 GGAATGTGGCTCCCGGGGTATCACGCTTTTACTGCCACGGAGAAATGCCCTTTTCCTC 1320
Qy 1321 TGGCTGATCATCTGAACCTCACTAATCATGCCATTGTTTTCAGACGTTGGTCAACTCTGTTA 1380
Db 1321 TGGCTGATCATCTGAACCTCACTAATCATGCCATTGTTTTCAGACGTTGGTCAACTCTGTTA 1380
```

```
Qy 1381 ACTCTAAGATTCTTAAGGCATGCTGTGTCCCGACAGAACTCAGTGTCTATCTCGATGCTGT 1440
Db 1381 ACTCTAAGATTCTTAAGGCATGCTGTGTCCCGACAGAACTCAGTGTCTATCTCGATGCTGT 1440
Qy 1441 ACCTTGACGAGAATGAAAAGGTTGTTATTAAGAACTATCAGGACATGGTTGTGGAGGTT 1500
Db 1441 ACCTTGACGAGAATGAAAAGGTTGTTATTAAGAACTATCAGGACATGGTTGTGGAGGTT 1500
Qy 1501 GTGGGTGTGCTAGTACAGCAAAATTAATAACATAAATATATATATA 1547
Db 1501 GTGGGTGTGCTAGTACAGCAAAATTAATAACATAAATATATATATA 1547
```

Search completed: January 10, 2006, 20:38:30
Job time : 685 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 10, 2006, 20:20:29 ; Search time 221 Seconds
(without alignments)
12442.932 Million cell updates/sec

Title: US-10-801-648-1

Perfect score: 1547

Sequence: 1 ggggactcttgaaactgca.....aatacataaatatatata 1547

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:*

- 1: /cgn2_6/ptodata/1/ina/1 COMB.seq.*
- 2: /cgn2_6/ptodata/1/ina/5 COMB.seq.*
- 3: /cgn2_6/ptodata/1/ina/6A COMB.seq.*
- 4: /cgn2_6/ptodata/1/ina/6B COMB.seq.*
- 5: /cgn2_6/ptodata/1/ina/6H COMB.seq.*
- 6: /cgn2_6/ptodata/1/ina/PTCUS COMB.seq.*
- 7: /cgn2_6/ptodata/1/ina/PP COMB.seq.*
- 8: /cgn2_6/ptodata/1/ina/RE COMB.seq.*
- 9: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|--------|-------------|--------|----|--------------------|
| 1 | 1547 | 100.0 | 1547 | 2 | US-08-377-292-2 |
| 2 | 1547 | 100.0 | 1607 | 3 | US-07-721-847A-3 |
| 3 | 1547 | 100.0 | 1607 | 3 | US-08-925-779-3 |
| 4 | 1547 | 100.0 | 1607 | 9 | 5166058-3 |
| 5 | 1547 | 100.0 | 3526 | 3 | US-09-976-594-11 |
| 6 | 1545.4 | 99.9 | 1607 | 2 | US-07-989-847-1 |
| 7 | 1545.4 | 99.9 | 1607 | 3 | US-08-469-411-1 |
| 8 | 1545.4 | 99.9 | 1607 | 3 | US-09-780-601A-1 |
| 9 | 1545.4 | 99.9 | 2185 | 3 | US-09-949-016-4668 |
| 10 | 1543.8 | 99.8 | 1607 | 2 | US-07-679-451-1 |
| 11 | 1227.2 | 79.3 | 1260 | 2 | US-07-841-646-4 |
| 12 | 1227.2 | 79.3 | 1260 | 2 | US-07-901-703-14 |
| 13 | 1227.2 | 79.3 | 1260 | 2 | US-08-147-023-4 |
| 14 | 1227.2 | 79.3 | 1260 | 2 | US-08-447-570-4 |
| 15 | 1227.2 | 79.3 | 1260 | 2 | US-08-449-700-4 |
| 16 | 1227.2 | 79.3 | 1260 | 3 | US-08-449-699A-4 |
| 17 | 1227.2 | 79.3 | 1260 | 3 | US-09-148-925C-4 |
| 18 | 1227.2 | 79.3 | 1260 | 3 | US-08-957-425-4 |
| 19 | 1227.2 | 79.3 | 1260 | 3 | US-10-321-799-4 |
| 20 | 1227.2 | 79.3 | 1260 | 6 | PCT-US93-05446-14 |
| 21 | 1045.2 | 67.6 | 1314 | 3 | US-08-713-556F-39 |
| 22 | 896.6 | 58.0 | 1233 | 2 | US-08-362-670B-27 |
| 23 | 896.6 | 58.0 | 1233 | 3 | US-08-333-576C-27 |
| 24 | 896.6 | 58.0 | 1233 | 3 | US-08-808-324-27 |

Sequence 27, Appl
Sequence 27, Appl
Sequence 1, Appl
Sequence 16410, A
Sequence 6, Appl
Sequence 6, Appl
Sequence 7, Appl
Sequence 35, Appl
Sequence 4, Appl
Sequence 6, Appl
Sequence 18, Appl
Sequence 6, Appl
Sequence 6, Appl
Sequence 6, Appl
Sequence 6, Appl
Sequence 6, Appl
Sequence 18, Appl
Sequence 1476, Ap

25 896.6 58.0 1233 3 US-09-945-182-27
26 896.6 58.0 1233 6 PCT-US94-14030A-27
27 880 56.9 14759 3 US-09-661-887-1
28 878.4 56.8 15203 3 US-09-949-016-16410
29 681.2 44.0 15144 3 US-08-458-434A-6
30 623.2 40.3 1992 2 US-08-455-550-6
31 416.4 26.9 955 2 US-08-455-550-3
32 385.4 24.9 1558 2 US-08-455-550-7
33 378 24.4 406 3 US-08-868-452-35
34 375 24.2 1751 2 US-08-377-292-4
35 375 24.2 1788 2 US-07-841-646-6
36 375 24.2 1788 2 US-07-901-703-18
37 375 24.2 1788 2 US-08-147-023-6
38 375 24.2 1788 2 US-08-447-570-6
39 375 24.2 1788 2 US-08-449-699A-6
40 375 24.2 1788 2 US-08-148-925C-6
41 375 24.2 1788 3 US-09-148-925C-6
42 375 24.2 1788 3 US-08-957-425-6
43 375 24.2 1788 3 US-10-321-799-6
44 375 24.2 1788 6 PCT-US93-05446-18
45 375 24.2 1945 3 US-09-949-016-1476

ALIGNMENTS

RESULT 1

US-08-377-292-2
; Sequence 2, Application US/08377292
; Patent No. 5693615
; GENERAL INFORMATION:
; APPLICANT: STONE, ROGER L.
; TITLE OF INVENTION: THERAPEUTIC FORMULAS FOR OSTEOINDUCTION
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; STREET: The Procter & Gamble Company
; ADDRESS: 11810 East Miami River Road
; CITY: Cincinnati
; STATE: Ohio
; COUNTRY: U.S.A.
; ZIP: 45239-8707
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/377,292
; FILING DATE: 23-JAN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/243,435
; FILING DATE:
; APPLICATION NUMBER: US/08/117,367
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Corstange, Brahm J.
; REGISTRATION NUMBER: 34,804
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 513-245-2858
; TELEFAX: 513-741-3012
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1547 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-377-292-2

Query Match 100.0%; Score 1547; DB 2; Length 1547;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1547; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo Sapiens
CELL TYPE: Osteosarcoma Cell Line
CELL LINE: U-2OS
IMMEDIATE SOURCE:
LIBRARY: U2OS cDNA in Lambda GT10
CLONE: Lambda U2OS-39
POSITION IN GENOME:
UNITS: bp
FEATURE:
NAME/KEY: CDS
LOCATION: 356..1546
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 1202..1543
FEATURE:
NAME/KEY: mRNA
LOCATION: 14..1607
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 356..424
US-07-721-847A-3
Query Match 100.0%; Score 1547; DB 3; Length 1607;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1547; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGGACTTCTTGAATCTTGAGGAGAAATAAATTGCGGACCCCACTTTTGGCGCGGTCCTT 60
DB 33 GGGGACTTCTTGAATCTTGAGGAGAAATAAATTGCGGACCCCACTTTTGGCGCGGTCCTT 92
QY 61 TGCCCGAGCGGAGCTGCTTCCGCACTCCGAGCCCAACCGCCCTCCACTCTTGGGCTT 120
DB 93 TGCCCGAGCGGAGCTGCTTCCGCACTCCGAGCCCAACCGCCCTCCACTCTTGGGCTT 152
QY 121 TGCCCGGACACTGAGACGCTGTTCCAGCGTGAAAGAGAGACTGCGCGCGCGGACCCCGG 180
DB 153 TGCCCGGACACTGAGACGCTGTTCCAGCGTGAAAGAGAGACTGCGCGCGCGGACCCCGG 212
QY 181 GAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 240
DB 213 GAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 272
QY 241 AGAGTTTTTCCATGTGGAGCGCTTTTCAATGAGACGTGTCCCGCGCTTCTTAGACGA 300
DB 273 AGAGTTTTTCCATGTGGAGCGCTTTTCAATGAGACGTGTCCCGCGCTTCTTAGACGA 332
QY 301 CTGCGGCTCTCTTAAAGGTCGACCATGTGGCGCGGACCGCTGTCTTAGCGTTGCTGC 360
DB 333 CTGCGGCTCTCTTAAAGGTCGACCATGTGGCGCGGACCGCTGTCTTAGCGTTGCTGC 392
QY 361 TTCCCGAGGCTCTCTTGGCGCGCGGCTGCTGTTCCGAGCTGGCGCGGAGGAGT 420
DB 393 TTCCCGAGGCTCTCTTGGCGCGCGGCTGCTGTTCCGAGCTGGCGCGGAGGAGT 452
QY 421 TCGCGCGCGGCTGCTGCGCGCGCGCTCTATCCAGCCCTCTGACGAGTCTGACGAGT 480
DB 453 TCGCGCGCGGCTGCTGCGCGCGCGCTCTATCCAGCCCTCTGACGAGGCTCTGACGAGT 512
QY 481 TCGAGTTGCGGCTGCTGAGCATGTTCCGCTCTGAAACAGAGACCCACCCCGAGCGGAGC 540
DB 513 TCGAGTTGCGGCTGCTGAGCATGTTCCGCTCTGAAACAGAGACCCACCCCGAGCGGAGC 572
QY 541 CGGTGGTGCCTCCCTACATGCTAGACCTGTATCGAGGCACTCAGGTGAGCGGCTCAC 600
DB 573 CGGTGGTGCCTCCCTACATGCTAGACCTGTATCGAGGCACTCAGGTGAGCGGCTCAC 632
QY 601 CGGCCCCAGACACCGGTTGGAGAGGCGAGCGGAGGCGGAGGCGGAGGCGGAGGCGGAG 660
DB 633 CGGCCCCAGACACCGGTTGGAGAGGCGAGCGGAGGCGGAGGCGGAGGCGGAGGCGGAG 692

QY 661 ACCATGAAGAACTCTTTGGAGAACTACACAGAAACGAGTGGGAAACAAACCCGAGATTCT 720
DB 693 ACCATGAAGAACTCTTTGGAGAACTACACAGAAACGAGTGGGAAACAAACCCGAGATTCT 752
QY 721 TCTTTAATTTAAGTTCTATCCCGAGGAGGAGTTTATCACCCTCAGCAGAGCTTCAGGTTT 780
DB 753 TCTTTAATTTAAGTTCTATCCCGAGGAGGAGTTTATCACCCTCAGCAGAGCTTCAGGTTT 812
QY 781 TCCGAGAACAGATGCAAGATGCTTTTGGAGAAACAAATAGCAGTTTCCATCACCGAAATTAATA 840
DB 813 TCCGAGAACAGATGCAAGATGCTTTTGGAGAAACAAATAGCAGTTTCCATCACCGAAATTAATA 872
QY 841 TTTATGAATCATATAAACCTGCAACAGCCAACTCCCGTACAGACACTTTTGG 900
DB 873 TTTATGAATCATATAAACCTGCAACAGCCAACTCCCGTACAGACACTTTTGG 932
QY 901 ACACGAGTTGCTGAATCAGAAATGCAAGCAGGTGGGAAAGTTTTCATGTCAACCCCGCTG 960
DB 933 ACACGAGTTGCTGAATCAGAAATGCAAGCAGGTGGGAAAGTTTTCATGTCAACCCCGCTG 992
QY 961 TGATGCGGTGACTGCAACAGGACACGCAACCACTGGAATTCGTGTGGAAGTGGGCCACT 1020
DB 993 TGATGCGGTGACTGCAACAGGACACGCAACCACTGGAATTCGTGTGGAAGTGGGCCACT 1052
QY 1021 TGGAGGAGAAACAAAGTGTCTCCAAGAGACATGTTAGGATAAGCAGGTCTTTTGCACCAAG 1080
DB 1053 TGGAGGAGAAACAAAGTGTCTCCAAGAGACATGTTAGGATAAGCAGGTCTTTTGCACCAAG 1112
QY 1081 ATGAACACAGCTGGTCAACAGATAGGCCAATTCGTAGTAACTTTTGGCCATGATGGAAG 1140
DB 1113 ATGAACACAGCTGGTCAACAGATAGGCCAATTCGTAGTAACTTTTGGCCATGATGGAAG 1172
QY 1141 GGCATCTCTCCACAAAAGAGAAAACGCTCAAGCCAAACACAAACAGCGGAAACGCCCTTA 1200
DB 1173 GGCATCTCTCCACAAAAGAGAAAACGCTCAAGCCAAACACAAACAGCGGAAACGCCCTTA 1232
QY 1201 AGTCAGCTGTAAGAGACACCCCTTTTGTACGTGGACTTCAGTGACGTGGGTGGAAATGACT 1260
DB 1233 AGTCAGCTGTAAGAGACACCCCTTTTGTACGTGGACTTCAGTGACGTGGGTGGAAATGACT 1292
QY 1261 GGATTTGGCTCCCGCGGGGTATACGCTTTTACTGCGCAGGAGAAATGCCCTTTTCTCTC 1320
DB 1293 GGATTTGGCTCCCGCGGGGTATACGCTTTTACTGCGCAGGAGAAATGCCCTTTTCTCTC 1352
QY 1321 TGGCTGATCATCTGAACCTCCACTAATCATGCAATGTTTTCAGACGTTGGTCAACTCTGTTA 1380
DB 1353 TGGCTGATCATCTGAACCTCCACTAATCATGCAATGTTTTCAGACGTTGGTCAACTCTGTTA 1412
QY 1381 ACTCTAAGATTCTTAAGGCATGCTGTGTCGCGACAGAACTCAGTGCTATCTCGATGCTGT 1440
DB 1413 ACTCTAAGATTCTTAAGGCATGCTGTGTCGCGACAGAACTCAGTGCTATCTCGATGCTGT 1472
QY 1441 ACCTTGACGAGAAATGAAAGGTTGTTAATAAGAACTATCAGGACATGTTGTGGAGGGTT 1500
DB 1473 ACCTTGACGAGAAATGAAAGGTTGTTAATAAGAACTATCAGGACATGTTGTGGAGGGTT 1532
QY 1501 GTGGGTGCTGTAGTACAGCAAAATTAATAACATAAATATATATA 1547
DB 1533 GTGGGTGCTGTAGTACAGCAAAATTAATAACATAAATATATATA 1579

RESULT 3
US-08-925-779-3
; Sequence 3, Application US/08925779
; Patent No. 6245889
; GENERAL INFORMATION:
; APPLICANT: Wang, Elizabeth A.
; APPLICANT: Rosen, Vicki A.
; APPLICANT: Wozney, John M.
; TITLE OF INVENTION: No. 6245889el BMP Products
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LEGAL AFFAIRS, GENETICS INSTITUTE, INC.

```
STREET: 87 CAMBRIDGE PARK DRIVE
CITY: CAMBRIDGE
STATE: MA
COUNTRY: USA
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/925,779
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION NUMBER: 07/721,847
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Kapinos, Ellen J
REGISTRATION NUMBER: 32,245
REFERENCE/DOCKET NUMBER: 5160C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-876-1170
TELEFAX: 617-876-5851
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1607 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo Sapiens
CELL TYPE: Osteosarcoma Cell Line
CELL LINE: U-2OS
IMMEDIATE SOURCE:
LIBRARY: U2OS cDNA in Lambda GT10
CLONE: Lambda U2OS-39
POSITION IN GENOME:
UNITS: bp
FEATURE:
NAME/KEY: CDS
LOCATION: 356..1546
FEATURE:
NAME/KEY: .mat_peptide
LOCATION: 1202..1543
FEATURE:
NAME/KEY: mRNA
LOCATION: 14..1607
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 356..424
US-08-925-779-3

Query Match 100.0%; Score 1547; DB 3; Length 1607;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1547; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGACTCTTGAACCTTCAGGGAGAAATACCTTCGGCACCCCACTTTTGGCGCGGTGCTT 60
Db 33 GGGGACTCTTGAACCTTCAGGGAGAAATACCTTCGGCACCCCACTTTTGGCGCGGTGCTT 92
Qy 61 TGCCCCGAGCGAGCTGCTTCGCCATCTCCGAGCCCAACCGCCCTCCACTTCCTCGGCCT 120
Db 93 TGCCCCGAGCGAGCTGCTTCGCCATCTCCGAGCCCAACCGCCCTCCACTTCCTCGGCCT 152
Qy 121 TGCCCGCACTGAGACGCTGTTCGACGCTGTAAGAGAGACTCGCGGCGCGCACCCGG 180
Db 153 TGCCCGCACTGAGACGCTGTTCGACGCTGTAAGAGAGAGACTCGCGGCGCGCACCCGG 212
Qy 181 GAGAAGGAGGAGGCAAGAAAGGNAACGACATTCGGTCTTCGGCCAGGTCTTTTGACC 240

213 GAGAAGGAGGAGGCAAGAAAGGNAACGACATTCGGTCTTCGGCCAGGTCTTTTGACC 272
241 AGAGTTTTTCCATGTGACGCTCTTTCAATGGACGCTGCCCGCGTCTTTTAGACGGA 300
273 AGAGTTTTTCCATGTGACGCTCTTTCAATGGACGCTGCCCGCGTCTTTTAGACGGA 332
301 CTGCGGTCTCTAAAGGTTCGACCAATGTGCGCGGACCCGCTGCTTCTTAGCTGTCTGC 360
333 CTGCGGTCTCTAAAGGTTCGACCAATGTGCGCGGACCCGCTGCTTCTTAGCTGTCTGC 392
361 TTCCCGAGGTCTCTGCGGCGCGGCTCGCTTCGTCGCGAGCTGGCGCGCAGGAAGT 420
393 TTCCCGAGGTCTCTGCGGCGCGGCTCGCTTCGTCGCGAGCTGGCGCGCAGGAAGT 452
421 TCGCGGCGGCTCTGTCGGGCGCGCCCTCATCCAGCCCTCTGACGAGTCTGAGCGAGT 480
453 TCGCGGCGGCTCTGTCGGGCGCGCCCTCATCCAGCCCTCTGACGAGTCTCTGAGCGAGT 512
481 TCGAGTTGCGGCTCTCAGCATGTTCGGCTCGAAGACAGAGACCCACCCGACGAGGACG 540
513 TCGAGTTGCGGCTCTCAGCATGTTCGGCTCGAAGACAGAGACCCACCCGACGAGGACG 572
541 CCGTGTGCGCCCTCATCATCTAGACCTGTATCGCAGCACTCAGGTGAGCGCGGCTCAC 600
573 CCGTGTGCGCCCTCATCATCTAGACCTGTATCGCAGCACTCAGGTGAGCGCGGCTCAC 632
601 CCGCCCGAGACCAACCGTTGGAGGGCAGCAGCCGAGCAACACTGTGCGCAGCTTCC 660
633 CCGCCCGAGACCAACCGTTGGAGGGCAGCAGCCGAGCAACACTGTGCGCAGCTTCC 692
661 ACATGAAGAAATCTTTGGAGAACTACAGAAACGAGTGGGAAAACAAACCCGAGATTCT 720
693 ACCATGAAGAAATCTTTGGAGAACTACAGAAACGAGTGGGAAAACAAACCCGAGATTCT 752
721 TCTTTAATTTAAGTTCTATCCCGAGGAGGTTTATCCTCAGCAGAGCTTCAGGTTT 780
753 TCTTTAATTTAAGTTCTATCCCGAGGAGGTTTATCCTCAGCAGAGCTTCAGGTTT 812
781 TCCGAGAACAGATGCAAGATGCTTTTAGGAAACAAATAGCAGTTTCATCACCAGATTATA 840
813 TCCGAGAACAGATGCAAGATGCTTTTAGGAAACAAATAGCAGTTTCATCACCAGATTATA 872
841 TTTATGAATCATAAACCTTGCAACAGCCAACTCGAAATTCCTCGTGCACGACTTTTGG 900
873 TTTATGAATCATAAACCTTGCAACAGCCAACTCGAAATTCCTCGTGCACGACTTTTGG 932
901 ACACGAGTTGGTGAATCAGAAATGCAAGAGGTGGGAAAGTTTGTATGTCAACCCCGCTG 960
933 ACACGAGTTGGTGAATCAGAAATGCAAGAGGTGGGAAAGTTTGTATGTCAACCCCGCTG 992
961 TGATGCGGTGGAATGCAAGAGGTGGGAAAGTTTGTATGTCAACCCCGCTG 1020
993 TGATGCGGTGGAATGCAAGAGGTGGGAAAGTTTGTATGTCAACCCCGCTG 1052
1021 TGAGGAGAAACAAAGGTGCTCCAGAGACATGTTAGGTAAGCAGGTCTTTGACCCAG 1080
1053 TGAGGAGAAACAAAGGTGCTCCAGAGACATGTTAGGTAAGCAGGTCTTTGACCCAG 1112
1081 ATGAACACAGCTGTCACAGATAGGCAATTCGTAGTAACCTTTTGGCCATGATGAAAG 1140
1113 ATGAACACAGCTGTCACAGATAGGCAATTCGTAGTAACCTTTTGGCCATGATGAAAG 1172
1141 GGCACTCTCTCCAAAGAGAAACAGTCAAGCAACAAACAAACAGCGGAAACGCTTTA 1200
1173 GGCACTCTCTCCAAAGAGAAACAGTCAAGCAACAAACAAACAGCGGAAACGCTTTA 1232
1201 AGTCACAGCTGTAAGACACCTTTTGTAGTGAATTCAGTGAAGTGGGTGGAATGACT 1260
1233 AGTCACAGCTGTAAGACACCTTTTGTAGTGAATTCAGTGAAGTGGGTGGAATGACT 1292
1261 GGATTTGGTCTCCCGCGGCTATCACGCTTTTACTGCCAGGAGAAATGCCCTTTTCTC 1320
```


;; TITLE OF INVENTION: Heterodimers, Compositions and Methods of Use.
;; NUMBER OF SEQUENCES: 30
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Legal Affairs, Genetics Institute, Inc.
;; STREET: 87 CambridgePark Drive
;; CITY: Cambridge
;; STATE: MA
;; COUNTRY: USA
;; ZIP: 02140-2387
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Tape
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/07/989,847
;; FILING DATE:
;; CLASSIFICATION: 436
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Kapinos, Ellen J.
;; REGISTRATION NUMBER: 32,245
;; REFERENCE/DOCKET NUMBER: GI-5192B
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 617-876-1170
;; TELEFAX: 617-876-5851
;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1607 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: double
;; TOPOLOGY: unknown
;; MOLECULE TYPE: DNA (genomic)
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 356..1543
;; US-07-989-847-1

Query Match 99.9%; Score 1545.4; DB 2; Length 1607;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1546; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

| | | | |
|----|-----|--|-----|
| Qy | 1 | GGGGACTCTTCTGAACTTGCAGGAGAGAACTTGGCGACCCCACTTTGGCGCGGTGCCTT | 60 |
| Db | 33 | GGGGACTCTTCTGAACTTGCAGGAGAGAACTTGGCGACCCCACTTTGGCGCGGTGCCTT | 92 |
| Qy | 61 | TGCCCCAGCGAGCTCTTCCGCACTTCCGAGCCCGACCGCCCTTCCACTCTCGGCT | 120 |
| Db | 93 | TGCCCCAGCGAGCTCTTCCGCACTTCCGAGCCCGACCGCCCTTCCACTCTCGGCT | 152 |
| Qy | 121 | TGCCCCGACACTGAGACGCTTCCGAGCGTGAAGAGAGAGACTGCGCGCGCGACCCGG | 180 |
| Db | 153 | TGCCCCGACACTGAGACGCTTCCGAGCGTGAAGAGAGAGACTGCGCGCGCGACCCGG | 212 |
| Qy | 181 | GAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG | 240 |
| Db | 213 | GAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG | 272 |
| Qy | 241 | AGAGTTTTTCCATGTGAGAGCTCTTTCATGTAGAGCTGCTCCCGCGGTCTTTAGACGA | 300 |
| Db | 273 | AGAGTTTTTCCATGTGAGAGCTCTTTCATGTAGAGCTGCTCCCGCGGTCTTTAGACGA | 332 |
| Qy | 301 | CTGCGGTCTCTTAAAGGTGACCATGTGCGCGGAGCCGCTGCTTCTAGCGTTGCTGC | 360 |
| Db | 333 | CTGCGGTCTCTTAAAGGTGACCATGTGCGCGGAGCCGCTGCTTCTAGCGTTGCTGC | 392 |
| Qy | 361 | TTCCCCCAGGTCTCTTGGCGGCGCGGTGCGCTGCTTCCGAGAGCTGGGCGCGCAGGAAGT | 420 |
| Db | 393 | TTCCCCCAGGTCTCTTGGCGGCGCGGTGCGCTGCTTCCGAGAGCTGGGCGCGCAGGAAGT | 452 |
| Qy | 421 | TGCGCGCGCGGTGCTGCGCGCGCGCCCTCATCCAGCCCTCTGACGAGGTCTTGACGAGT | 480 |
| Db | 453 | TGCGCGCGCGGTGCTGCGCGCGCGCCCTCATCCAGCCCTCTGACGAGGTCTTGACGAGT | 512 |

| | | | |
|----|------|--|------|
| Qy | 481 | TCGAGTTGCGGCTGCTCAGCATGTTTCGCGCTGAAACAGAGACCCACCCCGAGCGGACG | 540 |
| Db | 513 | TCGAGTTGCGGCTGCTCAGCATGTTTCGCGCTGAAACAGAGACCCACCCCGAGCGGACG | 572 |
| Qy | 541 | CCGTGGTCCCGCCCTCATAGCTGTATGAGAGGCACTCAGGTGAGCGCGGCTCAC | 600 |
| Db | 573 | CCGTGGTCCCGCCCTCATAGCTGTATGAGAGGCACTCAGGTGAGCGCGGCTCAC | 632 |
| Qy | 601 | CCGCCCCAGACCCCGGTTGGAGAGGCGAGCCAGCCGAGCCAACTGTCGCGAGCTTCC | 660 |
| Db | 633 | CCGCCCCAGACCCCGGTTGGAGAGGCGAGCCAGCCGAGCCAACTGTCGCGAGCTTCC | 692 |
| Qy | 661 | ACCATGAAGAACTCTTTGGAAGAACTTACACAGAAACGAGTGGGAAACAAACCGGAGATTCT | 720 |
| Db | 693 | ACCATGAAGAACTCTTTGGAAGAACTTACACAGAAACGAGTGGGAAACAAACCGGAGATTCT | 752 |
| Qy | 721 | TCTTTAATTAAAGTTCTATCCCCAGGAGAGTTTATCATCTCAGCAGAGCTTCAGGTTT | 780 |
| Db | 753 | TCTTTAATTAAAGTTCTATCCCCAGGAGAGTTTATCATCTCAGCAGAGCTTCAGGTTT | 812 |
| Qy | 781 | TCCGAGACACATGCAAGATGCTTTAGGAAACAATAGCAGTTTCCATCACCAGAAATTAATA | 840 |
| Db | 813 | TCCGAGACACATGCAAGATGCTTTAGGAAACAATAGCAGTTTCCATCACCAGAAATTAATA | 872 |
| Qy | 841 | TTTATGAATCATATAAACTCTGCAACAGCCAACTCGAAATTCCTCCGTCACAGACTTTTGG | 900 |
| Db | 873 | TTTATGAATCATATAAACTCTGCAACAGCCAACTCGAAATTCCTCCGTCACAGACTTTTGG | 932 |
| Qy | 901 | ACACAGGTTGGTGAATCAGAAATGCAAGCAGGTTGGGAAAGTTTGTATGTACACCCCGCTG | 960 |
| Db | 933 | ACACAGGTTGGTGAATCAGAAATGCAAGCAGGTTGGGAAAGTTTGTATGTACACCCCGCTG | 992 |
| Qy | 961 | TGATCGGTGACCTGCAAGGACACCGCAACCATGGAATTCGTGTGGAAGTGGCCCACT | 1020 |
| Db | 993 | TGATCGGTGACCTGCAAGGACACCGCAACCATGGAATTCGTGTGGAAGTGGCCCACT | 1052 |
| Qy | 1021 | TGGAGGAGAAACAAGGTGCTCTCAAGAGACATGTTAGGATAAGCAGGCTCTTTGCACCAAG | 1080 |
| Db | 1053 | TGGAGGAGAAACAAGGTGCTCTCAAGAGACATGTTAGGATAAGCAGGCTCTTTGCACCAAG | 1112 |
| Qy | 1081 | ATGAACACAGCTGCTCAGATAAGGCAATTTGCTAGTAACTTTTGGCCCATGATGGAAG | 1140 |
| Db | 1113 | ATGAACACAGCTGCTCAGATAAGGCAATTTGCTAGTAACTTTTGGCCCATGATGGAAG | 1172 |
| Qy | 1141 | GGCATCTCTCCACAAAGAGAAACGTCAGCCAAACACAAACAGCGGAAACCGCTTA | 1200 |
| Db | 1173 | GGCATCTCTCCACAAAGAGAAACGTCAGCCAAACACAAACAGCGGAAACCGCTTA | 1232 |
| Qy | 1201 | AGTCAGCTGTAAGAGACACCTTTTGTACGTGGAATTCAGTGACGTGGGGTGAATGACT | 1260 |
| Db | 1233 | AGTCAGCTGTAAGAGACACCTTTTGTACGTGGAATTCAGTGACGTGGGGTGAATGACT | 1292 |
| Qy | 1261 | GGATTTGGCTCCCGCGGGGTATACGCTTTTACTGCAAGGAGATGCCCCCTTTTCTCTC | 1320 |
| Db | 1293 | GGATTTGGCTCCCGCGGGGTATACGCTTTTACTGCAAGGAGATGCCCCCTTTTCTCTC | 1352 |
| Qy | 1321 | TGGCTGATCATCTGAACTCCCAATCATGCAATTTGTTTTCAGACGTTGGTCACTCTGTTA | 1380 |
| Db | 1353 | TGGCTGATCATCTGAACTCCCAATCATGCAATTTGTTTTCAGACGTTGGTCACTCTGTTA | 1412 |
| Qy | 1381 | ACTCTAAGATCTCTAAGGCACTGCTGTGTCGCGACAGAACTCAGTGCTATCTCGATGCTGT | 1440 |
| Db | 1413 | ACTCTAAGATCTCTAAGGCACTGCTGTGTCGCGACAGAACTCAGTGCTATCTCGATGCTGT | 1472 |
| Qy | 1441 | ACCTTGAAGAGAAAGGTTGTTTAAAGAACTATCAGGACATGTTGTGGAAGGTT | 1500 |
| Db | 1473 | ACCTTGAAGAGAAAGGTTGTTTAAAGAACTATCAGGACATGTTGTGGAAGGTT | 1532 |
| Qy | 1501 | GTGGGTGCTGTAGTACAGCAAAATTAATATATATATATATA | 1547 |
| Db | 1533 | GTGGGTGCTGTAGTACAGCAAAATTAATATATATATATATA | 1579 |

RESULT 7

US-08-469-411-1
; Sequence 1, Application US/08469411
; Patent No. 6190880
; GENERAL INFORMATION:
; APPLICANT: Israel, David
; Wolfman, Neil M.
; TITLE OF INVENTION: Recombinant Bone Morphogenetic Protein
; Heterodimers, Compositions and Methods of Use.
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Legal Affairs, Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140-2387
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Tape
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 06-Jun-1995
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Kapinos, Ellen J.
; REGISTRATION NUMBER: 32,245
; REFERENCE/DOCKET NUMBER: GI-5192B-CON
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-498-8622
; TELEFAX: 617-876-5851
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1607 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 356..1543
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-08-469-411-1

Query Match 99.9%; Score 1545.4; DB 3; Length 1607;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 1546; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

| | | | | |
|----|-----|---------------------------------|---------------------------------|-----|
| Qy | 1 | GGGACTTCTTGAACCTTCAGGGAGATAA | CTTGGCGACCCCACTTTTGGCGCGGTGCCTT | 60 |
| Db | 33 | GGGACTTCTTGAACCTTCAGGGAGATAA | CTTGGCGACCCCACTTTTGGCGCGGTGCCTT | 92 |
| Qy | 61 | TGCCCCAGCGAGCTGCTCGCATCTCCGAGCC | CAACCCCTCCCACTCTCCGCT | 120 |
| Db | 93 | TGCCCCAGCGAGCTGCTCGCATCTCCGAGCC | CAACCCCTCCCACTCTCCGCT | 152 |
| Qy | 121 | TGCCCCGACACTGAGACGCTGTTCACGCTG | AAAGAGAGACTCGCGCGCGGACCCGG | 180 |
| Db | 153 | TGCCCCGACACTGAGACGCTGTTCACGCTG | AAAGAGAGACTCGCGCGCGGACCCGG | 212 |
| Qy | 181 | GAGAGGAGGAGGCAAGAAAGGAAAGGAA | CGGACATTCGGTCTTGGCCAGGTCCTTGACC | 240 |
| Db | 213 | GAGAGGAGGAGGCAAGAAAGGAAAGGAA | CGGACATTCGGTCTTGGCCAGGTCCTTGACC | 272 |
| Qy | 241 | AGAGTTTTTCCATGTGGACGCTCTTTCAAT | GGAGCTGTCCCGCGTGTCTTCTTAGACGGA | 300 |
| Db | 273 | AGAGTTTTTCCATGTGGACGCTCTTTCAAT | GGAGCTGTCCCGCGTGTCTTCTTAGACGGA | 332 |
| Qy | 301 | CTCGGGTCTCTAAAGTFCGACCAATAGTG | GGCGGAGACCCGCTGTCTTCTAGCGTGTGC | 360 |
| Db | 333 | CTCGGGTCTCTAAAGTFCGACCAATAGTG | GGCGGAGACCCGCTGTCTTCTAGCGTGTGC | 392 |

| | | | | |
|----|------|-------------------------------|---|------|
| Qy | 361 | TTCCCCAGAGTCTCTCGGGCGCGCGCTG | GCCTCGTTCCGAGCTGCGCGCGCAGGAAGT | 420 |
| Db | 393 | TTCCCCAGAGTCTCTCGGGCGCGCGCTG | GCCTCGTTCCGAGCTGCGCGCGCAGGAAGT | 452 |
| Qy | 421 | TCGCGGCGGCTGCTCGGGCGCGCCCTCAT | CCCCAGCCCTCTGACGAGTCTCTGAGCGAGT | 480 |
| Db | 453 | TCGCGGCGGCTGCTCGGGCGCGCCCTCAT | CCCCAGCCCTCTGACGAGTCTCTGAGCGAGT | 512 |
| Qy | 481 | TCGAGTTGCGGCTGCTCAGCATGTTTCGG | CCCTGAAACAGAGACCCACCCAGCAGGACG | 540 |
| Db | 513 | TCGAGTTGCGGCTGCTCAGCATGTTTCGG | CCCTGAAACAGAGACCCACCCAGCAGGACG | 572 |
| Qy | 541 | CCGTGTCGCCCTCATGCTAGACCTGTAT | CGCAGGCACTCAGTTCAGCCGGCTCAC | 600 |
| Db | 573 | CCGTGTCGCCCTCATGCTAGACCTGTAT | CGCAGGCACTCAGTTCAGCCGGCTCAC | 632 |
| Qy | 601 | CCGCCCCAGACCAACCGGTTGGAGGGC | CAGCAGCCAGGCAACACCTGTGCGCAGCTTCC | 660 |
| Db | 633 | CCGCCCCAGACCAACCGGTTGGAGGGC | CAGCAGCCAGGCAACACCTGTGCGCAGCTTCC | 692 |
| Qy | 661 | ACCATGAAGAATCTTTGGAAGAACTAC | CAGAAACGAGTGGGAAAAAACAACCCGGAGATTCT | 720 |
| Db | 693 | ACCATGAAGAATCTTTGGAAGAACTAC | CAGAAACGAGTGGGAAAAAACAACCCGGAGATTCT | 752 |
| Qy | 721 | TCTTTAATTTAAGTTCTATCCCAACG | GAGGAGTTTATCAGCTCAGCAGAGCTTCAGGTTT | 780 |
| Db | 753 | TCTTTAATTTAAGTTCTATCCCAACG | GAGGAGTTTATCAGCTCAGCAGAGCTTCAGGTTT | 812 |
| Qy | 781 | TCCGAGAACAGATGCAAGATGCTTTTAG | AAAAAACAATAGCAGTTTCCATCACCAGATTATA | 840 |
| Db | 813 | TCCGAGAACAGATGCAAGATGCTTTTAG | AAAAAACAATAGCAGTTTCCATCACCAGATTATA | 872 |
| Qy | 841 | TTTATGAATCATAAAACTTGCAACAG | CCAACTCGAAATTTCCCGTGACACGACTTTTGG | 900 |
| Db | 873 | TTTATGAATCATAAAACTTGCAACAG | CCAACTCGAAATTTCCCGTGACACGACTTTTGG | 932 |
| Qy | 901 | ACACAGGTTGTTGAATCAGATGCAAG | AGAGTGGGAAAGTTTGTGATCAACCCCGCTG | 960 |
| Db | 933 | ACACAGGTTGTTGAATCAGATGCAAG | AGAGTGGGAAAGTTTGTGATCAACCCCGCTG | 992 |
| Qy | 961 | TGATGCGGTGGAATGCAACAGGCA | CACGCCAACAATGCTGTTGGTGGAAAGTGC | 1020 |
| Db | 993 | TGATGCGGTGGAATGCAACAGGCA | CACGCCAACAATGCTGTTGGTGGAAAGTGC | 1052 |
| Qy | 1021 | TGAGAGGAAACAAAGGTGCTCCAGAG | ACATGTTAGGATAAGCAGGTCTTTTGACCAAG | 1080 |
| Db | 1053 | TGAGAGGAAACAAAGGTGCTCCAGAG | ACATGTTAGGATAAGCAGGTCTTTTGACCAAG | 1112 |
| Qy | 1081 | ATGAACACAGCTGTCACAGTAAAG | CCCATTTGCTAGTAACTTTTGGCCATGATG | 1140 |
| Db | 1113 | ATGAACACAGCTGTCACAGTAAAG | CCCATTTGCTAGTAACTTTTGGCCATGATG | 1172 |
| Qy | 1141 | GGCATCTCTCCACAAAGAGAAAAAC | GTCAAGCCAAACAACAACAGCGGAAACGCCTTA | 1200 |
| Db | 1173 | GGCATCTCTCCACAAAGAGAAAAAC | GTCAAGCCAAACAACAACAGCGGAAACGCCTTA | 1232 |
| Qy | 1201 | AGTCACAGCTGTAAGAGACACCTTTT | GTACGTGAGCTTCAGTACGCTGGGTGGAATGACT | 1260 |
| Db | 1233 | AGTCACAGCTGTAAGAGACACCTTTT | GTACGTGAGCTTCAGTACGCTGGGTGGAATGACT | 1292 |
| Qy | 1261 | GGATTGTTGGCTCCCGCGGGGTATC | ACGCCCTTTTACTGCCAGGAGAAATGCCCTTTTCTC | 1320 |
| Db | 1293 | GGATTGTTGGCTCCCGCGGGGTATC | ACGCCCTTTTACTGCCAGGAGAAATGCCCTTTTCTC | 1352 |
| Qy | 1321 | TGGCTGATCATCTGAACCTCCAC | TAATCATGCAATGTTTTCAGACGTTGGTCAACTCTGTTA | 1380 |
| Db | 1353 | TGGCTGATCATCTGAACCTCCAC | TAATCATGCAATGTTTTCAGACGTTGGTCAACTCTGTTA | 1412 |
| Qy | 1381 | ACTCTAAGATTCCTAAGGCATGCTGT | TCGCGACAGAACTCAGTGTCTATCTCGATGCTGT | 1440 |
| Db | 1413 | ACTCTAAGATTCCTAAGGCATGCTGT | TCGCGACAGAACTCAGTGTCTATCTCGATGCTGT | 1472 |

QY 1441 ACCTTGACGAGAAATGAAAGGTTGTTATTAAGAACTATCAGGACATGTTGTGGAGGTT 1500
 Db 1473 ACCTTGACGAGAAATGAAAGGTTGTTATTAAGAACTATCAGGACATGTTGTGGAGGTT 1532
 QY 1501 GTGGGTGCTGCTAGTACAGCAAAATTAATACATAAATATATATATA 1547
 Db 1533 GTGGGTGCTGCTAGTACAGCAAAATTAATACATAAATATATATATA 1579

RESULT 8
 US-09-780-601A-1
 ; Sequence 1, Application US/09780601A
 ; Patent No. 6593109
 ; GENERAL INFORMATION:
 ; APPLICANT: Israel, David
 ; APPLICANT: Wolfman, Neil M.
 ; TITLE OF INVENTION: Recombinant Bone Morphogenetic Protein
 ; TITLE OF INVENTION: Heterodimers, Compositions and Methods of Use.
 ; NUMBER OF SEQUENCES: 30
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Legal Affairs, Genetics Institute, Inc.
 ; STREET: 87 CambridgePark Drive
 ; CITY: Cambridge
 ; STATE: MA
 ; COUNTRY: USA
 ; ZIP: 02140-2387
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Tape
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/780,601A
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/469,411
 ; FILING DATE: 06-Jun-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Kapinos, Ellen J.
 ; REGISTRATION NUMBER: 32,245
 ; REFERENCE/DOCKET NUMBER: GI-5192B-CON
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 617-498-8622
 ; TELEFAX: 617-876-5851
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1607 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: unknown
 ; MOLECULE TYPE: DNA (genomic)
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 356..1543
 ; US-09-780-601A-1

Query Match 99.9%; Score 1545.4; DB 3; Length 1607;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 1546; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GGGGACTCTTCAACTTGCAGGAGAAATACTTGGCGACCCCACTTGGCCGGTGCTTT 60
 Db 33 GGGGACTCTTCAACTTGCAGGAGAAATACTTGGCGACCCCACTTGGCCGGTGCTTT 92
 QY 61 TGCCCCAGCGAGCCTGCTTCCGCAATCTCCGAGCCCCCAGCGCCCTTCCACTCTCCGGCT 120
 Db 93 TGCCCCAGCGAGCCTGCTTCCGCAATCTCCGAGCCCCCAGCGCCCTTCCACTCTCCGGCT 152
 QY 121 TGCCCCGACACTGAGAGCGCTGTTCCGAGCGGTGAAAGAGAGAGAGAGAGAGAGAGAG 180
 Db 153 TGCCCCGACACTGAGAGCGCTGTTCCGAGCGGTGAAAGAGAGAGAGAGAGAGAGAGAG 212

QY 181 GAGAAGGAGGAGGCAAAAGAAAGGAAACGGAACATTCGGTCTTGGCCAGGTCCTTTGACC 240
 Db 213 GAGAAGGAGGAGGCAAAAGAAAGGAAACGGAACATTCGGTCTTGGCCAGGTCCTTTGACC 272
 QY 241 AGAGTTTTTCCATGTGAGCGCTCTTTCAATGGAAGTGTCCCGCGTGTCTTCTTAGACGGA 300
 Db 273 AGAGTTTTTCCATGTGAGCGCTCTTTCAATGGAAGTGTCCCGCGTGTCTTCTTAGACGGA 332
 QY 301 CTGCGGTCTCTTAAAGGTCGACCATGTGGCGGAGCCCGTGTCTTCTTAGGTTGCTGTC 360
 Db 333 CTGCGGTCTCTTAAAGGTCGACCATGTGGCGGAGCCCGTGTCTTCTTAGGTTGCTGTC 392
 QY 361 TTCCCCAGGTCCTCTCTGGCGGCGGCTGCTCTGTTCCGAGAGCTGGGCGCAGAGAGT 420
 Db 393 TTCCCCAGGTCCTCTCTGGCGGCGGCTGCTCTGTTCCGAGAGCTGGGCGCAGAGAGT 452
 QY 421 TCGCGGCGGCGTCTCTGGCGGCGGCTCTCTATCCGAGCCCTCTGACGAGTCTCTGAGCGAGT 480
 Db 453 TCGCGGCGGCGTCTCTGGCGGCGGCTCTCTATCCGAGCCCTCTGACGAGTCTCTGAGCGAGT 512
 QY 481 TCGAGTTGCGGCTCTCTAGCATGTTTGGGCTTGAACAGAGACCCACCCAGCAGGAGG 540
 Db 513 TCGAGTTGCGGCTCTCTAGCATGTTTGGGCTTGAACAGAGACCCACCCAGCAGGAGG 572
 QY 541 CCGTGTGCCCCCTTACATGCTAGACCTGTATCGCAGGCACTCAGGTGAGCGGGCTCAC 600
 Db 573 CCGTGTGCCCCCTTACATGCTAGACCTGTATCGCAGGCACTCAGGTGAGCGGGCTCAC 632
 QY 601 CGGCCAGAGACACCGGTTGAGAGGCGAGCCAGCGAGCCAACTCTGTGGCAGCTTCC 660
 Db 633 CGGCCAGAGACACCGGTTGAGAGGCGAGCCAGCGAGCCAACTCTGTGGCAGCTTCC 692
 QY 661 ACCATGAGAGATCTTTGGAAGAACTTACCAGAAACGAGTGGGAAACAAACCCGAGATCT 720
 Db 693 ACCATGAGAGATCTTTGGAAGAACTTACCAGAAACGAGTGGGAAACAAACCCGAGATCT 752
 QY 721 TCTTTAATTTAAGTTCTATCCCGAGGAGGAGTTTATCACCTCAGCAGAGCTTCAAGTTT 780
 Db 753 TCTTTAATTTAAGTTCTATCCCGAGGAGGAGTTTATCACCTCAGCAGAGCTTCAAGTTT 812
 QY 781 TCCGAGAAACAGATGCAAGATGCTTTAGGAAACAAATAGCAGTTTCCATCAGCGAATTAATA 840
 Db 813 TCCGAGAAACAGATGCAAGATGCTTTAGGAAACAAATAGCAGTTTCCATCAGCGAATTAATA 872
 QY 841 TTTATGAATCATAAACCTGCAACAGCCAACTCGAATTCCTCGTACCAGACTTTTGG 900
 Db 873 TTTATGAATCATAAACCTGCAACAGCCAACTCGAATTCCTCGTACCAGACTTTTGG 932
 QY 901 ACACGAGTTGGTGAATCAGAAATGCAAGCAGGTGGGAAAGTTTGTATGTACCCCCGCTG 960
 Db 933 ACACGAGTTGGTGAATCAGAAATGCAAGCAGGTGGGAAAGTTTGTATGTACCCCCGCTG 992
 QY 961 TGATGCGGTGGAATGCAACAGGAGACGCGCAACCAATGGATTGTTGTTGAAAGTGGCCACT 1020
 Db 993 TGATGCGGTGGAATGCAACAGGAGACGCGCAACCAATGGATTGTTGTTGAAAGTGGCCACT 1052
 QY 1021 TGGAGGAAACAAAGGTGTCTCCAGAGACATGTTGGTAAGCAGGTCTTTGACCCAG 1080
 Db 1053 TGGAGGAAACAAAGGTGTCTCCAGAGACATGTTGGTAAGCAGGTCTTTGACCCAG 1112
 QY 1081 ATGAACACAGCTGGTACAGATAAGGCCATTTGCTAGTAACTTTTGGCCATGATGGAAG 1140
 Db 1113 ATGAACACAGCTGGTACAGATAAGGCCATTTGCTAGTAACTTTTGGCCATGATGGAAG 1172
 QY 1141 GGCATCTCTCCAAAAAGAGAAAAAGCTCAGCCAAACACAAAACAGCGGAAAAACGCTTTA 1200
 Db 1173 GGCATCTCTCCAAAAAGAGAAAAAGCTCAGCCAAACACAAAACAGCGGAAAAACGCTTTA 1232
 QY 1201 AGTCAGCTGTAAAGAGACACCTTTGTACGTGAGCTTCACTGAGCTGGGTGGAGTACT 1260
 Db 1233 AGTCAGCTGTAAAGAGACACCTTTGTACGTGAGCTTCACTGAGCTGGGTGGAGTACT 1292
 QY 1261 GGATTTGGCTCCCCCGGGGTATCACGCTTTTACTGCGCAGGAGAAATGCCCCCTTTTCCTC 1320

```
Db 1293 GGAATGTTGGCTCCCGGGGATACAGCCTTTTACTGCCAGGAGAAATGCCCTTTTCTC 1352
Qy 1321 TGGCTGATCATCTGAACTCCCACTAATCATGTCATGTTGTTGAGACGTTGGTCAACTCTGTGA 1380
Db 1353 TGGCTGATCATCTGAACTCCCACTAATCATGTCATGTTGTTGAGACGTTGGTCAACTCTGTGA 1412
Qy 1381 ACTCTAGATTCCTAAGGCACTGTTGTTCCCGACAGAACTCAGTCTATCTCGATGCTGT 1440
Db 1413 ACTCTAAGATTCCTAAGGCACTGTTGTTCCCGACAGAACTCAGTCTATCTCGATGCTGT 1472
Qy 1441 ACCTTTGACGAGATTCGAAAGGTTGTTAATAAGAACTATCAGGACATGTTGTGAGGGTT 1500
Db 1473 ACCTTTGACGAGATTCGAAAGGTTGTTAATAAGAACTATCAGGACATGTTGTGAGGGTT 1532
Qy 1501 GTGGGTGTCGTAGTACGCAAAATTAATAACATAAATATATATA 1547
Db 1533 GTGGGTGTCGTAGTACGCAAAATTAATAACATAAATATATATA 1579

RESULT 9
US-09-949-016-4668
; Sequence 4668, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C0001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4668
; LENGTH: 2185
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-4668
```

```
Query Match 99.9%; Score 1545.4; DB 3; Length 2185;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1546; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGGGACTTCTTGAACCTTGCGGAGAAATTAACCTTGCGCACCCCACTTTTGGCGCGGTGCTT 60
Db 45 GGGGACTTCTTGAACCTTGCGGAGAAATTAACCTTGCGCACCCCACTTTTGGCGCGGTGCTT 104
Qy 61 TGCCCCAGCGAGGCTGCTTCCCATCTCCGAGCCCAACCCGCTCCACCTCTCGGCT 120
Db 105 TGCCCCAGCGAGGCTGCTTCCCATCTCCGAGCCCAACCCGCTCCACCTCTCGGCT 164
Qy 121 TGCCCGACACTGAGACGCTGTTCCAGCGTGAAGAGAGACTGCGGCGCGGCAACCGG 180
Db 165 TGCCCGACACTGAGACGCTGTTCCAGCGTGAAGAGAGACTGCGGCGCGGCAACCGG 224
Qy 181 GAGAAGGAGGAGGCAAGAAAGAAAGCAAGCAATTCGGTCTTGGCCAGGTCTTTTGACC 240
Db 225 GAGAAGGAGGAGGCAAGAAAGAAAGCAAGCAATTCGGTCTTGGCCAGGTCTTTTGACC 284
Qy 241 AGAGTTTTTCAATGTGACGCTCTTTTCAATGCACTGTCCCGCGGTCTTCTTAGACGA 300
Db 285 AGAGTTTTTCAATGTGACGCTCTTTTCAATGCACTGTCCCGCGGTCTTCTTAGACGA 344
Qy 301 CTGCGGTCTCTAAGGTCGACCAATGTTGGCCGGAACCCGCTGTCTTCTAGCTGTGTC 360
Db 345 CTGCGGTCTCTAAGGTCGACCAATGTTGGCCGGAACCCGCTGTCTTCTAGCTGTGTC 404
```

```
Qy 361 TTCCCCAGGTCCTCCGCGCGCGCGCTGGCTCGTTCCGAGCTGCGCGCGCAGGAGT 420
Db 405 TTCCCCAGGTCCTCCGCGCGCGCGCTGGCTCGTTCCGAGCTGCGCGCGCAGGAGT 464
Qy 421 TCGCGCGCGGCTGCTCGCGCGCGCGCTCATCCAGCCCTCTGACGAGGTCTCTGACGAGT 480
Db 465 TCGCGCGCGGCTGCTCGCGCGCGCGCTCATCCAGCCCTCTGACGAGGTCTCTGACGAGT 524
Qy 481 TCGAGTTGCGGCTGCTCAGCATGTTGCGCCCTGAAAAAGAGACCCACCCGAGGAGACG 540
Db 525 TCGAGTTGCGGCTGCTCAGCATGTTGCGCCCTGAAAAAGAGACCCACCCGAGGAGACG 584
Qy 541 CCGTGTGCCCCCTCATGCTAGACCTGTATGCGAGCACTCAGGTGAGCCGGCTCAC 600
Db 585 CCGTGTGCCCCCTCATGCTAGACCTGTATGCGAGCACTCAGGTGAGCCGGCTCAC 644
Qy 601 CCGCCCCAGACCCCGTTGGAGAGGCGAGCCAGCCGAGCCAACTGTGTGCGAGCTTCC 660
Db 645 CCGCCCCAGACCCCGTTGGAGAGGCGAGCCAGCCGAGCCAACTGTGTGCGAGCTTCC 704
Qy 661 ACCATGAAGAATCTTTGGAAGAACTACAGAAAGAGTGGGAAAAACAACCCGAGATCT 720
Db 705 ACCATGAAGAATCTTTGGAAGAACTACAGAAAGAGTGGGAAAAACAACCCGAGATCT 764
Qy 721 TCTTTAATTTAAGTTCTATCCCGAGGAGGAGTTTATCACCTCAGCAGAGCTTCAGGTTT 780
Db 765 TCTTTAATTTAAGTTCTATCCCGAGGAGGAGTTTATCACCTCAGCAGAGCTTCAGGTTT 824
Qy 781 TCCGAGAACAGATGCAAGATGCTTTTAGGAAACAATAGCAGTTTCCATCACCAGATTATA 840
Db 825 TCCGAGAACAGATGCAAGATGCTTTTAGGAAACAATAGCAGTTTCCATCACCAGATTATA 884
Qy 841 TTTATGAATAATCAATAAACCTTGCAACAGCCAACTCGAAATTTCCCGTGCAGCAGCTTTGG 900
Db 885 TTTATGAATAATCAATAAACCTTGCAACAGCCAACTCGAAATTTCCCGTGCAGCAGCTTTGG 944
Qy 901 ACACGAGTTGTTGAATCAGAAATGCAAGAGGTTGGGAAAGTTTGTATGTACCCCGCTG 960
Db 945 ACACGAGTTGTTGAATCAGAAATGCAAGAGGTTGGGAAAGTTTGTATGTACCCCGCTG 1004
Qy 961 TGATGCGGTGGACTGCA CAGGAGCACGCCCAACCAATGGAATTCGTGGTGAAGTGGCCACT 1020
Db 1005 TGATGCGGTGGACTGCA CAGGAGCACGCCCAACCAATGGAATTCGTGGTGAAGTGGCCACT 1064
Qy 1021 TGGAGGAGAAACAAGGTGCTCCAGAGACATGTTAGGTAAGCAGGTCTTTGACCAAG 1080
Db 1065 TGGAGGAGAAACAAGGTGCTCCAGAGACATGTTAGGTAAGCAGGTCTTTGACCAAG 1124
Qy 1081 ATGAACACAGCTGCTCAGATAGGCGCATTTGCTAGTAACTTTTGGCCATGATGGAAG 1140
Db 1125 ATGAACACAGCTGCTCAGATAGGCGCATTTGCTAGTAACTTTTGGCCATGATGGAAG 1184
Qy 1141 GGCAATCTCTCCAAAAAGAGAAAAAGCTCAGCCAAACAACAACAGCGGAAACGCTTA 1200
Db 1185 GGCAATCTCTCCAAAAAGAGAAAAAGCTCAGCCAAACAACAACAGCGGAAACGCTTA 1244
Qy 1201 AGTCAGCTGTAAGAGACACCTTTTGTAGTGAATTCAGTGAATTCAGTGGGTGGAATGACT 1260
Db 1245 AGTCAGCTGTAAGAGACACCTTTTGTAGTGAATTCAGTGAATTCAGTGGGTGGAATGACT 1304
Qy 1261 GGATTTGGCTCCCGCGGGTATCAGCCCTTTTACTGCCAGGAGATGCCCTTTTCTC 1320
Db 1305 GGATTTGGCTCCCGCGGGTATCAGCCCTTTTACTGCCAGGAGATGCCCTTTTCTC 1364
Qy 1321 TGGCTGATCATCTGAACTCCCACTAATCATGTCATGTTGTTGAGACGTTGGTCAACTCTGTTA 1380
Db 1365 TGGCTGATCATCTGAACTCCCACTAATCATGTCATGTTGTTGAGACGTTGGTCAACTCTGTTA 1424
Qy 1381 ACTCTAAGATTCCTAAGGCACTGTTGTTCCCGACAGAACTCAGTGTCTATCTCGATGCTGT 1440
Db 1425 ACTCTAAGATTCCTAAGGCACTGTTGTTCCCGACAGAACTCAGTGTCTATCTCGATGCTGT 1484
Qy 1441 ACCTTGACGAGATGAAAAAGGTTGTTAATAAGAACTATCAGGACATGTTGTGAGGGTT 1500
```

Db 1485 ACCTTGACGAGATGAAGAGGTTGTATTAAAGAACTATCAGGACATGTTGTGGGGTT 1544
Qy 1501 GTGGGTGTCGTAGTACAGCAAAATTAATAACATAATATATATATA 1547
Db 1545 GTGGGTGTCGTAGTACAGCAAAATTAATAACATAATATATATATA 1591

RESULT 10

US-07-679-451-1
; Sequence 1, Application US/07679451
; Patent No. 531898
; GENERAL INFORMATION:
; APPLICANT: Israel, David I.
; TITLE OF INVENTION: IMPROVED PRODUCTION OF RECOMBINANT
; TITLE OF INVENTION: BONE-INDUCING PROTEINS
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Legal Affairs, Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140-2387
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/679,451
; FILING DATE: 19910402
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/179,100
; FILING DATE: 08-APR-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: McDaniels, Patricia A.
; REGISTRATION NUMBER: 33,194
; REFERENCE/DOCKET NUMBER: GI 5180
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-876-1170
; TELEFAX: 617-876-5851
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1607 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: homo sapiens
; IMMEDIATE SOURCE:
; CLONE: HUMBP11-CDNA-39
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: 1..355
; FEATURE:
; NAME/KEY: 3'UTR
; LOCATION: 1544..1607
; PUBLICATION INFORMATION:
; DOCUMENT NUMBER: US 5,013,649
; FILING DATE: 08-APR-1988
; PUBLICATION DATE: 07-MAY-1991

US-07-679-451-1

Query Match 99.8%; Score 1543.8; DB 2; Length 1607;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1545; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 GGGGACTTCTTGAACCTTGAGGGAGAAATCTTGGCGACCCCACTTTGGCGCGGTGCCTT 60
Db 33 GGGGACTTCTTGAACCTTGAGGGAGAAATCTTGGCGACCCCACTTTGGCGCGGTGCCTT 92

Qy 61 TGCCCCAGCGAGCCTCTCGCCATCTCGAGCCCAACGCGCCCTCCACTCTCTCGGCCT 120
Db 93 TGCCCCAGCGAGCCTCTCTCGCCATCTCGAGCCCAACGCGCCCTCCACTCTCTCGGCCT 152
Qy 121 TGCCCGACACTGAGACGCTGTTCCAGCGTGAAGAGAGACTGCGGCGCGGCAACCGG 180
Db 153 TGCCCGACACTGAGACGCTGTTCCAGCGTGAAGAGAGACTGCGGCGCGGCAACCGG 212
Qy 181 GAGAGGAGGAGGCAAGAGAAAGCAATTCGGTCTCTTGCGCCAGGTCTCTTGACC 240
Db 213 GAGAGGAGGAGGCAAGAGAAAGCAATTCGGTCTCTTGCGCCAGGTCTCTTGACC 272
Qy 241 AGAGTTTTTCCATGTGACGCTCTTTCAATGAGAGTGTCCCCGGGTGCTCTTTAGACGGA 300
Db 273 AGAGTTTTTCCATGTGACGCTCTTTCAATGAGAGTGTCCCCGGGTGCTCTTTAGACGGA 332
Qy 301 CTGCGGTCTCTTAAAGTFCGACATAGTGGCGGAGACCGCTGCTCTTAGGTGCTGC 360
Db 333 CTGCGGTCTCTTAAAGTFCGACATAGTGGCGGAGACCGCTGCTCTTAGGTGCTGC 392
Qy 361 TTCCCCAGGTCTCTTGCGGCGGCGGCTGCTGCTTCCGAGCTGGCGCGCAGGAAGT 420
Db 393 TTCCCCAGGTCTCTTGCGGCGGCGGCTGCTGCTTCCGAGCTGGCGCGCAGGAAGT 452
Qy 421 TCGCGGCGGCGTCTGTCGGGCGGCGCTCATCCAGCCCTCTGAGCAGAGTCTCTGAGCGAGT 480
Db 453 TCGCGGCGGCGTCTGTCGGGCGGCGCTCATCCAGCCCTCTGAGCAGAGTCTCTGAGCGAGT 512
Qy 481 TCGAGTTGCGGCTCTCAGCATAGTTCGGCTTGAAACAGAGACCCACCCAGCAGGAGCG 540
Db 513 TCGAGTTGCGGCTCTCAGCATAGTTCGGCTTGAAACAGAGACCCACCCAGCAGGAGCG 572
Qy 541 CCGTGGTGGCCCCCTACATGCTAGACCTGTATCGCAGGCATCTCAGGTGAGCGGGCTCAC 600
Db 573 CCGTGGTGGCCCCCTACATGCTAGACCTGTATCGCAGGCATCTCAGGTGAGCGGGCTCAC 632
Qy 601 CCGCCCCAGACACCGGTTGGAGAGGCGCAGCCAGCCAGCCAACTCTGTGCGCAGCTTCC 660
Db 633 CCGCCCCAGACACCGGTTGGAGAGGCGCAGCCAGCCAGCCAACTCTGTGCGCAGCTTCC 692
Qy 661 ACCATGAAGAACTTTTGAAGAACTACCAAGAAACGAGTGGGAAACAAACCGGAGATTCT 720
Db 693 ACCATGAAGAACTTTTGAAGAACTACCAAGAAACGAGTGGGAAACAAACCGGAGATTCT 752
Qy 721 TCTTTAATTTAAGTTCTATCCCGAGGAGTTTATCACCTCAGCAGAGCTTTCAGGTTT 780
Db 753 TCTTTAATTTAAGTTCTATCCCGAGGAGTTTATCACCTCAGCAGAGCTTTCAGGTTT 812
Qy 781 TCCGAGAACAGATGCAAGATGCTTTAGGAAACAAATAGCAGTTTCCATCACCGAAATTAATA 840
Db 813 TCCGAGAACAGATGCAAGATGCTTTAGGAAACAAATAGCAGTTTCCATCACCGAAATTAATA 872
Qy 841 TTTATGAATCATAAACCTCGAACAGCCAACTCGAAATTCCTGTAACAGACTTTTGG 900
Db 873 TTTATGAATCATAAACCTCGAACAGCCAACTCGAAATTCCTGTAACAGACTTTTGG 932
Qy 901 ACACAGGTTGGTGAATCAGAAATGCAAGCAGGTGGGAAAGTTTTCATGTCAACCCCGCTG 960
Db 933 ACACAGGTTGGTGAATCAGAAATGCAAGCAGGTGGGAAAGTTTTCATGTCAACCCCGCTG 992
Qy 961 TGATCGGTGGACTGACAGGAGACCGCAACCATGGATTCTGTGTGGAAGTGGGCCACT 1020
Db 993 TGATCGGTGGACTGACAGGAGACCGCAACCATGGATTCTGTGTGGAAGTGGGCCACT 1052
Qy 1021 TGGAGGAGAAACAAAGGTCTCTCAAGAGACATGTTAGGATAGCAGGTCTTTGCAACCAAG 1080
Db 1053 TGGAGGAGAAACAAAGGTCTCTCAAGAGACATGTTAGGATAGCAGGTCTTTGCAACCAAG 1112
Qy 1081 ATGAACACAGCTGCTCAGATAAGGCCAATTCGTAGTAATCTTTGGCCATGATGGAAG 1140
Db 1113 ATGAACACAGCTGCTCAGATAAGGCCAATTCGTAGTAATCTTTGGCCATGATGGAAG 1172

QY 1141 GGCATCTCTCCACAAAAGAGAAAACGTCAGGCCAAACACAAACAGCGGAAACGCCCTTA 1200
Db 1173 GGCATCTCTCCACAAAAGAGAAAACGTCAGGCCAAACACAAACAGCGGAAACGCCCTTA 1232
QY 1201 AGTCCAGCTGTAAGAGACACCCCTTTGTAGTGGACTTCAGTGACGTGGGGTGGAAATGACT 1260
Db 1233 AGTCCAGCTGTAAGAGACACCCCTTTGTAGTGGACTTCAGTGACGTGGGGTGGAAATGACT 1292
QY 1261 GGATGTGGCTCCCGCGGGGTATCAGCCTTTTACTGCGACGAGAAATGCCCTTTTCCTC 1320
Db 1293 GGATGTGGCTCCCGCGGGGTATCAGCCTTTTACTGCGACGAGAAATGCCCTTTTCCTC 1352
QY 1321 TGGCTGATCATCTGAATCCCACTAATCATGATCCATTTTTCAGACGTTGCTCAACTCTGTTA 1380
Db 1353 TGGCTGATCATCTGAATCCCACTAATCATGATCCATTTTTCAGACGTTGCTCAACTCTGTTA 1412
QY 1381 ACTCTAAGATTCCTAAGGCATGCTGTGTCGCCGACAGAACTCAGTGCTATCTCGATGCTGT 1440
Db 1413 ACTCTAAGATTCCTAAGGCATGCTGTGTCGCCGACAGAACTCAGTGCTATCTCGATGCTGT 1472
QY 1441 ACCTTGACGAGAAAGAAAGTTGTATTAAGAACTATCAGACATGTTGTGAGGGTT 1500
Db 1473 ACCTTGACGAGAAAGAAAGTTGTATTAAGAACTATCAGACATGTTGTGAGGGTT 1532
QY 1501 GTGGGTGTCGTAGTACAGCAAAATTAATACATAAATATATATATA 1547
Db 1533 GTGGGTGTCGTAGTACAGCAAAATTAATACATAAATATATATATA 1579

RESULT 11

US-07-841-646-4

; Sequence 4, Application US/07841646

; Patent No. 5266683

; GENERAL INFORMATION:

; APPLICANT: OPPERMANN, HERMANN

; APPLICANT: OZKAYNAK, ENGIN

; APPLICANT: KUBERASAMPATH, THANGAVEL

; APPLICANT: RUEGER, DAVID C.

; APPLICANT: PANG, ROY H.L.

; TITLE OF INVENTION: OSTEOGENIC DEVICES

; NUMBER OF SEQUENCES: 33

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: TESTA, HURWITZ & THIBEAULT

; STREET: 53 STATE STREET

; CITY: BOSTON

; STATE: MASSACHUSETTS

; COUNTRY: U.S.A.

; ZIP: 02109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/841,646

; FILING DATE: 19920221

; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 810,560

; FILING DATE: 20-DEC-1991

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 827,052

; FILING DATE: 28-JAN-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 660,162

; FILING DATE: 22-FEB-1991

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 621,988

; FILING DATE: 04-DEC-1990

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 621,849

; FILING DATE: 04-DEC-1990

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 621,849

; FILING DATE: 04-DEC-1990

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 616,374
; FILING DATE: 21-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 600,024
; FILING DATE: 18-OCT-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 599,543
; FILING DATE: 18-OCT-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 579,865
; FILING DATE: 07-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 569,920
; FILING DATE: 20-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 483,913
; FILING DATE: 22-FEB-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 422,613
; FILING DATE: 17-OCT-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 315,342
; FILING DATE: 23-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 232,630
; FILING DATE: 15-AUG-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 179,460
; FILING DATE: 08-APR-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: PITCHER, EDMUND R.
; REGISTRATION NUMBER: 27,829
; REFERENCE/DOCKET NUMBER: CRP-001CP6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/248-7100
; TELEFAX: 617/248-7100
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1260 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: HOMO SAPIENS
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 9..1196
; OTHER INFORMATION: /function= "OSTEOGENIC PROTEIN"
; OTHER INFORMATION: /product= "CBMP2A"
; OTHER INFORMATION: /note= "CBMP2A (CDNA) "
US-07-841-646-4

Query Match 79.3%; Score 1227.2; DB 2; Length 1260;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 1229; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

| | | | |
|----|-----|--|-----|
| QY | 316 | GGTCGACCATGGTGGCGGACCGCGCTGCTTCTAGCGTTGCTGCTTCTTCCCGAGGTCTCC | 375 |
| Db | 1 | GGTCGACCATGGTGGCGGACCGCGCTGCTTCTAGCGTTGCTGCTTCTTCCCGAGGTCTCC | 60 |
| QY | 376 | TGGCGCGCGCGCTGGGCTTCGTCGAGAGTGGGCGCGAGAAATTCGCGCGCGGTGCT | 435 |
| Db | 61 | TGGCGCGCGCGCTGGGCTTCGTCGAGAGTGGGCGCGAGAAATTCGCGCGCGGTGCT | 120 |
| QY | 436 | CGGCGCGCGCGCTCATCCAGGCTTCGACGAGTTCGAGAGTTCGAGTTGGGCTGC | 495 |
| Db | 121 | CGGCGCGCGCGCTCATCCAGGCTTCGACGAGTTCGAGAGTTCGAGTTGGGCTGC | 180 |
| QY | 496 | TCAGCATGTTGGGCTTGAAACAGAGACCCCGCGAGGAGCGCGTGTGTCGCCCT | 555 |

| | | | |
|----|------|---|------|
| Db | 181 | TCAGCATGTTGGCGCTGAAACAGANGACCCACCCCGACGAGCGCGTGGTGCCTCCCT | 240 |
| Qy | 556 | ACATGCTAGACCTGTATGCGAGGCACTCAGGTGAGCGGGCTCACCGCCCCAGACCAAC | 615 |
| Db | 241 | ACATGCTAGACCTGTATGCGAGGCACTCGGGTCAAGCGGGCTCACCGCCCCAGACCAAC | 300 |
| Qy | 616 | GGTTGGAGAGGGCAGCAGCGGACCAACTGTGGCAGCTTCCACCATGAAGAATCTT | 675 |
| Db | 301 | GGTTGGAGAGGGCAGCAGCGGACCAACTGTGGCAGCTTCCACCATGAAGAATCTT | 360 |
| Qy | 676 | TGGAAGAACTACCAAGAAACGAGTGGGAAAAACAACCGGAGATCTCTCTTTAAATTAAGTT | 735 |
| Db | 361 | TGGAAGAACTACCAAGAAACGAGTGGGAAAAACAACCGGAGATCTCTCTTTAAATTAAGTT | 420 |
| Qy | 736 | CTATCCCCACGGAGGAGTTTATCACTTCAGCAGAGCTTCAGGTTTCCGAGAAACAGATGC | 795 |
| Db | 421 | CTATCCCCACGGAGGAGTTTATCACTTCAGCAGAGCTTCAGGTTTCCGAGAAACAGATGC | 480 |
| Qy | 796 | AAGATGCTTTAGGAAAAAATAGCAGTTTCCATCACCGAAATTAATATTTATGAATCATAA | 855 |
| Db | 481 | AAGATGCTTTAGGAAAAAATAGCAGTTTCCATCACCGAAATTAATATTTATGAATCATAA | 540 |
| Qy | 856 | AACCTGCAACAGCCAACTCGAAATTCCTCGTGACAGACTTTTGGACACACAGGTTGGTGA | 915 |
| Db | 541 | AACCTGCAACAGCCAACTCGAAATTCCTCGTGACAGACTTTTGGACACACAGGTTGGTGA | 600 |
| Qy | 916 | ATCAGATGCAACAGCAGTGGGAAAGTTTGAATGTCACCCCGCTGTGATCGGTGGACTG | 975 |
| Db | 601 | ATCAGATGCAACAGCAGTGGGAAAGTTTGAATGTCACCCCGCTGTGATCGGTGGACTG | 660 |
| Qy | 976 | CACAGGACACGCCAACCATGGAATTCGTGGTGAAGTGGGCCACTTTCGAGGAGAAACAAG | 1035 |
| Db | 661 | CACAGGACACGCCAACCATGGAATTCGTGGTGAAGTGGGCCACTTTCGAGGAGAAACAAG | 720 |
| Qy | 1036 | GTGTCTCAAGAGACATGTTAGGATAAGCAGGTTCTTTGCACCAAGATGAACACAGCTGGT | 1095 |
| Db | 721 | GTGTCTCAAGAGACATGTTAGGATAAGCAGGTTCTTTGCACCAAGATGAACACAGCTGGT | 780 |
| Qy | 1096 | CACAGATAAGGCCATTCGTACTTAATTTGGCCATGATGAAAAGGCGATCTCTCCACA | 1155 |
| Db | 781 | CACAGATAAGGCCATTCGTACTTAATTTGGCCATGATGAAAAGGCGATCTCTCCACA | 840 |
| Qy | 1156 | AAAGAGAAAAACGTCAGGCAACAAACAGACGCGAAAACGCTTTAAGTCAGCTGTAAGA | 1215 |
| Db | 841 | AAAGAGAAAAACGTCAGGCAACAAACAGACGCGAAAACGCTTTAAGTCAGCTGTAAGA | 900 |
| Qy | 1216 | GACACCTTTGTATGCTGACCTTCAGTGAAGTGGGGTGGATGACTGATTTGGCTCCCC | 1275 |
| Db | 901 | GACACCTTTGTATGCTGACCTTCAGTGAAGTGGGGTGGATGACTGATTTGGCTCCCC | 960 |
| Qy | 1276 | CGGGGTATCAGCCCTTTTACTGCAACGAGAGAAATCCCTTTTCTCTCGCTGATCATCTGA | 1335 |
| Db | 961 | CGGGGTATCAGCCCTTTTACTGCAACGAGAGAAATCCCTTTTCTCTCGCTGATCATCTGA | 1020 |
| Qy | 1336 | ACTCCACTAAATCATGCCAATGTTTCCAGAGTTGGTCAACTCTGTTAACTTAAGATTCCTA | 1395 |
| Db | 1021 | ACTCCACTAAATCATGCCAATGTTTCCAGAGTTGGTCAACTCTGTTAACTTAAGATTCCTA | 1080 |
| Qy | 1396 | AGGCATGCTGTGTCGGACAGAACTCAGTGTATCTCGATGCTGACTTTCGACGAGATG | 1455 |
| Db | 1081 | AGGCATGCTGTGTCGGACAGAACTCAGTGTATCTCGATGCTGACTTTCGACGAGATG | 1140 |
| Qy | 1456 | AAAAGGTTGTATTAAGAACTATCAGGACATGGTTTGGAGGGTGTGGGGTGTGCCTAGT | 1515 |
| Db | 1141 | AAAAGGTTGTATTAAGAACTATCAGGACATGGTTTGGAGGGTGTGGGGTGTGCCTAGT | 1200 |
| Qy | 1516 | ACAGCAAAATTAATACATAAATATATATATA | 1547 |
| Db | 1201 | ACAGCAAAATTAATACATAAATATATATATA | 1232 |

```

: Sequence 14. Application US/07901703
: Patent No. 534654
: GENERAL INFORMATION:
: APPLICANT: RUEGER, DAVID C
: APPLICANT: KUBERASAMPATH, THANGAVEL
: APPLICANT: OPPERMANN, HERMANN
: APPLICANT: OZAKAYAK, ENGIN
: TITLE OP INVENTION: PROSTHETIC DEVICES HAVING ENHANCED
: TITLE OP INVENTION: OSTEOGENIC PROPERTIES
: NUMBER OF SEQUENCES: 22
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: TESTA, HURWITZ & THIBEAULT
: STREET: EXCHANGE PLACE, 53 STATE STREET
: CITY: BOSTON
: STATE: MA
: COUNTRY: USA
: ZIP: 02109
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent in Release #1.0, Version #1.25
: CURRENT APPLICATION NUMBER: US/07/901,703
: APPLICATION NUMBER: 19920616
: FILING DATE: 19920616
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: PITCHER ESQ, EDMUND R
: REGISTRATION NUMBER: 27,829
: REFERENCE/DOCKET NUMBER: STR-057
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 617/248-7000
: INFORMATION FOR SEQ ID NO: 14:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1260 base pairs
: TYPE: NUCLEIC ACID
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: HYPOTHETICAL: NO
: ANTI-SENSE: NO
: ORIGINAL SOURCE:
: ORGANISM: HOMO SAPIENS
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 9..1196
: OTHER INFORMATION: /function= "OSTEOGENIC PROTEIN"
: OTHER INFORMATION: /product= "BMP2A"
: OTHER INFORMATION: /note= "BMP2A (CDNA) "
: US-07-901-703-14

```

| | Query Match | 79.3% | Score 1227.2 | DB 2 | Length 1260 |
|----|-----------------------|---|--------------|----------|-------------|
| | Best Local Similarity | 99.8% | Pred. No. 0 | | |
| | Matches 1229 | Conservative 0 | Mismatches 3 | Indels 0 | Gaps 0 |
| QY | 316 | GGTGACATGTTGGCGCGGACCGCTGCTTCTTAGAGTTGCTGCTTCCCGAGTTCCTCC | 375 | | |
| DB | 1 | GGTGACATGTTGGCGCGGACCGCTGCTTCTTAGAGTTGCTGCTTCCCGAGTTCCTCC | 60 | | |
| QY | 376 | TGGCGCGCGCGCTGGGCTCTGTTCCGAGCTGGGCCCGCAGGAAGTTTCGCGCGCGTGGT | 435 | | |
| DB | 61 | TGGCGCGCGCGCTGGGCTCTGTTCCGAGCTGGGCCCGCAGGAAGTTTCGCGCGCGTGGT | 120 | | |
| QY | 436 | CGGCGCGGCGCTCATCCGAGCCCTCTGACGAGGTCCTGAGCGAGTTTCGAGTTGCGGCTGC | 495 | | |
| DB | 121 | CGGCGCGGCGCTCATCCGAGCCCTCTGACGAGGTCCTGAGCGAGTTTCGAGTTGCGGCTGC | 180 | | |
| QY | 496 | TCAGCATGTTCCGGCTGAAACAGAGACCCACCCCGCAGGAGCGCGTGGTGCAGCCCT | 555 | | |
| DB | 181 | TCAGCATGTTCCGGCTGAAACAGAGACCCACCCCGCAGGAGCGCGTGGTGCAGCCCT | 240 | | |
| QY | 556 | ACATGCTAGACTCTGATCGCAGGCACTCAGGTCAGCCGGGCTCACCCGCGCCCGACCAACC | 615 | | |

Db 241 ACATGCTAGACTGTATCGCAGGACCTCGGGTCAGCGGGCTCACCCGCCCCAGACACC 300
Qy 616 GGTGGAGAGGCGAGCGAGCGCAACACTGTGGCGAGCTTCCACATCAAGATCTT 675
Db 301 GGTGGAGAGGCGAGCGAGCGCAACACTGTGGCGAGCTTCCACCATGAAGATCTT 360
Qy 676 TGGAGACTACCCAGAACGAGTGGAAAAACAACCGGAGATCTCTTTAAATTAAGTT 735
Db 361 TGGAGAACTACCCAGAACGAGTGGAAAAACAACCGGAGATCTCTTTAAATTAAGTT 420
Qy 736 CTATCCCCACGAGGAGTTTATCACTCAGCAGAGCTTCAGGTTTCCGAGAACAGATGC 795
Db 421 CTATCCCCACGAGGAGTTTATCACTCAGCAGAGCTTCAGGTTTCCGAGAACAGATGC 480
Qy 796 AAGATGCTTTAGGAAACAATAGAGTTTCCATCACCGAATTAATATTATGAATCATAA 855
Db 481 AAGATGCTTTAGGAAACAATAGAGTTTCCATCACCGAATTAATATTATGAATCATAA 540
Qy 856 AACCTGCAACAGCCAACTCGAAATTCGCCGTGACAGACTTTTGGACACCAAGTTGGTA 915
Db 541 AACCTGCAACAGCCAACTCGAAATTCGCCGTGACAGACTTTTGGACACCAAGTTGGTA 600
Qy 916 ATCAGATGCAAGCAGGTTGGAAAGTTTGTATGTCACCCCGCTGTGATGCGGTGACTG 975
Db 601 ATCAGATGCAAGCAGGTTGGAAAGTTTGTATGTCACCCCGCTGTGATGCGGTGACTG 660
Qy 976 CACAGGACAGCCCAACCATGATTCGTGGTGGAGTGGCCCACTTGGAGAGAGAAACAAG 1035
Db 661 CACAGGACAGCCCAACCATGATTCGTGGTGGAGTGGCCCACTTGGAGAGAGAAACAAG 720
Qy 1036 GTGTCTCAAGAGACATGTTAGGATAAGCAGGTCTTTGACCAAGAGTGAACACAGCTGGT 1095
Db 721 GTGTCTCAAGAGACATGTTAGGATAAGCAGGTCTTTGACCAAGAGTGAACACAGCTGGT 780
Qy 1096 CACAGATAAGGCCATTGTAGTAACTTTTGGCCATGATGAAAGGGCATCTCTCCACA 1155
Db 781 CACAGATAAGGCCATTGTAGTAACTTTTGGCCATGATGAAAGGGCATCTCTCCACA 840
Qy 1156 AAAGAGAAAAAGTCAAGCAGCAACAAACAGCGGAAACGCCTTAAGTCCAGCTGTAAGA 1215
Db 841 AAAGAGAAAAAGTCAAGCAGCAACAAACAGCGGAAACGCCTTAAGTCCAGCTGTAAGA 900
Qy 1216 GACACCTTTTGTAGTGAACCTTCACTGACGTGGGGTGAAGTCACTGATTTGGCTCCCC 1275
Db 901 GACACCTTTTGTAGTGAACCTTCACTGACGTGGGGTGAAGTCACTGATTTGGCTCCCC 960
Qy 1276 CGGGGTATCAGCCCTTTTACTGCCACGAGAAATGCCCTTTTCTCTGGCTGATCATCTGA 1335
Db 961 CGGGGTATCAGCCCTTTTACTGCCACGAGAAATGCCCTTTTCTCTGGCTGATCATCTGA 1020
Qy 1336 ACTCACTAATCATGCCAATTTGTTCAGAGCTTGGTCAACTGTGTTAACTCTTAAGATTCTTA 1395
Db 1021 ACTCACTAATCATGCCAATTTGTTCAGAGCTTGGTCAACTGTGTTAACTCTTAAGATTCTTA 1080
Qy 1396 AGGATGCTGTGTCGCCAGACACTCAGTGTCTATCTCGATCTGTACCTTACCGAGATG 1455
Db 1081 AGGATGCTGTGTCGCCAGACACTCAGTGTCTATCTCGATCTGTACCTTACCGAGATG 1140
Qy 1456 AAAAGGTTGTATTAAAGAACTATCAGGACATGGTTGTGGAGGGTTGTGGGTGTGCTAGT 1515
Db 1141 AAAAGGTTGTATTAAAGAACTATCAGGATATGGTTGTGGAGGGTTGTGGGTGTGCTAGT 1200
Qy 1516 ACAGAAAAATTAATAATACATAATATATATA 1547
Db 1201 ACAGAAAAATTAATAATACATAATATATATA 1232

RESULT 13
US-08-147-023-4
; Sequence 4, Application US/08147023
; Patent No. 546845
; GENERAL INFORMATION:
; APPLICANT: OPPERMANN, HERMANN

APPLICANT: OZKAYNAK, ENGIN
APPLICANT: KUBERASAMPATH, THANGAVEL
APPLICANT: RUEGER, DAVID C.
APPLICANT: PANG, ROY H.L.
TITLE OF INVENTION: OSTEOGENIC DEVICES
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: TESTA, HORWITZ & THIBEAULT
STREET: 53 STATE STREET
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: U.S.A.
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/08/147,023
APPLICATION NUMBER: US 810,560
FILING DATE: 20-DEC-1991
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 827,052
FILING DATE: 28-JAN-1992
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 660,162
FILING DATE: 22-FEB-1991
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 621,849
FILING DATE: 04-DEC-1990
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 616,374
FILING DATE: 21-NOV-1990
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 600,024
FILING DATE: 18-OCT-1990
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 599,543
FILING DATE: 18-OCT-1990
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 579,865
FILING DATE: 07-SEP-1990
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 569,920
FILING DATE: 20-AUG-1990
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 483,913
FILING DATE: 22-FEB-1990
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 422,613
FILING DATE: 17-OCT-1989
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 315,342
FILING DATE: 23-FEB-1989
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 232,630
FILING DATE: 15-AUG-1988
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 179,460
FILING DATE: 08-APR-1988
ATTORNEY/AGENT INFORMATION:
NAME: PITCHER, EDMUND R.
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: CRP-001CP6
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/248-7000

TELEFAX: 617/248-7100
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1260 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: HOMO SAPIENS
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 9..1196
; OTHER INFORMATION: /function= "OSTEOGENIC PROTEIN"
; OTHER INFORMATION: /product= "CBMP2A"
; OTHER INFORMATION: /note= "CBMP2A (CDNA)"
US-08-147-023-4

Query Match 79.3%; Score 1227.2; DB 2; Length 1260;
Best Local Similarity 99.8%; Pred. No. 0; Mismatches 3; Indels 0; Gaps 0;
Matches 1229; Conservative 0;

QY 316 GGTGACCATGTTGGCGGACCGCTGCTCTTAGCGTTGCTGCTCCCGAGGTCCTCC 375
DB 1 GGTGACCATGTTGGCGGACCGCTGCTCTTAGCGTTGCTGCTCCCGAGGTCCTCC 60

QY 376 TGGGCGGCGCGCTGCGCTGCTTCCGAGCTGGCGCGAGGTTCCGCGGCGTCTGT 435
DB 61 TGGGCGGCGCGCTGCGCTGCTTCCGAGCTGGCGCGAGGTTCCGCGGCGTCTGT 120

QY 436 CGGCGCGCGCTCATCCAGCCCTCTGACGAGTCTGACGAGTTCGAGTTGCGGCTGC 495
DB 121 CGGCGCGCGCTCATCCAGCCCTCTGACGAGTCTGACGAGTTCGAGTTGCGGCTGC 180

QY 496 TCAGCATGTTGGCTGAAACAGAGACCCAGGAGGAGCGCGGTCGCCCT 555
DB 181 TCAGCATGTTGGCTGAAACAGAGACCCAGGAGGAGCGCGGTCGCCCT 240

QY 556 ACATCTAGACCTGTATCGAGGCACTCAGGTGAGCGGCTCACCCGCGCCAGACCA 615
DB 241 ACATCTAGACCTGTATCGAGGCACTCAGGTGAGCGGCTCACCCGCGCCAGACCA 300

QY 616 GGTGAGAGGCGAGCGGCGGAGCACTGTGGGAGCTTCCACCATGAGATCTT 675
DB 301 GGTGAGAGGCGAGCGGCGGAGCACTGTGGGAGCTTCCACCATGAGATCTT 360

QY 676 TGGAGAACTACAGAAACGAGTGGGAAACAAACCGGAGATCTCTTTAATTAAGTT 735
DB 361 TGGAGAACTACAGAAACGAGTGGGAAACAAACCGGAGATCTCTTTAATTAAGTT 420

QY 736 CTATCCCGAGGAGGTTTATCAGCTCAGCAGAGCTTCAGGTTTCCGAGAACAGATGC 795
DB 421 CTATCCCGAGGAGGTTTATCAGCTCAGCAGAGCTTCAGGTTTCCGAGAACAGATGC 480

QY 796 AAGATGCTTTAGAAACAAATAGCAGTTTCCATCAACGAATTAATTAATGAATCA 855
DB 481 AAGATGCTTTAGAAACAAATAGCAGTTTCCATCAACGAATTAATTAATGAATCA 540

QY 856 AACCTGCACAGCAGCACTCGAAATTCGCGTGCAGCAGCTTTTGGACACAGGTTGGA 915
DB 541 AACCTGCACAGCAGCACTCGAAATTCGCGTGCAGCAGCTTTTGGACACAGGTTGGA 600

QY 916 ATCAGAAATCAAGCAGGTTGGGAAAGTTTGTATGTACCCCGCTGTGATCGGTCG 975
DB 601 ATCAGAAATCAAGCAGGTTGGGAAAGTTTGTATGTACCCCGCTGTGATCGGTCG 660

QY 976 CACAGGAGCAGCGCAACCAATGATTCGTTGGTGAAGTGCCCACTTGGAGGAGAAAC 1035
DB 661 CACAGGAGCAGCGCAACCAATGATTCGTTGGTGAAGTGCCCACTTGGAGGAGAAAC 720

QY 1036 GTGCTCTCAAGAGACATGTTAGGATAGCAGGTCCTTTGACCAAGATGAACAGCTGT 1095

DB 721 GTGCTCTCAAGAGACATGTTAGGATAGCAGGTCCTTTGACCAAGATGAACACAGCTGT 780

QY 1096 CACAGATAGGCCCATTTGCTAGTAATCTTTGGCCATGATGGAAAGGCGATCTCTCCACA 1155

DB 781 CACAGATAGGCCCATTTGCTAGTAATCTTTGGCCATGATGGAAAGGCGATCTCTCTCCACA 840

QY 1156 AAAGAGAAAAACGTCAGGCCAAACAAACAGCGGAAACGCTTAAAGTCCAGCTGTAAGA 1215

DB 841 AAAGAGAAAAACGTCAGGCCAAACAAACAGCGGAAACGCTTAAAGTCCAGCTGTAAGA 900

QY 1216 GACACCCCTTTGTCAGTGGACTTTCAGTGACGTGGGGTGGAAATGACTGGATTTGGTCCCC 1275

DB 901 GACACCCCTTTGTCAGTGGACTTTCAGTGACGTGGGGTGGAAATGACTGGATTTGGTCCCC 960

QY 1276 CGGGGTATCAGCGCTTTTACTGCCACCGAGAAATGCCCTTTCTCTGCTGATCATCTGA 1335

DB 961 CGGGGTATCAGCGCTTTTACTGCCACCGAGAAATGCCCTTTCTCTGCTGATCATCTGA 1020

QY 1336 ACTCCACTAATCATGCGCATTTGTCAGACGTTGGTCAACTCTGTTAACTTAAGATTCTTA 1395

DB 1021 ACTCCACTAATCATGCGCATTTGTCAGACGTTGGTCAACTCTGTTAACTTAAGATTCTTA 1080

QY 1396 AGGCATGCTGTGTCGCGACAGAACTCAGTCTGCTATCTCGATGCTGTACCTTGACGAGATG 1455

DB 1081 AGGCATGCTGTGTCGCGACAGAACTCAGTCTGCTATCTCGATGCTGTACCTTGACGAGATG 1140

QY 1456 AAAAGGTTGTTAAAGAACTATCAGGACATGTTGCGAGGGTTGTGGGTTGCTGCTAGT 1515

DB 1141 AAAAGGTTGTTAAAGAACTATCAGGATATGTTGTCGAGGGTTGTGGGTTGCTGCTAGT 1200

QY 1516 ACAGCAAAATTAATATACATAATATATATA 1547

DB 1201 ACAGCAAAATTAATATACATAATATATATA 1232

RESULT 14
US-08-447-570-4
; Sequence 4, Application US/08447570
; Patent No. 5714589
; GENERAL INFORMATION:
; APPLICANT: OPPERMAN, HERMANN
; APPLICANT: OZKAYNAK, ENGIN
; APPLICANT: KUBERASAMPATH, THANGAVEL
; APPLICANT: RUEGER, DAVID C.
; APPLICANT: PANG, ROY H.L.
; TITLE OF INVENTION: OSTEOGENIC DEVICES
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TESTA, HURWITZ & THIBEAULT
; STREET: 53 STATE STREET
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: U.S.A.
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/447,570
; FILING DATE: 21-FEB-1992
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 810,560
; FILING DATE: 20-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 827,052
; FILING DATE: 28-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 660,162
; FILING DATE: 22-FEB-1991

```
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 621,988
;; FILING DATE: 04-DEC-1990
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 621,849
;; FILING DATE: 04-DEC-1990
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 616,374
;; FILING DATE: 21-NOV-1990
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 600,024
;; FILING DATE: 18-OCT-1990
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 599,543
;; FILING DATE: 18-OCT-1990
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 579,865
;; FILING DATE: 07-SEP-1990
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 569,920
;; FILING DATE: 20-AUG-1990
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 483,913
;; FILING DATE: 22-FEB-1990
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 315,342
;; FILING DATE: 23-FEB-1989
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 232,630
;; FILING DATE: 15-AUG-1988
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 179,460
;; FILING DATE: 08-APR-1988
;; ATTORNEY/AGENT INFORMATION:
;; NAME: FITCHER, EDMUND R.
;; REGISTRATION NUMBER: 27,829
;; REFERENCE/DOCKET NUMBER: CRP-001CP6
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 617/248-7000
;; TELEFAX: 617/248-7100
;; INFORMATION FOR SEQ ID NO: 4:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1260 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: cDNA
;; HYPOTHEetical: NO
;; ANTI-SENSE: NO
;; ORIGINAL SOURCE:
;; ORGANISM: HOMO SAPIENS
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 9..1196
;; OTHER INFORMATION: /function= "OSTEOGENIC PROTEIN"
;; OTHER INFORMATION: /product= "CBMP2A"
;; OTHER INFORMATION: /note= "CBMP2A (CDNA)"
US-08-447-570-4

Query Match 79.3%; Score 1227.2; DB 2; Length 1260;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1229; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 316 GGTGACCATGGTGGCGGACCGGCTGTCTTCTAGCGTTGCTGCTTCCCGGAGTCTCC 375
DB 1 GGTGACCATGGTGGCGGAGCCGCGTGTCTTCTAGCGTTGCTGCTTCCCGGAGTCTCC 60

QY 376 TGGGCGGCGCGGCTGGGCTCGTTCGGGAGCTGGGCGGAGGAGTTCCGCGGCGGCTGCT 435
DB 61 TGGGCGGCGGCGGCTGGGCTCGTTCGGGAGCTGGGCGGAGGAGTTCCGCGGCGGCTGCT 120

;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 621,988
;; FILING DATE: 04-DEC-1990
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 621,849
;; FILING DATE: 04-DEC-1990
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 616,374
;; FILING DATE: 21-NOV-1990
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 600,024
;; FILING DATE: 18-OCT-1990
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 599,543
;; FILING DATE: 18-OCT-1990
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 579,865
;; FILING DATE: 07-SEP-1990
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 569,920
;; FILING DATE: 20-AUG-1990
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 483,913
;; FILING DATE: 22-FEB-1990
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 315,342
;; FILING DATE: 23-FEB-1989
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 232,630
;; FILING DATE: 15-AUG-1988
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 179,460
;; FILING DATE: 08-APR-1988
;; ATTORNEY/AGENT INFORMATION:
;; NAME: FITCHER, EDMUND R.
;; REGISTRATION NUMBER: 27,829
;; REFERENCE/DOCKET NUMBER: CRP-001CP6
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 617/248-7000
;; TELEFAX: 617/248-7100
;; INFORMATION FOR SEQ ID NO: 4:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1260 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: cDNA
;; HYPOTHEtical: NO
;; ANTI-SENSE: NO
;; ORIGINAL SOURCE:
;; ORGANISM: HOMO SAPIENS
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 9..1196
;; OTHER INFORMATION: /function= "OSTEOGENIC PROTEIN"
;; OTHER INFORMATION: /product= "CBMP2A"
;; OTHER INFORMATION: /note= "CBMP2A (CDNA)"
US-08-447-570-4

QY 316 GGTGACCATGGTGGCGGACCGGCTGTCTTCTAGCGTTGCTGCTTCCCGGAGTCTCC 375
DB 1 GGTGACCATGGTGGCGGAGCCGCGTGTCTTCTAGCGTTGCTGCTTCCCGGAGTCTCC 60

QY 376 TGGGCGGCGGCTGGGCTCGTTCGGGAGCTGGGCGGAGGAGTTCCGCGGCGGCTGCT 435
DB 61 TGGGCGGCGGCGGCTGGGCTCGTTCGGGAGCTGGGCGGAGGAGTTCCGCGGCGGCTGCT 120
```

Qy 1516 ACAGCAAAATTAATAACATATAATATATATATA 1547
Db 1201 ACAGCAAAATTAATAACATATAATATATATA 1232

RESULT 15
US-08-449-700-4
Sequence 4, Application US/08449700
Patent No. 5863758
GENERAL INFORMATION:
APPLICANT: OPPERMAN, HERMANN
APPLICANT: OZKANAK, ENGIN
APPLICANT: KUBERASAPATH, THANGAVEL
APPLICANT: RUEGER, DAVID C.
APPLICANT: PANG, ROY H.L.
TITLE OF INVENTION: OSTEOGENIC DEVICES
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESS: TESTA, HURWITZ & THIBEAULT
STREET: 53 STATE STREET
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: U.S.A.
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/449,700
FILING DATE: 21-FEB-1992
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 810,560
FILING DATE: 20-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 827,052
FILING DATE: 28-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 660,162
FILING DATE: 22-FEB-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 621,988
FILING DATE: 04-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 621,849
FILING DATE: 04-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 616,374
FILING DATE: 21-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 600,024
FILING DATE: 18-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 599,543
FILING DATE: 18-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 579,865
FILING DATE: 07-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 569,920
FILING DATE: 20-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 483,913
FILING DATE: 22-FEB-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 422,613
FILING DATE: 17-OCT-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 315,342
FILING DATE: 23-FEB-1989
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 232,630
FILING DATE: 15-AUG-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 179,460
FILING DATE: 08-APR-1988
ATTORNEY/AGENT INFORMATION:
NAME: PITCHER, EDMUND R.
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: CRP-001CP6
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/248-7000
TELEFAX: 617/248-7100
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1260 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: HOMO SAPIENS
FEATURE:
NAME/KEY: CDS
LOCATION: 9..1196
OTHER INFORMATION: /function= "OSTEOGENIC PROTEIN"
OTHER INFORMATION: /product= "CBMP2A"
OTHER INFORMATION: /note= "CBMP2A (CDNA)"
US-08-449-700-4

Query Match 79.3%; Score 1227.2; DB 2; Length 1260;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1229; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 316 GGTGACCATGGTGGCGGGGACCCGCTGCTCTTAGCGTTGCTGCTCCCGAGTCTCC 375
Db 1 GGTGACCATGGTGGCGGGGACCCGCTGCTCTTAGCGTTGCTGCTCCCGAGTCTCC 60
Qy 376 TGGGCGGCGGCTGGCTCGTTCGGAGCTGGGCGGAGAGTTCGGCGGGGCTGCT 435
Db 61 TGGGCGGCGGCTGGCTCGTTCGGAGCTGGGCGGAGAGTTCGGCGGGGCTGCT 120
Qy 436 CGGCGCGGCTCATCCAGCCCTCTGACGAGTCTCTGAGCGAGTTCGAGTTGCGGCTGC 495
Db 121 CGGCGCGGCTCATCCAGCCCTCTGACGAGTCTCTGAGCGAGTTCGAGTTGCGGCTGC 180
Qy 496 TCAGCATGTTGGCTGAAACAGAGACCCACCCCGAGGAGCGCGTGGTCCCGCT 555
Db 181 TCAGCATGTTGGCTGAAACAGAGACCCACCCCGAGGAGCGCGTGGTCCCGCT 240
Qy 556 ACATCTAGACTGTATCGCAGGCACTCAGGTCAGCGGGCTCACCCGCCAGACACC 615
Db 241 ACATCTAGACTGTATCGCAGGCACTCAGGTCAGCGGGCTCACCCGCCAGACACC 300
Qy 616 GGTGGAGAGGCGCAGCGGCACTGTCGCGAGCTTCACCATGAAGATCTT 675
Db 301 GGTGGAGAGGCGCAGCGGCACTGTCGCGAGCTTCACCATGAAGATCTT 360
Qy 676 TGGAGAACTACCGAGAAACGAGTGGGAAAAACACCCGAGATCTCTTTTAATTAAGTT 735
Db 361 TGGAGAACTACCGAGAAACGAGTGGGAAAAACACCCGAGATCTCTTTTAATTAAGTT 420
Qy 736 CTATCCCGAGGAGTTTATCCTCAGCAGAGTTCAGGTTTTCGAGAACAGATGC 795
Db 421 CTATCCCGAGGAGTTTATCCTCAGCAGAGTTCAGGTTTTCGAGAACAGATGC 480
Qy 796 AAGATGCTTTAGGAAACAATAGCAGTTTCCATCACCGAATTAATTTATGAATCATAA 855
Db 481 AAGATGCTTTAGGAAACAATAGCAGTTTCCATCACCGAATTAATTTATGAATCATAA 540
Qy 856 AACCTGCAACGCCAACTCGAAATTCGCCGTGACAGACTTTTGACACCGAGTTGGTGA 915

Db 541 AACCTGCAACAGCCAACCTCGAAATTCGCCGTGACCAGTCTTTTGGACACACAGGTTGGTGA 600
Qy 916 ATCAGAATGCAGAGGTGGAAAGTTTGTATGTCACCCCGGCTGTGTATGCGGTGGACTG 975
Db 601 ATCAGAATGCAGAGGTGGAAAGTTTGTATGTCACCCCGGCTGTGTATGCGGTGGACTG 660
Qy 976 CACAGGGACAGCGCCAAACCATGGATTCTGTGTGGAGTGGCCCACTTGGAGGAGAAACAAG 1035
Db 661 CACAGGGACAGCGCCAAACCATGGATTCTGTGTGGAGTGGCCCACTTGGAGGAGAAACAAG 720
Qy 1036 GTGTCTCCAGAGACATGTTAGGATAAGCAGGTCTTTGCCACCAAGATGAACACAGCTGGT 1095
Db 721 GTGTCTCCAGAGACATGTTAGGATAAGCAGGTCTTTGCCACCAAGATGAACACAGCTGGT 780
Qy 1096 CACAGATAAGGCCATTTGCTAGTAACTTTTGGCCATGATGGAAAGGGGATCCTCTCCACA 1155
Db 781 CACAGATAAGGCCATTTGCTAGTAACTTTTGGCCATGATGGAAAGGGGATCCTCTCCACA 840
Qy 1156 AAGAGAAAAACGTCAAGCCAAACACAAACAGCGGAAACGCCCTTAAGTCCAGCTGTAAGA 1215
Db 841 AAGAGAAAAACGTCAAGCCAAACACAAACAGCGGAAACGCCCTTAAGTCCAGCTGTAAGA 900
Qy 1216 GACACCCCTTTGTAGCTGACTTTCAGTGACGTGGGTGGAAATGACTGGATTGTGGCTCCCC 1275
Db 901 GACACCCCTTTGTAGCTGACTTTCAGTGACGTGGGTGGAAATGACTGGATTGTGGCTCCCC 960
Qy 1276 CGGGGTATCAGCCCTTTTACTGCCACGGAGAAATGCCCTTTTCCTCTGGCTGATCATCTGA 1335
Db 961 CGGGGTATCAGCCCTTTTACTGCCACGGAGAAATGCCCTTTTCCTCTGGCTGATCATCTGA 1020
Qy 1336 ACTCCACTAATCATGCCATTTGTTCCAGAGCTTGTGCTCAACTCTGTTAACTCTAAGATTCTTA 1395
Db 1021 ACTCCACTAATCATGCCATTTGTTCCAGAGCTTGTGCTCAACTCTGTTAACTCTAAGATTCTTA 1080
Qy 1396 AGGCATGCTGTGTCCCGACAGAACTCAGTGTCTATCTCGATGCTGTACCTTGACGAGAATG 1455
Db 1081 AGGCATGCTGTGTCCCGACAGAACTCAGTGTCTATCTCGATGCTGTACCTTGACGAGAATG 1140
Qy 1456 AAAAGGTTGTATTAAAGAACTATCAGGACATGGTTGTGGAGGGTTGTGGGTGTCGCTAGT 1515
Db 1141 AAAAGGTTGTATTAAAGAACTATCAGGATATGGTTGTGGAGGGTTGTGGGTGTCGCTAGT 1200
Qy 1516 ACAGCAAAATTAATACATAAATATATATA 1547
Db 1201 ACAGCAAAATTAATACATAAATATATATA 1232

Search completed: January 10, 2006, 23:27:39
Job time : 224 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 10, 2006, 20:27:12 ; Search time 924 Seconds
(without alignments)
13844.943 Million cell updates/sec

Title: US-10-801-648-1
Perfect score: 1547
Sequence: 1 ggggactcttggaactgtca.....aatacataaatatatata 1547

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA Main:
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq.*
4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.*
5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq.*
8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq.*
9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq.*
10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match % | Length | ID | Description |
|------------|--------|---------------|--------|----|--------------------|
| 1 | 1547 | 100.0 | 1547 | 5 | US-10-044-716-1 |
| 2 | 1547 | 100.0 | 1547 | 6 | US-10-286-152A-1 |
| 3 | 1547 | 100.0 | 1547 | 6 | US-10-139-814-1 |
| 4 | 1547 | 100.0 | 1547 | 6 | US-10-366-345-10 |
| 5 | 1547 | 100.0 | 1547 | 6 | US-10-295-027-159 |
| 6 | 1547 | 100.0 | 1547 | 7 | US-10-302-812-19 |
| 7 | 1547 | 100.0 | 1547 | 7 | US-10-283-975A-403 |
| 8 | 1547 | 100.0 | 1547 | 7 | US-10-692-824-1 |
| 9 | 1547 | 100.0 | 1547 | 8 | US-10-801-648-1 |
| 10 | 1547 | 100.0 | 1547 | 9 | US-10-489-740-36 |
| 11 | 1547 | 100.0 | 1547 | 9 | US-10-492-380-1 |
| 12 | 1547 | 100.0 | 1547 | 9 | US-10-917-265-1 |
| 13 | 1547 | 100.0 | 1547 | 9 | US-10-886-947-1 |
| 14 | 1547 | 100.0 | 1607 | 3 | US-09-804-625-3 |
| 15 | 1547 | 100.0 | 1607 | 6 | US-10-397-214-3 |
| 16 | 1547 | 100.0 | 1607 | 9 | US-10-397-214-3 |
| 17 | 1545.4 | 99.9 | 1607 | 6 | US-10-375-150-1 |
| 18 | 1314.8 | 85.0 | 2154 | 6 | US-10-210-951-45 |
| 19 | 1314.8 | 85.0 | 2154 | 6 | US-10-211-884-45 |
| 20 | 1314.8 | 85.0 | 2154 | 6 | US-10-211-858-45 |
| 21 | 1227.2 | 79.3 | 1260 | 2 | US-08-957-425-4 |
| 22 | 1227.2 | 79.3 | 1260 | 6 | US-10-321-799-4 |
| 23 | 1227.2 | 79.3 | 1260 | 7 | US-10-428-997A-4 |

| | | | | | | |
|----|--------|------|--------|---|---------------------|-------------------|
| 24 | 1045.2 | 67.6 | 1314 | 3 | US-09-935-144-39 | Sequence 39, Appl |
| 25 | 1026.2 | 66.3 | 1541 | 7 | US-10-302-812-17 | Sequence 17, Appl |
| 26 | 896.6 | 58.0 | 1233 | 3 | US-09-945-182-27 | Sequence 27, Appl |
| 27 | 896.6 | 58.0 | 1233 | 7 | US-10-779-635-27 | Sequence 27, Appl |
| 28 | 880 | 56.9 | 14759 | 3 | US-03-952-360-1 | Sequence 1, Appl |
| 29 | 880 | 56.9 | 14759 | 6 | US-10-346-723-1 | Sequence 1, Appl |
| 30 | 880 | 56.9 | 173308 | 9 | US-10-756-149-629 | Sequence 629, App |
| 31 | 576 | 37.2 | 576 | 6 | US-10-029-386-20679 | Sequence 20679, A |
| 32 | 538 | 34.8 | 538 | 6 | US-10-029-386-6968 | Sequence 6968, Ap |
| 33 | 440.2 | 28.5 | 508 | 3 | US-09-918-995-21456 | Sequence 21456, A |
| 34 | 380.8 | 24.6 | 1432 | 9 | US-10-169-050-63 | Sequence 63, Appl |
| 35 | 380.8 | 24.6 | 8611 | 9 | US-10-169-050-17 | Sequence 17, Appl |
| 36 | 378 | 24.4 | 381 | 5 | US-10-189-302-1 | Sequence 1, Appl |
| 37 | 378 | 24.4 | 381 | 7 | US-10-354-856-1 | Sequence 23, Appl |
| 38 | 375 | 24.2 | 1400 | 7 | US-10-302-812-23 | Sequence 30, Appl |
| 39 | 375 | 24.2 | 1569 | 6 | US-10-264-049-90 | Sequence 3, Appl |
| 40 | 375 | 24.2 | 1751 | 5 | US-10-189-302-3 | Sequence 1309, Ap |
| 41 | 375 | 24.2 | 1751 | 7 | US-10-240-425-1309 | Sequence 201, App |
| 42 | 375 | 24.2 | 1751 | 8 | US-10-278-698-201 | Sequence 717, App |
| 43 | 375 | 24.2 | 1751 | 8 | US-10-278-698-717 | Sequence 6, Appl |
| 44 | 375 | 24.2 | 1788 | 2 | US-08-957-425-6 | Sequence 6, Appl |
| 45 | 375 | 24.2 | 1788 | 6 | US-10-321-799-6 | Sequence 6, Appl |

ALIGNMENTS

RESULT 1
US-10-044-716-1
; Sequence 1, Application US/10044716
; Publication No. US2002015986A1
; GENERAL INFORMATION:
; APPLICANT: LANGENFELD, John
; TITLE OF INVENTION: BONE MORPHOGENETIC PROTEIN-2 IN THE TREATMENT AND DIAGNOSIS OF CA
; FILE REFERENCE: 270/07005
; CURRENT APPLICATION NUMBER: US/10/044,716
; CURRENT FILING DATE: 2002-01-11
; PRIOR APPLICATION NUMBER: US60/261,252
; PRIOR FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1547
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: source
; LOCATION: (1)..(1547)
; OTHER INFORMATION: Homo sapiens: Taxon:9606
; NAME/KEY: gene
; LOCATION: (1)..(1547)
; OTHER INFORMATION: BMP2
; NAME/KEY: CDS
; LOCATION: (324)..(1514)
; OTHER INFORMATION:
; NAME/KEY: misc feature
; LOCATION: (429)..(1127)
; OTHER INFORMATION: Region: TGF-beta propeptide
; NAME/KEY: variation
; LOCATION: (432)..(432)
; OTHER INFORMATION: Allele = "T"; Allele = "G"
; NAME/KEY: variation
; LOCATION: (584)..(584)
; OTHER INFORMATION: Allele = "A"; Allele = "G"
; NAME/KEY: variation
; LOCATION: (893)..(893)
; OTHER INFORMATION: Allele = "T"; Allele = "A"
; NAME/KEY: misc feature
; LOCATION: (1209)..(1511)
; OTHER INFORMATION: TGF-beta; Region: Transforming growth factor beta like domain
; NAME/KEY: misc feature
; LOCATION: (1209)..(1511)
; OTHER INFORMATION: TGF-beta; Region: Transforming growth factor-beta (TGF-beta) family

US-10-044-716-1

```
Query Match      100.0%; Score 1547; DB 5; Length 1547;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1547; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGACTCTTCTGAACTTGCAGGAGATAAATCTTGCACACCCCACTTTTGGCGCGGTGCTTT 60
Db 1 GGGGACTCTTCTGAACTTGCAGGAGATAAATCTTGCACACCCCACTTTTGGCGCGGTGCTTT 60

Qy 61 TGGCCCGAGCGAGCTGCTTCCGATCTCCGAGCCCAACCGCCCTCCACTCTCCGCGCT 120
Db 61 TGGCCCGAGCGAGCTGCTTCCGATCTCCGAGCCCAACCGCCCTCCACTCTCCGCGCT 120

Qy 121 TGGCCCGACACTGAGACGCTGTTCCGAGCTGTAAGAGAGAGACTGCGGCGCGGACCCGG 180
Db 121 TGGCCCGACACTGAGACGCTGTTCCGAGCTGTAAGAGAGAGACTGCGGCGCGGACCCGG 180

Qy 181 GAGAAGGAGGAGGCAAGAAAAGAAACGACATTCGGTCTTGGCCAGAGTCCCTTTGACC 240
Db 181 GAGAAGGAGGAGGCAAGAAAAGAAACGACATTCGGTCTTGGCCAGAGTCCCTTTGACC 240

Qy 241 AGAGTTTTTCCATGATGGACGCTCTTTCAATGGAGAGTGTCCCGCGTGTCTTTAGACGGA 300
Db 241 AGAGTTTTTCCATGATGGAGCGCTCTTTCAATGGAGAGTGTCCCGCGTGTCTTTAGACGGA 300

Qy 301 CTGGCGTCTCTTAAAGTTCGACATGTTGGCGCGGACCCGCTGTCCTTAGCGTTGCTGC 360
Db 301 CTGGCGTCTCTTAAAGTTCGACATGTTGGCGCGGACCCGCTGTCCTTAGCGTTGCTGC 360

Qy 361 TTCCCGAGTCTCTTGGCGCGGCGCTGCTTCAATGGAGAGTGTCCCGAGTGTCCGCGGAGAGT 420
Db 361 TTCCCGAGTCTCTTGGCGCGGCGGCTGCTTCAATGGAGAGTGTCCCGAGTGTCCGCGGAGAGT 420

Qy 421 TCGCGGCGGCGTCTGTCGCGCGCGCCCTCATCCAGACCTCTGAGAGAGTCTGAGCGAGT 480
Db 421 TCGCGGCGGCGTCTGTCGCGCGCGCCCTCATCCAGACCTCTGAGAGAGTCTGAGCGAGT 480

Qy 481 TCGAGTTTGGCGCTGCTAGCATGTTTGGCGCTGAAACAGAGACCCACCCCGAGCGAGCG 540
Db 481 TCGAGTTTGGCGCTGCTAGCATGTTTGGCGCTGAAACAGAGACCCACCCCGAGCGAGCG 540

Qy 541 CCGTGGTGCCCGCTTACATGCTAGACCTGTATCGAGGACCTCAGGTGAGCGCGGCTCAC 600
Db 541 CCGTGGTGCCCGCTTACATGCTAGACCTGTATCGAGGACCTCAGGTGAGCGCGGCTCAC 600

Qy 601 CCGCCCGAGACACCGGTTGAGAGGCGAGCCAGCGGACCAACACTGTGCGCAGCTTCC 660
Db 601 CCGCCCGAGACACCGGTTGAGAGGCGAGCCAGCGGACCAACACTGTGCGCAGCTTCC 660

Qy 661 ACCATGAAGATCTTTGGAAGAACTACAGAAACGAGTGGGAAACCAACCGGAGATTCT 720
Db 661 ACCATGAAGATCTTTGGAAGAACTACAGAAACGAGTGGGAAACCAACCGGAGATTCT 720

Qy 721 TCTTTAATTTAAGTTCTATCCCGAGGAGTGTATCACCTCAGCAGAGCTTCAGGTTT 780
Db 721 TCTTTAATTTAAGTTCTATCCCGAGGAGTGTATCACCTCAGCAGAGCTTCAGGTTT 780

Qy 781 TCCGAGAACAGATGCAAGATGCTTTAGGAAACAAATAGCAGTTCATCACCGAATTAAATA 840
Db 781 TCCGAGAACAGATGCAAGATGCTTTAGGAAACAAATAGCAGTTCATCACCGAATTAAATA 840

Qy 841 TTTATGAAATCATAAAACCTTCGAACAGCCAACTCGAAATTCCTCCGTCGACAGACTTTTGG 900
Db 841 TTTATGAAATCATAAAACCTTCGAACAGCCAACTCGAAATTCCTCCGTCGACAGACTTTTGG 900

Qy 901 ACACGAGTTGGTGAATCAGAACTCAAGCAGGTGGGAAAGTTTGTATGTCACCCCGCTG 960
Db 901 ACACGAGTTGGTGAATCAGAACTCAAGCAGGTGGGAAAGTTTGTATGTCACCCCGCTG 960

Qy 961 TGATGCGGTGGACTGCAACAGGGAACAGCCAACTGGAATTCGTTGGTGAAGTGGCCCACT 1020
Db 961 TGATGCGGTGGACTGCAACAGGGAACAGCCAACTGGAATTCGTTGGTGAAGTGGCCCACT 1020
```

```
Qy 1021 TGGAGGAGAAACAAGGTGTCTCCAGAGACATGTTAGGATAAGCAGGTCTTTTCACCAAG 1080
Db 1021 TGGAGGAGAAACAAGGTGTCTCCAGAGACATGTTAGGATAAGCAGGTCTTTTCACCAAG 1080

Qy 1081 ATGAACAACAGCTGCTCAGATTAAGGCAATGCTAGTAACTTTTGGCCATGATGGAAGAAG 1140
Db 1081 ATGAACAACAGCTGCTCAGATTAAGGCAATGCTAGTAACTTTTGGCCATGATGGAAGAAG 1140

Qy 1141 GGCAATCCTCTCCACAAAGAGAAAAACGTCAGGCAAAACAACACAGCGGAAACGCTTTA 1200
Db 1141 GGCAATCCTCTCCACAAAGAGAAAAACGTCAGGCAAAACAACACAGCGGAAACGCTTTA 1200

Qy 1201 AGTCCAGCTGTAAGAGACACCCCTTTGTACGTGGAATCTCAGTGAGCTGGGTGGATGACT 1260
Db 1201 AGTCCAGCTGTAAGAGACACCCCTTTGTACGTGGAATCTCAGTGAGCTGGGTGGATGACT 1260

Qy 1261 GGATTTGGGTCTCCCGCGGCTATCACGCTTTTACTGCCACGAGAGATGCCCTTTTCTCTC 1320
Db 1261 GGATTTGGGTCTCCCGCGGCTATCACGCTTTTACTGCCACGAGAGATGCCCTTTTCTCTC 1320

Qy 1321 TGGCTGATCATCTGAACTCCACTAATCATGCCATTTGTTCAAGCGTTGGTCAACTCTGTGA 1380
Db 1321 TGGCTGATCATCTGAACTCCACTAATCATGCCATTTGTTCAAGCGTTGGTCAACTCTGTGA 1380

Qy 1381 ACTCTAAGATTCCTTAAGGCAATGCTGTCTCCGACAGAACTCAGTGCTATCTCGATGCTGT 1440
Db 1381 ACTCTAAGATTCCTTAAGGCAATGCTGTCTCCGACAGAACTCAGTGCTATCTCGATGCTGT 1440

Qy 1441 ACCTTGACGAGAAATGAAAAGCTTGTATTAAAGAACTATCAGGACATGTTGTGGAGGTT 1500
Db 1441 ACCTTGACGAGAAATGAAAAGCTTGTATTAAAGAACTATCAGGACATGTTGTGGAGGTT 1500

Qy 1501 GTGGGTGCTGCTAGTCAGCAAAATTAATAATACATAATATATATA 1547
Db 1501 GTGGGTGCTGCTAGTCAGCAAAATTAATAATACATAATATATATA 1547
```

RESULT 2
US-10-286-152A-1
; Sequence 1, Application US/10286152A
; Publication No. US20030134308A1
; GENERAL INFORMATION:
; APPLICANT: Alcon Research, Ltd.
; APPLICANT: Clark, Abbot F.
; TITLE OF INVENTION: Bone Morphogenic Proteins (BMP), BMP Receptors and BMP Binding Pr
; TITLE OF INVENTION: and Their Use in the Diagnosis and Treatment of Glaucoma
; FILE REFERENCE: 2312 US
; CURRENT APPLICATION NUMBER: US/10/286,152A
; CURRENT FILING DATE: 2002-02-28
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1547
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-286-152A-1

```
Query Match      100.0%; Score 1547; DB 6; Length 1547;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1547; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGACTCTTCTGAACTTGCAGGAGATAAATCTTGCACACCCCACTTTTGGCGCGGTGCTTT 60
Db 1 GGGGACTCTTCTGAACTTGCAGGAGATAAATCTTGCACACCCCACTTTTGGCGCGGTGCTTT 60

Qy 61 TGGCCCGAGCGAGCTGCTTCCGATCTCCGAGCCCAACCGCCCTCCACTCTCCGCGCT 120
Db 61 TGGCCCGAGCGAGCTGCTTCCGATCTCCGAGCCCAACCGCCCTCCACTCTCCGCGCT 120

Qy 121 TGGCCCGACACTGAGACGCTGTTCCGAGCTGTAAGAGAGAGACTGCGGCGCGGACCCGG 180
Db 121 TGGCCCGACACTGAGACGCTGTTCCGAGCTGTAAGAGAGAGACTGCGGCGCGGACCCGG 180
```


181 GAGAGGAGGAGGCAAAAGAAAGAAACGACATTCGGTCTTGGCCAGGTCTTTGACC 240
 Db |
 181 GAGAGGAGGAGGCAAAAGAAAGAAACGACATTCGGTCTTGGCCAGGTCTTTGACC 240
 Qy |
 241 AGAGTTTTTCCATGTGGACGCTCTTTTCAATGGAACGTGTCCCGCGTCTTTTAGACGA 300
 Db |
 241 AGAGTTTTTCCATGTGGACGCTCTTTTCAATGGAACGTGTCCCGCGTCTTTTAGACGA 300
 Qy |
 301 CTGCGGTCTCTTAAGGTTCGACCATGTTGGCCGGAACCGTCTTCTTAGGTGCTGC 360
 Db |
 301 CTGCGGTCTCTTAAGGTTCGACCATGTTGGCCGGAACCGTCTTCTTAGGTGCTGC 360
 Qy |
 361 TTCCCCAGGTCTCTTGGCGGCGGCTGGCTCTTGGGAGCTGGGCGCGCAGGAAGT 420
 Db |
 361 TTCCCCAGGTCTCTTGGCGGCGGCTGGCTCTTGGGAGCTGGGCGCGCAGGAAGT 420
 Qy |
 421 TCGCGCGGCGTCTTGGCGGCGGCTCTTGGGAGCTGGGCGCGCAGGAAGT 480
 Db |
 421 TCGCGCGGCGTCTTGGCGGCGGCTCTTGGGAGCTGGGCGCGCAGGAAGT 480
 Qy |
 481 TCGAGTTGGGCTGTCTGACATGTTTCGGCTGAAACAGAGACCCACCCGACGAGGAG 540
 Db |
 481 TCGAGTTGGGCTGTCTGACATGTTTCGGCTGAAACAGAGACCCACCCGACGAGGAG 540
 Qy |
 541 CCGTGTGCCCCCTTACATGCTAGACCTGTATCGCAGGCACCTCAGGTGAGCGGCTCAC 600
 Db |
 541 CCGTGTGCCCCCTTACATGCTAGACCTGTATCGCAGGCACCTCAGGTGAGCGGCTCAC 600
 Qy |
 601 CGCGCCCGACACACCGGTTGGAGGGGAGCGGAGCCGAGCCAACTGTGGCAGCTTCC 660
 Db |
 601 CGCGCCCGACACACCGGTTGGAGGGGAGCGGAGCCGAGCCAACTGTGGCAGCTTCC 660
 Qy |
 661 ACCATGAGAAATCTTTGGAAGAACTACCGAAGAACGAGTGGGAAACAAACCGGAGTCT 720
 Db |
 661 ACCATGAGAAATCTTTGGAAGAACTACCGAAGAACGAGTGGGAAACAAACCGGAGTCT 720
 Qy |
 721 TCTTTAATTAAGTTCTATCCCGGAGGAGTTTATCCTCAGCAGGCTTCAGGTTT 780
 Db |
 721 TCTTTAATTAAGTTCTATCCCGGAGGAGTTTATCCTCAGCAGGCTTCAGGTTT 780
 Qy |
 781 TCCGAGAACAGATGCAAGATGCTTTAGGAAACAAATAGCAGTTTCCATCACCGAATTAATA 840
 Db |
 781 TCCGAGAACAGATGCAAGATGCTTTAGGAAACAAATAGCAGTTTCCATCACCGAATTAATA 840
 Qy |
 841 TTTATGAATCATATAAACTCTGCAACAGCCAACTCGAAATTCCTCGTACGACGACTTTGG 900
 Db |
 841 TTTATGAATCATATAAACTCTGCAACAGCCAACTCGAAATTCCTCGTACGACGACTTTGG 900
 Qy |
 901 ACACAGGTTGGTGAATCAGATGCAAGCAGGTGGGAAAGTTTGTATGTCACCCCGCTG 960
 Db |
 901 ACACAGGTTGGTGAATCAGATGCAAGCAGGTGGGAAAGTTTGTATGTCACCCCGCTG 960
 Qy |
 961 TGATCGGTGGAGTGCACAGGAGACCGCCAAACATGGATTCTGTGGTGGAGTGGCCACT 1020
 Db |
 961 TGATCGGTGGAGTGCACAGGAGACCGCCAAACATGGATTCTGTGGTGGAGTGGCCACT 1020
 Qy |
 1021 TGGAGAGAGAAACAAGGTGCTCAAGAGACATGTTAGGATAAGCAGGTCTTTGCAACCAAG 1080
 Db |
 1021 TGGAGAGAGAAACAAGGTGCTCAAGAGACATGTTAGGATAAGCAGGTCTTTGCAACCAAG 1080
 Qy |
 1081 ATGAACAGCTGGTCAAGATAAGCCATTTCTAGTAATTTTGGCCATGATGGAAG 1140
 Db |
 1081 ATGAACAGCTGGTCAAGATAAGCCATTTCTAGTAATTTTGGCCATGATGGAAG 1140
 Qy |
 1141 GGCATCTCTCCACAAAAGAGAAACAGTCAAGCCAAACACAAACAGCGGAAACGCTTA 1200
 Db |
 1141 GGCATCTCTCCACAAAAGAGAAACAGTCAAGCCAAACACAAACAGCGGAAACGCTTA 1200
 Qy |
 1201 AGTCCAGCTGTAAGAGACACCTTTGTACGTGAGCTTCAGTGACGCTGGGGTGGAAATGACT 1260
 Db |
 1201 AGTCCAGCTGTAAGAGACACCTTTGTACGTGAGCTTCAGTGACGCTGGGGTGGAAATGACT 1260

RESULT 3

US-10-139-814-1
 ; Sequence 1, Application US/10139814
 ; Publication No. US20030134790A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Langenfeld, John
 ; TITLE OF INVENTION: BONE MORPHOGENETIC PROTEIN-2 IN THE TREATMENT AND DIAGNOSIS OF
 ; TITLE OF INVENTION: CANCER
 ; FILE REFERENCE: 273/136 Michael J. Wise
 ; CURRENT APPLICATION NUMBER: US/10/139,814
 ; PRIOR FILING DATE: 2002-05-02
 ; PRIOR APPLICATION NUMBER: US60/261,252
 ; PRIOR FILING DATE: 2001-01-12
 ; PRIOR APPLICATION NUMBER: US10/044,716
 ; PRIOR FILING DATE: 2002-01-11
 ; NUMBER OF SEQ ID NOS: 18
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 1
 ; LENGTH: 1547
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: source
 ; LOCATION: (1)..(1547)
 ; OTHER INFORMATION: Homo sapiens: Taxon:9606
 ; FEATURE:
 ; NAME/KEY: Gene
 ; LOCATION: (1)..(1547)
 ; OTHER INFORMATION: BMP2
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (324)..(1514)
 ; OTHER INFORMATION:
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (429)..(1127)
 ; OTHER INFORMATION: Region: TGF-beta propeptide
 ; FEATURE:
 ; NAME/KEY: variation
 ; LOCATION: (432)..(432)
 ; OTHER INFORMATION: Allele = "T"; Allele = "G"
 ; FEATURE:
 ; NAME/KEY: variation
 ; LOCATION: (584)..(584)
 ; OTHER INFORMATION: Allele = "A"; Allele = "G"
 ; FEATURE:
 ; NAME/KEY: variation
 ; LOCATION: (893)..(893)
 ; OTHER INFORMATION: Allele = "T"; Allele = "A"
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (1205)..(1511)

OTHER INFORMATION: TGF-beta; Region: Transforming growth factor beta like domain
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1205)..(1511)
; OTHER INFORMATION: TGF-beta; Region: Transforming growth factor-beta (TGF-beta) family
US-10-139-814-1

Query Match 100.0%; Score 1547; DB 6; Length 1547;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1547; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGACTTCTTGAACCTTGCAGGAGAAATAAATTGCGCACCCCACTTTGCGCGCGTGCCTT 60
Db 1 GGGGACTTCTTGAACCTTGCAGGAGAAATAAATTGCGCACCCCACTTTGCGCGCGTGCCTT 60

Qy 61 TGCCCCAGCGAGGCTGTTGCCATCTCCAGAGCCCAACCGCCCTCCATCTCTCGGCT 120
Db 61 TGCCCCAGCGAGGCTGTTGCCATCTCCAGAGCCCAACCGCCCTCCATCTCTCGGCT 120

Qy 121 TGCCCCGACACTGAGACGCTGTTCCAGCGTGAAGAAGAGACTGCGGCGCGGACCCGG 180
Db 121 TGCCCCGACACTGAGACGCTGTTCCAGCGTGAAGAAGAGACTGCGGCGCGGACCCGG 180

Qy 181 GAGAGGAGGAGGCAAGAAAGGAAACGGAATTCGGTCTTGGCGCCAGGTCTCTTGACC 240
Db 181 GAGAGGAGGAGGCAAGAAAGGAAACGGAATTCGGTCTTGGCGCCAGGTCTCTTGACC 240

Qy 241 AGAGTTTTCATGTGACGCTCTTTTCAATGGAAGCTGTCGCCGCTCTTTAGACGGA 300
Db 241 AGAGTTTTCATGTGACGCTCTTTTCAATGGAAGCTGTCGCCGCTCTTTAGACGGA 300

Qy 301 CTGCGGTCTCTAAAGTTCAGACCTGTTGGCGCGGAGCCCGTCTCTTCTAGCGTTGCTGC 360
Db 301 CTGCGGTCTCTAAAGTTCAGACCTGTTGGCGCGGAGCCCGTCTCTTCTAGCGTTGCTGC 360

Qy 361 TTCCCCAGGTCTCTTGGCGCGGCGGCTGCGCTCTGTTTCCGAGCTTGGCGCGGAGGAGT 420
Db 361 TTCCCCAGGTCTCTTGGCGCGGCGGCTGCGCTCTGTTTCCGAGCTTGGCGCGGAGGAGT 420

Qy 421 TCGCGGCGGCTGCTGCGGCGGCGGCTCTATCCAGCCCTCTGACGAGTCTGACGAGT 480
Db 421 TCGCGGCGGCTGCTGCGGCGGCGGCTCTATCCAGCCCTCTGACGAGTCTGACGAGT 480

Qy 481 TCGAGTTGCGGCTCTCAGCATGTTCCGCTGAAACAGAGACCCACCCAGCAGGAGCG 540
Db 481 TCGAGTTGCGGCTCTCAGCATGTTCCGCTGAAACAGAGACCCACCCAGCAGGAGCG 540

Qy 541 CCGTGTGCCCCCTACATGCTAGACCTGTATCGCAGCACTCAGGTGAGCGCGGCTCAC 600
Db 541 CCGTGTGCCCCCTACATGCTAGACCTGTATCGCAGCACTCAGGTGAGCGCGGCTCAC 600

Qy 601 CCGGCGCAGACACCGGTTGAGAGGGGAGCCAGCGAGCCAACTGTGCGCAGCTTCC 660
Db 601 CCGGCGCAGACACCGGTTGAGAGGGGAGCCAGCGAGCCAACTGTGCGCAGCTTCC 660

Qy 661 ACCATGAGATCTTTGGAAGAACTACAGAAAGCTTGGAAACCAACCCGAGATCT 720
Db 661 ACCATGAGATCTTTGGAAGAACTACAGAAAGCTTGGAAACCAACCCGAGATCT 720

Qy 721 TCTTTAATTTAAGTTCTATCCCGCAGGAGGTTTATCACCTCAGCAGAGCTTCAGGTTT 780
Db 721 TCTTTAATTTAAGTTCTATCCCGCAGGAGGTTTATCACCTCAGCAGAGCTTCAGGTTT 780

Qy 781 TCCGAGAACAGATGAGATGCTTTAGAAACAATAGCAGTTTTCATCACCGAATTAATA 840
Db 781 TCCGAGAACAGATGAGATGCTTTAGAAACAATAGCAGTTTTCATCACCGAATTAATA 840

Qy 841 TTTATGAATCATAAACCTGCAACAGCCACTCGAAATTCGCCGTCACAGACTTTGG 900
Db 841 TTTATGAATCATAAACCTGCAACAGCCACTCGAAATTCGCCGTCACAGACTTTGG 900

Qy 901 ACACGAGTTGGTGAATCAGAAATCAAGCAGGTGGGAAAGTTTGTGATGTACACCCCGCTG 960
Db 901 ACACGAGTTGGTGAATCAGAAATCAAGCAGGTGGGAAAGTTTGTGATGTACACCCCGCTG 960

Db 901 ACACGAGTTGGTGAATCAGAAATCAAGCAGGTGGGAAAGTTTGTGATGTACACCCCGCTG 960
Qy 961 TGATCGCGTGGACTGCAACAGGACACGCCAACCAATGGAATTCGTGGTGAAGTGGCCACT 1020
Db 961 TGATCGCGTGGACTGCAACAGGACACGCCAACCAATGGAATTCGTGGTGAAGTGGCCACT 1020

Qy 1021 TGAGAGGAGAAACAAGGTGCTCTCCAGAGACATGTTAGGATAAGCAGGTCTTTGACCAAG 1080
Db 1021 TGAGAGGAGAAACAAGGTGCTCTCCAGAGACATGTTAGGATAAGCAGGTCTTTGACCAAG 1080

Qy 1081 ATGAACACAGCTGCTGTCACAGATAAGGCCATTTGCTAGTAACCTTTGGCCATGATGAAAG 1140
Db 1081 ATGAACACAGCTGCTGTCACAGATAAGGCCATTTGCTAGTAACCTTTGGCCATGATGAAAG 1140

Qy 1141 GGCATCTCTCCAAAAGAGAAAACGTCAGCCAAACACAAACAGCGGAAACGCTTTA 1200
Db 1141 GGCATCTCTCCAAAAGAGAAAACGTCAGCCAAACACAAACAGCGGAAACGCTTTA 1200

Qy 1201 AGTCACGCTGTAAGAGACACCTTTGTACGTGGACTTTCAGTGACGTGGGTGGAATGACT 1260
Db 1201 AGTCACGCTGTAAGAGACACCTTTGTACGTGGACTTTCAGTGACGTGGGTGGAATGACT 1260

Qy 1261 GGAATTTGGTCTCCCGCGGGGTATCACGCTTTTACTGCCACGAGAAATGCCCTTTCTC 1320
Db 1261 GGAATTTGGTCTCCCGCGGGGTATCACGCTTTTACTGCCACGAGAAATGCCCTTTCTC 1320

Qy 1321 TGGCTGATCATCTGAACTCCACTAATCATGCGCATTTGTTAGACGTTGGTCACTCTGTTA 1380
Db 1321 TGGCTGATCATCTGAACTCCACTAATCATGCGCATTTGTTAGACGTTGGTCACTCTGTTA 1380

Qy 1381 ACTTAAGATTCTTAAGCGATGCTGTCGCCGACAGAACTCAGTGCTATCTCGATGCTGT 1440
Db 1381 ACTTAAGATTCTTAAGCGATGCTGTCGCCGACAGAACTCAGTGCTATCTCGATGCTGT 1440

Qy 1441 ACCTTGAACGAGAAATGAAAAGGTTGTATTAAAGAACTATCAGGACATGTTGTGAGGGTT 1500
Db 1441 ACCTTGAACGAGAAATGAAAAGGTTGTATTAAAGAACTATCAGGACATGTTGTGAGGGTT 1500

Qy 1501 GTGGGTCTGCTAGTAGCAGCAAAATTAATAATACATAAATATATATA 1547
Db 1501 GTGGGTCTGCTAGTAGCAGCAAAATTAATAATACATAAATATATATA 1547

RESULT 4
US-10-366-345-10
; Sequence 10, Application US/10366345
; Publication No. US20030224501A1
; GENERAL INFORMATION:
; APPLICANT: Young, et al.
; TITLE OF INVENTION: Bone Morphogenetic Protein Polynucleotides, Polypeptides and
; TITLE OF INVENTION: Antibodies
; FILE REFERENCE: PT189
; CURRENT APPLICATION NUMBER: US/10/366,345
; CURRENT FILING DATE: 2003-02-14
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 1547
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-366-345-10

Query Match 100.0%; Score 1547; DB 6; Length 1547;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1547; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGACTTCTTGAACCTTGCAGGAGAAATAAATTGCGCACCCCACTTTGCGCGGCTGCCTT 60
Db 1 GGGGACTTCTTGAACCTTGCAGGAGAAATAAATTGCGCACCCCACTTTGCGCGGCTGCCTT 60

Qy 61 TGCCCCAGCGAGGCTGCTTTGCGCATCTCCGAGCCCAACCGCCCTCCATCTCTCGGCT 120
Db 61 TGCCCCAGCGAGGCTGCTTTGCGCATCTCCGAGCCCAACCGCCCTCCATCTCTCGGCT 120

QY 121 TCCCGCACACTGACGCTGTTCCAGCGTGAAAGAGAGAGACTGCGCGCGCGGACCCCGG 180
DB 121 TCCCGCACACTGACGCTGTTCCAGCGTGAAAGAGAGAGACTGCGCGCGCGGACCCCGG 180
QY 181 GAG 240
DB 181 GAG 240
QY 241 AGAGTTTTTCCATGTGGAGCGCTCTTTCAATGGAGCGTGTCCCGCGTGTCTTTAGACGGA 300
DB 241 AGAGTTTTTCCATGTGGAGCGCTCTTTCAATGGAGCGTGTCCCGCGTGTCTTTAGACGGA 300
QY 301 CTGCGGCTCTCTAAAGGTGAGACCTGCTGAGCGGAGAGAGAGAGAGAGAGAGAGAG 360
DB 301 CTGCGGCTCTCTAAAGGTGAGACCTGCTGAGCGGAGAGAGAGAGAGAGAGAGAGAG 360
QY 361 TTCCCGCAGGCTCTCTGCGCGCGCGGCTGAGCGGAGAGAGAGAGAGAGAGAGAGAG 420
DB 361 TTCCCGCAGGCTCTCTGCGCGCGCGGCTGAGCGGAGAGAGAGAGAGAGAGAGAGAG 420
QY 421 TCGCGCGCGGCTGCTGCGCGCGCGGCTGAGCGGAGAGAGAGAGAGAGAGAGAGAG 480
DB 421 TCGCGCGCGGCTGCTGCGCGCGCGGCTGAGCGGAGAGAGAGAGAGAGAGAGAGAG 480
QY 481 TCGAGTTCGCGCTGCTGAGCGAGTGTTCGCGCTGAAACAGAGAGAGAGAGAGAGAGAG 540
DB 481 TCGAGTTCGCGCTGCTGAGCGAGTGTTCGCGCTGAAACAGAGAGAGAGAGAGAGAGAG 540
QY 541 CGGTGCTGCGGCTGCTGAGCGAGTGTTCGCGCTGAAACAGAGAGAGAGAGAGAGAGAG 600
DB 541 CGGTGCTGCGGCTGCTGAGCGAGTGTTCGCGCTGAAACAGAGAGAGAGAGAGAGAGAG 600
QY 601 CGCGCCAGAGACCGGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
DB 601 CGCGCCAGAGACCGGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
QY 661 ACCATGAGAGATCTTTGAGAGATCTTACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
DB 661 ACCATGAGAGATCTTTGAGAGATCTTACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
QY 721 TCTTTAATTTAAGTTCTATCCCGAGAGAGTGTTCACCTGAGAGAGAGAGAGAGAG 780
DB 721 TCTTTAATTTAAGTTCTATCCCGAGAGAGTGTTCACCTGAGAGAGAGAGAGAGAG 780
QY 781 TCCGAGAGAGATGAGAGATCTTTAGAGAGATCTTACAGAGAGAGAGAGAGAGAGAG 840
DB 781 TCCGAGAGAGATGAGAGATCTTTAGAGAGATCTTACAGAGAGAGAGAGAGAGAGAG 840
QY 841 TTTATGAATCATATAAAGCTGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
DB 841 TTTATGAATCATATAAAGCTGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
QY 901 ACACAGAGTGTGTGAATCAGAGATGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960
DB 901 ACACAGAGTGTGTGAATCAGAGATGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960
QY 961 TGAATGCGGTGAGTGCACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
DB 961 TGAATGCGGTGAGTGCACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
QY 1021 TGGAG 1080
DB 1021 TGGAG 1080
QY 1081 ATGAACACAGCTGGTGCACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140
DB 1081 ATGAACACAGCTGGTGCACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140
QY 1141 GGCATCTCTCCACAAAG 1200
DB 1141 GGCATCTCTCCACAAAG 1200

RESULT 5

US-10-295-027-159
; Sequence 159, Application US/10295027
; Publication No. US20030232350A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glyne, Richard
; APPLICANT: Hevezi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; FILE REFERENCE: 018501-012500US
; CURRENT APPLICATION NUMBER: US/10/295,027
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 09/663,733
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/335,394
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/332,464
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/334,393
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/340,376
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/347,211
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/347,349
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/355,250
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/356,714
; PRIOR FILING DATE: 2002-02-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 159
; LENGTH: 1547
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-295-027-159

| | | | | | | |
|-----------------------|-----|--|--------------|------------|--------------|-------------------|
| Query Match | | 100.0%; | Score 1547; | DB 6; | Length 1547; | |
| Best Local Similarity | | 100.0%; | Pred. No. 0; | | | |
| Matches 1547; | | Conservative | 0; | Mismatches | 0; | Indels 0; Gaps 0; |
| Qy | 1 | GGGACCTCTTGAACCTTCAGGGAGATAAATCTTGGCACCCCACTTTTGGCGCGGTGCCTT | 60 | | | |
| Db | 1 | GGGACCTCTTGAACCTTCAGGGAGATAAATCTTGGCACCCCACTTTTGGCGCGGTGCCTT | 60 | | | |
| Qy | 61 | TGCCCCAGCGAGCGCTTCCGCCATCTCCAGAGCCCAACCGCCCTCCACCTCTCCGCGCT | 120 | | | |
| Db | 61 | TGCCCCAGCGAGCGCTTCCGCCATCTCCAGAGCCCAACCGCCCTCCACCTCTCCGCGCT | 120 | | | |
| Qy | 121 | TGCCCCAGCTGAGACGCTTCCAGAGTGAAAGAGAGACTGGCGGCGCGGACCCGG | 180 | | | |
| Db | 121 | TGCCCCAGCTGAGACGCTTCCAGAGTGAAAGAGAGACTGGCGGCGCGGACCCGG | 180 | | | |
| Qy | 181 | GAGAGGAGGAGGCAAGAAAGAAACGACATTCGGTCTTGGCCAGGTCCTTTTGACC | 240 | | | |
| Db | 181 | GAGAGGAGGAGGCAAGAAAGAAACGACATTCGGTCTTGGCCAGGTCCTTTTGACC | 240 | | | |
| Qy | 241 | AGAGTTTTCATGTGACGCTCTTTCAATGGACGTGTCCCGCGTCTTTAGACGGA | 300 | | | |
| Db | 241 | AGAGTTTTCATGTGACGCTCTTTCAATGGACGTGTCCCGCGTCTTTAGACGGA | 300 | | | |
| Qy | 301 | CTGCGGTCTCTAAAGTTCGACCATGTGGCGGCGGACCGCTGTCTTACGCTTGTCTGC | 360 | | | |
| Db | 301 | CTGCGGTCTCTAAAGTTCGACCATGTGGCGGCGGACCGCTGTCTTACGCTTGTCTGC | 360 | | | |
| Qy | 361 | TTCCCGAGTCTCTCTGGCGGCGGCTGCGCTCTGTTCCGGAGCTGGCGCGCAGGAGT | 420 | | | |
| Db | 361 | TTCCCGAGTCTCTCTGGCGGCGGCTGCGCTCTGTTCCGGAGCTGGCGCGCAGGAGT | 420 | | | |
| Qy | 421 | TCGCGGCGGCGTCTGCGGCGGCGGCTCATCCAGCCCTCTGACGAGTCTCTGACGAGT | 480 | | | |
| Db | 421 | TCGCGGCGGCGTCTGCGGCGGCGGCTCATCCAGCCCTCTGACGAGTCTCTGACGAGT | 480 | | | |
| Qy | 481 | TCGAGTTGCGGCTGCTCAGCATGTTCGGCTTGAACAGAGACCCACCGCAGGAGACG | 540 | | | |
| Db | 481 | TCGAGTTGCGGCTGCTCAGCATGTTCGGCTTGAACAGAGACCCACCGCAGGAGACG | 540 | | | |
| Qy | 541 | CCGTGGTCCCGCTTACATGCTAGACCTGTATCGCAGCACTCAGCTCAGCGCGGCTCAC | 600 | | | |
| Db | 541 | CCGTGGTCCCGCTTACATGCTAGACCTGTATCGCAGCACTCAGCTCAGCGCGGCTCAC | 600 | | | |
| Qy | 601 | CCGCCCCAGACCAACCGTTGAGAGGGCAGCCAGCCAGCACAACCTGTGCGCAGCTTCC | 660 | | | |
| Db | 601 | CCGCCCCAGACCAACCGTTGAGAGGGCAGCCAGCCAGCACAACCTGTGCGCAGCTTCC | 660 | | | |
| Qy | 661 | ACCATGAAGATCTTTGGAAGACTTACAGAAACGAGTGGGAAACCAACCCGAGATCT | 720 | | | |
| Db | 661 | ACCATGAAGATCTTTGGAAGACTTACAGAAACGAGTGGGAAACCAACCCGAGATCT | 720 | | | |
| Qy | 721 | TCCTTAATTTAAGTTCTATCCCGAGGAGTTTATCACCTCAGCAGAGCTTCAGGTTT | 780 | | | |
| Db | 721 | TCCTTAATTTAAGTTCTATCCCGAGGAGTTTATCACCTCAGCAGAGCTTCAGGTTT | 780 | | | |
| Qy | 781 | TCCGAGAACAGATGCAAGATCTTTAGGAAACAATAGCAGTTTCCATCACCAGATTAATA | 840 | | | |
| Db | 781 | TCCGAGAACAGATGCAAGATCTTTAGGAAACAATAGCAGTTTCCATCACCAGATTAATA | 840 | | | |
| Qy | 841 | TTTATGAATCATTAACCTGCAACAGCACTCGAAATTCCTCGTGACACGATTTTGG | 900 | | | |
| Db | 841 | TTTATGAATCATTAACCTGCAACAGCACTCGAAATTCCTCGTGACACGATTTTGG | 900 | | | |
| Qy | 901 | ACACAGGTGTGATCAGAAATGCAAGCAGTGGGAAAGTTTGTATGTACACCCCGCTG | 960 | | | |
| Db | 901 | ACACAGGTGTGATCAGAAATGCAAGCAGTGGGAAAGTTTGTATGTACACCCCGCTG | 960 | | | |
| Qy | 961 | TGATCGGTTGATGCAACAGGACACGCAACATAGGATTCGTGTGGAAGTGGCCCACT | 1020 | | | |
| Db | 961 | TGATCGGTTGATGCAACAGGACACGCAACATAGGATTCGTGTGGAAGTGGCCCACT | 1020 | | | |

| | | | | | | |
|----|------|--|------|--|--|--|
| Qy | 1021 | TGGAGGAGAAACAGGTGTCTCCAAGAGACATGTTAGGATAAGCAGCTCTTTGCCACCAAG | 1080 | | | |
| Db | 1021 | TGGAGGAGAAACAGGTGTCTCCAAGAGACATGTTAGGATAAGCAGCTCTTTGCCACCAAG | 1080 | | | |
| Qy | 1081 | ATGAACACAGCTGTCTCAGATAAGGCCATTTGCTAGTAACTTTTGGCCATGATCGAAAG | 1140 | | | |
| Db | 1081 | ATGAACACAGCTGTCTCAGATAAGGCCATTTGCTAGTAACTTTTGGCCATGATCGAAAG | 1140 | | | |
| Qy | 1141 | GGCATCTCTCCAACAAAGAGAAAACGTCAGGCCAAACACAAACAGCGGAAACGCCTTA | 1200 | | | |
| Db | 1141 | GGCATCTCTCCAACAAAGAGAAAACGTCAGGCCAAACACAAACAGCGGAAACGCCTTA | 1200 | | | |
| Qy | 1201 | AGTCCAGCTGTAGAGACACCTTTTACGTGGACTTTTACGTGGAGTTCAGTGGGTGGAACT | 1260 | | | |
| Db | 1201 | AGTCCAGCTGTAGAGACACCTTTTACGTGGACTTTTACGTGGAGTTCAGTGGGTGGAACT | 1260 | | | |
| Qy | 1261 | GGATTGTGGTCCCGCGGGGTATCACGCTTTTACTGCCAGGAGAAATGCCCTTTTCTC | 1320 | | | |
| Db | 1261 | GGATTGTGGTCCCGCGGGGTATCACGCTTTTACTGCCAGGAGAAATGCCCTTTTCTC | 1320 | | | |
| Qy | 1321 | TGGCTGATCATCTGAACTCCCACTAAATCATGCACTTTTACTGCCACGAGATGCGCTTCTGTTA | 1380 | | | |
| Db | 1321 | TGGCTGATCATCTGAACTCCCACTAAATCATGCACTTTTACTGCCACGAGATGCGCTTCTGTTA | 1380 | | | |
| Qy | 1381 | ACTCTAAGATTCCTAAGGAGCATGCTGTCCCGAGCACTCAGTCTATCTCGATGCTGT | 1440 | | | |
| Db | 1381 | ACTCTAAGATTCCTAAGGAGCATGCTGTCCCGAGCACTCAGTCTATCTCGATGCTGT | 1440 | | | |
| Qy | 1441 | ACCTTGACGAGATGAAAAGGTTGTATTAAGAACTATCAGGACATGTTGTGAGGGTT | 1500 | | | |
| Db | 1441 | ACCTTGACGAGATGAAAAGGTTGTATTAAGAACTATCAGGACATGTTGTGAGGGTT | 1500 | | | |
| Qy | 1501 | GTGGGTGTGCTAGTACAGCAAAATTAATAACATAAATATATATA 1547 | | | | |
| Db | 1501 | GTGGGTGTGCTAGTACAGCAAAATTAATAACATAAATATATATA 1547 | | | | |

RESULT 6
US-10-302-812-19
; Sequence 19, Application US/10302812
; Publication No. US20040087016A1
; GENERAL INFORMATION:
; APPLICANT: Keating et al.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR CELL DEDIFFERENTIATION AND
; TITLE OF INVENTION: TISSUE REGENERATION
; FILE REFERENCE: HYDR-P02-004
; CURRENT APPLICATION NUMBER: US/10/302,812
; CURRENT FILING DATE: 2002-11-21
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 1547
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-302-812-19

| | | | | | | |
|-----------------------|-----|--|--------------|------------|--------------|-------------------|
| Query Match | | 100.0%; | Score 1547; | DB 7; | Length 1547; | |
| Best Local Similarity | | 100.0%; | Pred. No. 0; | | | |
| Matches 1547; | | Conservative | 0; | Mismatches | 0; | Indels 0; Gaps 0; |
| Qy | 1 | GGGACCTCTTGAACCTTCAGGGAGATAAATCTTGGCACCCCACTTTTGGCGCGGTGCCTT | 60 | | | |
| Db | 1 | GGGACCTCTTGAACCTTCAGGGAGATAAATCTTGGCACCCCACTTTTGGCGCGGTGCCTT | 60 | | | |
| Qy | 61 | TGCCCCAGCGAGCGCTTTCGCCATCTCCGAGCCCCACCGCCCTCCATCTCTCGGCGCT | 120 | | | |
| Db | 61 | TGCCCCAGCGAGCGCTTTCGCCATCTCCGAGCCCCACCGCCCTCCATCTCTCGGCGCT | 120 | | | |
| Qy | 121 | TGCCCCAGCTGAGACGCTGTTCAGCGTGAAAGAGAGACTGCGGCGCGGACCCGG | 180 | | | |
| Db | 121 | TGCCCCAGCTGAGACGCTGTTCAGCGTGAAAGAGAGACTGCGGCGCGGACCCGG | 180 | | | |
| Qy | 181 | GAGAGGAGGAGGCAAGAAAGAAACGACATTCGGTCTTGGCCAGGTCCTTTTGACC | 240 | | | |

Qy 361 TTCCCCAGGTCCTCTCGGCGCGCGGCTGCTCGCTCGTTCCGAGCTGCGCGCAGGAGT 420
Db |||||
Qy 361 TTCCCCAGGTCCTCTCGGCGCGCGGCTGCTCGCTCGTTCCGAGCTGCGCGCAGGAGT 420
Db |||||
Qy 421 TCGCGGCGGCGCTCGTTCGGCGCGCGCCCTCATCCAGCCCTCTGAGCAGGTCCTGAGCGAGT 480
Db |||||
Qy 421 TCGCGGCGGCGCTCGTTCGGCGCGCGCCCTCATCCAGCCCTCTGAGCAGGTCCTGAGCGAGT 480
Db |||||
Qy 481 TCGAGTTGCGGCTGCTGAGCATGTTTCGGCTGGAACAGAGAGACCCACCCGAGCGAGCG 540
Db |||||
Qy 481 TCGAGTTGCGGCTGCTGAGCATGTTTCGGCTGGAACAGAGAGACCCACCCGAGCGAGCG 540
Db |||||
Qy 541 CCGTGGTGCCTTACATGCTAGACCTGTATCGCAGGCTCTGAGGCTGAGCGCGGCTCAC 600
Db |||||
Qy 541 CCGTGGTGCCTTACATGCTAGACCTGTATCGCAGGCTCTGAGGCTGAGCGCGGCTCAC 600
Db |||||
Qy 601 CCGCCCCAGACCCCGGTTGAGAGGGCAGCCAGCCGAGCCCAACACTGTGCGCAGCTTCC 660
Db |||||
Qy 601 CCGCCCCAGACCCCGGTTGAGAGGGCAGCCAGCCGAGCCCAACACTGTGCGCAGCTTCC 660
Db |||||
Qy 661 ACCATGAAGAATCTTTGGAAGAACTACAGAAAAGAGTGGGAAAACAAACCCGAGATTCT 720
Db |||||
Qy 661 ACCATGAAGAATCTTTGGAAGAACTACAGAAAAGAGTGGGAAAACAAACCCGAGATTCT 720
Db |||||
Qy 721 TCTTTAATTTAAGTTCTATCCCAAGGAGGTTTATCACCTCAGCAGAGCTTCAGGTTT 780
Db |||||
Qy 721 TCTTTAATTTAAGTTCTATCCCAAGGAGGTTTATCACCTCAGCAGAGCTTCAGGTTT 780
Db |||||
Qy 781 TCCGAGAACAGATGCAAGATCTTTAGGAAACAATAGCAGTTTCCATCACCGAATTAAATA 840
Db |||||
Qy 781 TCCGAGAACAGATGCAAGATCTTTAGGAAACAATAGCAGTTTCCATCACCGAATTAAATA 840
Db |||||
Qy 841 TTTATGAATCATTAACCTGCAACAGCCAACTCGAAATCCCGTGCACAGACTTTTGG 900
Db |||||
Qy 841 TTTATGAATCATTAACCTGCAACAGCCAACTCGAAATCCCGTGCACAGACTTTTGG 900
Db |||||
Qy 901 ACACAGGTTGGTGAATCAGAACTCAAGCAGGTCGGAAGTTTGTGATCAACCCCGCTG 960
Db |||||
Qy 901 ACACAGGTTGGTGAATCAGAACTCAAGCAGGTCGGAAGTTTGTGATCAACCCCGCTG 960
Db |||||
Qy 961 TGATGCGGTGACTGCAAGGAGACAGCCAAACCATGATGATTCGTGTGGAAGTGCCCACT 1020
Db |||||
Qy 961 TGATGCGGTGACTGCAAGGAGACAGCCAAACCATGATGATTCGTGTGGAAGTGCCCACT 1020
Db |||||
Qy 1021 TGGAGGAGAAACAAGTGTCTCAGAGACATGTTAGGATGAGCAGGTCCTTTGACCAAG 1080
Db |||||
Qy 1021 TGGAGGAGAAACAAGTGTCTCAGAGACATGTTAGGATGAGCAGGTCCTTTGACCAAG 1080
Db |||||
Qy 1081 ATGAACACAGCTGGTCAAGATAGGCCATTTAGTAACTTTTGGCCATGATGGAAG 1140
Db |||||
Qy 1081 ATGAACACAGCTGGTCAAGATAGGCCATTTAGTAACTTTTGGCCATGATGGAAG 1140
Db |||||
Qy 1141 GGCACTCTCTCCACAAAGAGAAAACGTCAGGCCAAACACAAACAGCGGAAACGCCTTA 1200
Db |||||
Qy 1141 GGCACTCTCTCCACAAAGAGAAAACGTCAGGCCAAACACAAACAGCGGAAACGCCTTA 1200
Db |||||
Qy 1201 AGTCAGCTGTAAGAGACACCCCTTTGACGTGGAATGAGTCAAGTGGGGTGGAAATGACT 1260
Db |||||
Qy 1201 AGTCAGCTGTAAGAGACACCCCTTTGACGTGGAATGAGTCAAGTGGGGTGGAAATGACT 1260
Db |||||
Qy 1261 GGATTTGGCTCCCCGGGGTATCAGCGCTTTTACTGCGAGGAGATGCCCTTTTCCTC 1320
Db |||||
Qy 1261 GGATTTGGCTCCCCGGGGTATCAGCGCTTTTACTGCGAGGAGATGCCCTTTTCCTC 1320
Db |||||
Qy 1321 TGGCTGATCATCTGAACTCCACTAATCATGTCATTTGTCAGACGTTGTCACCTCTGTTA 1380
Db |||||
Qy 1321 TGGCTGATCATCTGAACTCCACTAATCATGTCATTTGTCAGACGTTGTCACCTCTGTTA 1380
Db |||||
Qy 1381 ACTTAAGATTCCTAAGGATGCTGTGTCGCGACAGAACTCAGTGTATCTCGATGCTGT 1440
Db |||||
Qy 1381 ACTTAAGATTCCTAAGGATGCTGTGTCGCGACAGAACTCAGTGTATCTCGATGCTGT 1440
Db |||||
Qy 1441 ACCTTGACGAGATGAAAAGGTGTGTTTAAAGAACTATCAGGACATGCTTGTGAGGGTT 1500

Db 1441 ACCTTGACGAGATGAAAAGGTGTGTTTAAAGAACTATCAGGACATGCTTGTGAGGGTT 1500
Qy 1501 GTGGGTGCTGCTAGTACAGCAAAATTAATAACATAATATATATA 1547
Db |||||
Db 1501 GTGGGTGCTGCTAGTACAGCAAAATTAATAACATAATATATATA 1547
Db |||||
RESULT 8
US-10-692-824-1
; Sequence 1, Application US/10692824
; Publication No. US20040126375A1
; GENERAL INFORMATION:
; APPLICANT: Langenfeld, John
; TITLE OF INVENTION: BONE MORPHOGENETIC PROTEIN-2 IN THE TREATMENT AND DIAGNOSIS OF
; TITLE OF INVENTION: CANCER
; FILE REFERENCE: 54704.8036.US03
; CURRENT APPLICATION NUMBER: US/10/692,824
; CURRENT FILING DATE: 2003-10-23
; PRIOR APPLICATION NUMBER: US60/261,252
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: US10/044,716
; PRIOR FILING DATE: 2002-01-11
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 1547
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: source
; LOCATION: (1)..(1547)
; OTHER INFORMATION: Homo sapiens: Taxon:9606
; FEATURE:
; NAME/KEY: gene
; LOCATION: (1)..(1547)
; OTHER INFORMATION: BMP2
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (324)..(1514)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (429)..(1127)
; OTHER INFORMATION: Region: TGF-beta propeptide
; FEATURE:
; NAME/KEY: variation
; LOCATION: (432)..(432)
; OTHER INFORMATION: Allele = "T"; Allele = "G"
; FEATURE:
; NAME/KEY: variation
; LOCATION: (584)..(584)
; OTHER INFORMATION: Allele = "A"; Allele = "g"
; FEATURE:
; NAME/KEY: variation
; LOCATION: (893)..(893)
; OTHER INFORMATION: Allele = "T"; Allele = "A"
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1209)..(1511)
; OTHER INFORMATION: TGF-beta; Region: Transforming growth factor beta like domain
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1209)..(1511)
; OTHER INFORMATION: TGF-beta; Region: Transforming growth factor-beta (TGF-beta) family
US-10-692-824-1
Query Match 100.0%; Score 1547; DB 7; Length 1547;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1547; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GGGGACTTCTTGAACCTTGCAGGGAGATAAATTGCGACACCCCACTTTGCGCGGTCCTT 60
Db 1 GGGGACTTCTTGAACCTTGCAGGGAGATAAATTGCGACACCCCACTTTGCGCGGTCCTT 60

Db 181 GAGAAAGGAGGAGCAAGAAAAGGAAACGGAACATTCGGTCCCTTGCGCCAGGTCCTTTTGACC 240
Qy 241 AGAGTTTTTCATGTGAGCGCTCTTTCAATGGAAGTGTCGCCGGGTGCTTCTTAGACGGA 300
Db 241 AGAGTTTTTCATGTGAGCGCTCTTTCAATGGAAGTGTCGCCGGGTGCTTCTTAGACGGA 300
Qy 301 CTGCGGTCTCTTAAGGTCGACCAATGTGTGGCCGGGACCCGGTCTTCTAGCGTTGCTGC 360
Db 301 CTGCGGTCTCTTAAGGTCGACCAATGTGTGGCCGGGACCCGGTCTTCTAGCGTTGCTGC 360
Qy 361 TTCCCCAGGTCCTCTCTGCGCGCGCGGCTGGTCCCTCGTTCCGAGCTGGCGCGCAGGAAGT 420
Db 361 TTCCCCAGGTCCTCTCTGCGCGCGCGGCTGGTCCCTCGTTCCGAGCTGGCGCGCAGGAAGT 420
Qy 421 TCGCGCGCGGCTGCTGCGGCGCGCCCTCATCCAGCCCTCTGACGAGTCTTAGAGCGAGT 480
Db 421 TCGCGCGCGGCTGCTGCGGCGCGCCCTCATCCAGCCCTCTGACGAGTCTTAGAGCGAGT 480
Qy 481 TCGAGTTGCGGCTGCTGAGCATGTTCGGCTGGAACAGAGACCCACCCAGCAGGAGCG 540
Db 481 TCGAGTTGCGGCTGCTGAGCATGTTCGGCTGGAACAGAGACCCACCCAGCAGGAGCG 540
Qy 541 CCGTGGTCCCGCCCTACATGCTAGACCTGTATCGCAGGCACTCAGGTCAGCGCGGCTCAC 600
Db 541 CCGTGGTCCCGCCCTACATGCTAGACCTGTATCGCAGGCACTCAGGTCAGCGCGGCTCAC 600
Qy 601 CCGGCCAGACACCGGTTGAGAGGGCAGCCAGCGAGCCAAACACTGTGGCGAGCTTCC 660
Db 601 CCGGCCAGACACCGGTTGAGAGGGCAGCCAGCGAGCCAAACACTGTGGCGAGCTTCC 660
Qy 661 ACCATGAGAACTCTTGAAGAACTACACAGAAACGAGTGGGAACAAACCCCGAGATTCT 720
Db 661 ACCATGAGAACTCTTGAAGAACTACACAGAAACGAGTGGGAACAAACCCCGAGATTCT 720
Qy 721 TCTTTAATTTAAGTTCTATCCCGCAGGAGGATTTATCACCTCAGCAGAGCTTCAGGTTT 780
Db 721 TCTTTAATTTAAGTTCTATCCCGCAGGAGGATTTATCACCTCAGCAGAGCTTCAGGTTT 780
Qy 781 TCCGAGAACAGATGCAAGATGCTTTAGGAACAATAGCAGTTTCCATCCCGAATTAATA 840
Db 781 TCCGAGAACAGATGCAAGATGCTTTAGGAACAATAGCAGTTTCCATCCCGAATTAATA 840
Qy 841 TTTATGAATCATAAACCTGCAACAGCAACTCGAAATTCGCCGTGACCAAGCTTTTG 900
Db 841 TTTATGAATCATAAACCTGCAACAGCAACTCGAAATTCGCCGTGACCAAGCTTTTG 900
Qy 901 ACACGAGTTGGTGAATCAGAAATGCAAGCAGGTGGGAAAGTTTATGATGTACACCCCGCTG 960
Db 901 ACACGAGTTGGTGAATCAGAAATGCAAGCAGGTGGGAAAGTTTATGATGTACACCCCGCTG 960
Qy 961 TGATGCGGTGACGTGCAACAGGGAACGCAACCATGGAATTCGTTGAGTGCACCCCGCTG 1020
Db 961 TGATGCGGTGACGTGCAACAGGGAACGCAACCATGGAATTCGTTGAGTGCACCCCGCTG 1020
Qy 1021 TGGAGGAGAAACAGGTGCTCCAGAGACATGTTAGATAAGCAGGTCCTTTCACCAAG 1080
Db 1021 TGGAGGAGAAACAGGTGCTCCAGAGACATGTTAGATAAGCAGGTCCTTTCACCAAG 1080
Qy 1081 ATGAACACAGCTGGTCAAGATAAGGCCATTTAGTAACTTTTGGCCATGATGGAAG 1140
Db 1081 ATGAACACAGCTGGTCAAGATAAGGCCATTTAGTAACTTTTGGCCATGATGGAAG 1140
Qy 1141 GGCAATCTCTCAAAAAGAGAAAACGTCAGGCCAAACACAAACAGCGGAAAACGCTTTA 1200
Db 1141 GGCAATCTCTCAAAAAGAGAAAACGTCAGGCCAAACACAAACAGCGGAAAACGCTTTA 1200
Qy 1201 AGTCAGCTGTAAGAGACACCTTTGTACGTGGACTTCAGTGAGCTGGGGTGGAAATGACT 1260
Db 1201 AGTCAGCTGTAAGAGACACCTTTGTACGTGGACTTCAGTGAGCTGGGGTGGAAATGACT 1260
Qy 1261 GGAATGTGGCTCCCGGGGTATCACGCTTTTACTGCGCAGGAGATGCCCCCTTTTCTC 1320
Db 1261 GGAATGTGGCTCCCGGGGTATCACGCTTTTACTGCGCAGGAGATGCCCCCTTTTCTC 1320

RESULT 10

US-10-489-740-36
; Sequence 36, Application US/10489740
; Publication No. US20050112574A1
; GENERAL INFORMATION:
; APPLICANT: Bionomics Limited
; TITLE OF INVENTION: P9
; FILE REFERENCE: Angiogenesis_PCT
; CURRENT APPLICATION NUMBER: US/10/489,740
; CURRENT FILING DATE: 2004-03-15
; NUMBER OF SEQ ID NOS: 216
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 36
; LENGTH: 1547
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-489-740-36

Query Match 100.0%; Score 1547; DB 9; Length 1547;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1547; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGACTCTTTGAACTTGCAGGGAGAAATAACTTGCACACCCCACTTTTGGCGCGGTGCCCTT 60
Db 1 GGGGACTCTTTGAACTTGCAGGGAGAAATAACTTGCACACCCCACTTTTGGCGCGGTGCCCTT 60
Qy 61 TGCCCCAGCGGAGCCTGCTTCGCCATCTCCGAGCCCCACCGCCCCCTCCTCCTCGGCT 120
Db 61 TGCCCCAGCGGAGCCTGCTTCGCCATCTCCGAGCCCCACCGCCCCCTCCTCCTCGGCT 120
Qy 121 TGCCCCGACACTGAGACCGCTGTTCCAGCGTGAAAGAGAGACTCGCGCGCGGCACCCGG 180
Db 121 TGCCCCGACACTGAGACCGCTGTTCCAGCGTGAAAGAGAGACTCGCGCGCGGCACCCGG 180
Qy 181 GAGAAAGGAGGAGGCAAGAAAAGGAAACGGAACATTCGGTCCCTTGGCCAGGTCCTTTTGACC 240
Db 181 GAGAAAGGAGGAGGCAAGAAAAGGAAACGGAACATTCGGTCCCTTGGCCAGGTCCTTTTGACC 240
Qy 241 AGAGTTTTTCATGTGAGCGCTCTTTCAATGGAAGTGTCGCCGGGTGCTTCTTAGACGGA 300
Db 241 AGAGTTTTTCATGTGAGCGCTCTTTCAATGGAAGTGTCGCCGGGTGCTTCTTAGACGGA 300
Qy 301 CTGCGGTCTCTTAAGGTCGACCAATGTGTGGCCGGGACCCGGTCTTCTAGCGTTGCTGC 360
Db 301 CTGCGGTCTCTTAAGGTCGACCAATGTGTGGCCGGGACCCGGTCTTCTAGCGTTGCTGC 360
Qy 361 TTCCCCAGGTCCTCTCTGCGCGCGCGGCTGGTCCCTCGTTCCGAGCTGGCGCGCAGGAAGT 420
Db 361 TTCCCCAGGTCCTCTCTGCGCGCGCGGCTGGTCCCTCGTTCCGAGCTGGCGCGCAGGAAGT 420
Qy 421 TCGCGCGCGGCTGCTGCGGCGCGCCCTCATCCAGCCCTCTGACGAGTCTTAGAGCGAGT 480
Db 421 TCGCGCGCGGCTGCTGCGGCGCGCCCTCATCCAGCCCTCTGACGAGTCTTAGAGCGAGT 480
Qy 481 TCGAGTTGCGGCTGCTCAGCATGTTTCGGCTGGAACAGAGACCCACCCAGCAGGAGCG 540

481 TCAGTTGGCGTGTCTCAGCATGTTTCGGCTGAAACAGAGACCCACCCAGCAGGAGC 540
541 CGGTGGTCCCGCTACATGCTAGACCTGTATCGCAGGCACTCAGGTGAGCGGGCTCAC 600
541 CGGTGGTCCCGCTACATGCTAGACCTGTATCGCAGGCACTCAGGTGAGCGGGCTCAC 600
601 CGCGCCCAAGACACCGGTTGGAGAGGCGAGCCAGCGAGCCAACTGTGGCAGCTTCC 660
601 CGCGCCCAAGACACCGGTTGGAGAGGCGAGCCAGCGAGCCAACTGTGGCAGCTTCC 660
661 ACCATGAAGATCTTTTGAAGAACTTACAGAAACAGGTGGGAAACAAACCCGAGATTCT 720
661 ACCATGAAGATCTTTTGAAGAACTTACAGAAACAGGTGGGAAACAAACCCGAGATTCT 720
721 TCTTTAAATTTAAGTTCTATCCCAAGGAGGTTTATCACCCTCAGCAGGCTTCAGGTTT 780
721 TCTTTAAATTTAAGTTCTATCCCAAGGAGGTTTATCACCCTCAGCAGGCTTCAGGTTT 780
781 TCCGAGAACAGATGCAAGATGCTTTAGGAAACAAATAGCAGTTTCCATCACCGAATTAATA 840
781 TCCGAGAACAGATGCAAGATGCTTTAGGAAACAAATAGCAGTTTCCATCACCGAATTAATA 840
841 TTTATGAATCATATAAACTGCAACAGCCAACTCGAAATTCGCCGTGACAGACTTTTGG 900
841 TTTATGAATCATATAAACTGCAACAGCCAACTCGAAATTCGCCGTGACAGACTTTTGG 900
901 ACACAGGTTGGTGAATCAGATGCAAGCAGGTGGGAAAGTTTTCATGTACCCCGCTG 960
901 ACACAGGTTGGTGAATCAGATGCAAGCAGGTGGGAAAGTTTTCATGTACCCCGCTG 960
961 TGATCGGTGGATGTCACAGGAGACCGCAACATGGAATTCGTGGTGAAGTGGCCCACT 1020
961 TGATCGGTGGATGTCACAGGAGACCGCAACATGGAATTCGTGGTGAAGTGGCCCACT 1020
1021 TGGAGGAGAAACAAGGTGCTCACAAGACATGTTTAGGATAAGCAGGTCTTTGCAACCAAG 1080
1021 TGGAGGAGAAACAAGGTGCTCACAAGACATGTTTAGGATAAGCAGGTCTTTGCAACCAAG 1080
1081 ATGAACACAGCTGGTCAAGATAAGCCATTCCTAGTAACTTTTGGCCATGATGAAAG 1140
1081 ATGAACACAGCTGGTCAAGATAAGCCATTCCTAGTAACTTTTGGCCATGATGAAAG 1140
1141 GGCATCTCTTCCAAAAGAGAAACGTCAGGCAACACAAAACAGCGGAAACGCCCTTA 1200
1141 GGCATCTCTTCCAAAAGAGAAACGTCAGGCAACACAAAACAGCGGAAACGCCCTTA 1200
1201 AGTCCAGCTGTAAGAGACACCCCTTTGTACGTGGAATTCAGTGACGTGGGTGGAATGACT 1260
1201 AGTCCAGCTGTAAGAGACACCCCTTTGTACGTGGAATTCAGTGACGTGGGTGGAATGACT 1260
1261 GGAATGTGGCTCCCGGGGTATCAGCCTTTTACGTGCAACAGGAGATGCCCTTTTCCCTC 1320
1261 GGAATGTGGCTCCCGGGGTATCAGCCTTTTACGTGCAACAGGAGATGCCCTTTTCCCTC 1320
1321 TGGCTGATCATCTGAACTTCACTAATCATGCAATTCATGCAAGCTTGGTCAACTCTGTTA 1380
1321 TGGCTGATCATCTGAACTTCACTAATCATGCAATTCATGCAAGCTTGGTCAACTCTGTTA 1380
1381 ACTCTAAGATTCCTAAGGCATGCTGTGTCCTCCGACAGAACTCAGTGCTATCTCGATGCTGT 1440
1381 ACTCTAAGATTCCTAAGGCATGCTGTGTCCTCCGACAGAACTCAGTGCTATCTCGATGCTGT 1440
1441 ACTCTGACAGAAATGAAAGGTTGTAATAAGAACTATCAGGACATGGTTGTGGAGGTT 1500
1441 ACTCTGACAGAAATGAAAGGTTGTAATAAGAACTATCAGGACATGGTTGTGGAGGTT 1500
1501 GTGGGTGCTGCTAGTACGCAAAATTAATACATAAATATATATA 1547
1501 GTGGGTGCTGCTAGTACGCAAAATTAATACATAAATATATATA 1547

US-10-492-380-1
; Sequence 1, Application US/10492380
; Publication No. US2005011858A1
; GENERAL INFORMATION:
; APPLICANT: Alcon Research, Ltd.
; TITLE OF INVENTION: Bone Morphogenic Proteins (BMP), BMP Receptors and BMP Binding
; TITLE OF INVENTION: Proteins and Their Use in the Diagnosis and Treatment of Glaucom
; FILE REFERENCE: 2312 US
; CURRENT APPLICATION NUMBER: US/10/492,380
; CURRENT FILING DATE: 2004-04-12
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
; LENGTH: 1547
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-492-380-1

Query Match 100.0%; Score 1547; DB 9; Length 1547;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1547; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGGACTCTTTGAACTTTCAGGAGAAATACTTGGCAGCCCACTTTTGGCGCGGTGCCTT 60
Db 1 GGGGACTCTTTGAACTTTCAGGAGAAATACTTGGCAGCCCACTTTTGGCGCGGTGCCTT 60
QY 61 TGCCCCCAGCGAGCTGCTTCGCCATCTCCGAGCCCACTTCCTCCCTCCCTCCCTCCCT 120
Db 61 TGCCCCCAGCGAGCTGCTTCGCCATCTCCGAGCCCACTTCCTCCCTCCCTCCCTCCCT 120
QY 121 TGCCCGACACTGAGACGCTGTTCCAGCGTGAAGAGAGACTGCGCGCGCGGACCCCGG 180
Db 121 TGCCCGACACTGAGACGCTGTTCCAGCGTGAAGAGAGACTGCGCGCGCGGACCCCGG 180
QY 181 GAGAGAGAGAGGCAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 240
Db 181 GAGAGAGAGAGGCAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 240
QY 241 AGAGTTTTTCCATGTGGACGCTCTTCAATGAGAGTGTCCCGGTGCTCTTAGACCGA 300
Db 241 AGAGTTTTTCCATGTGGACGCTCTTCAATGAGAGTGTCCCGGTGCTCTTAGACCGA 300
QY 301 CTGCGGTCTCTTAAAGGTGCAACATGCTGGCGCGGACCCGCTGCTCTTAGCGTTGCTGC 360
Db 301 CTGCGGTCTCTTAAAGGTGCAACATGCTGGCGCGGACCCGCTGCTCTTAGCGTTGCTGC 360
QY 361 TTCCCCAGGTCTCTCTGGCGCGCGGCTGCGCTCGTTCCGAGCTGGGCGCAGGAAGT 420
Db 361 TTCCCCAGGTCTCTCTGGCGCGCGGCTGCGCTCGTTCCGAGCTGGGCGCAGGAAGT 420
QY 421 TCGCGCGCGGCTGCTGGCGCGCGGCTCATCCAGCCCTCTGACGAGGTCTGAGCGAGT 480
Db 421 TCGCGCGCGGCTGCTGGCGCGCGGCTCATCCAGCCCTCTGACGAGGTCTGAGCGAGT 480
QY 481 TCGAGTTGCGGCTGCTCAGCATGTTTCGGCTGAAACAGAGACCCACCCAGCAGGAGC 540
Db 481 TCGAGTTGCGGCTGCTCAGCATGTTTCGGCTGAAACAGAGACCCACCCAGCAGGAGC 540
QY 541 CCGTGGTCCCGCTTACATGCTAGACCTGTATCGCAGGCACTCAGGTGAGCGCGGCTCAC 600
Db 541 CCGTGGTCCCGCTTACATGCTAGACCTGTATCGCAGGCACTCAGGTGAGCGCGGCTCAC 600
QY 601 CGCGCCCAAGACACCGGTTGGAGAGGCGAGCCAGCGAGCCAACTGTGGCAGCTTCC 660
Db 601 CGCGCCCAAGACACCGGTTGGAGAGGCGAGCCAGCGAGCCAACTGTGGCAGCTTCC 660
QY 661 ACCATGAAGATCTTTTGAAGAACTTACAGAAACAGGTGGGAAACAAACCCGAGATTCT 720
Db 661 ACCATGAAGATCTTTTGAAGAACTTACAGAAACAGGTGGGAAACAAACCCGAGATTCT 720
QY 721 TCTTTAAATTTAAGTTCTATCCCAAGGAGGTTTATCACCCTCAGCAGGCTTCAGGTTT 780

Db 721 TCCTTAATTTAAGTTCTATCCCGAGGAGTTTATCACCTCAGCAGAGCTTCAGGTTT 780
Qy 781 TCCGAGAACAGATGCAAGATGCTTTAGGAAACAATAGCAGTTTCCATCACCGAATTAATA 840
Db 781 TCCGAGAACAGATGCAAGATGCTTTAGGAAACAATAGCAGTTTCCATCACCGAATTAATA 840
Qy 841 TTTATGAATCATATAAACCTGCAACAGCCCACTCGAAATTCCTCGTGCAGCAGCTTTTGG 900
Db 841 TTTATGAATCATATAAACCTGCAACAGCCCACTCGAAATTCCTCGTGCAGCAGCTTTTGG 900
Qy 901 ACACGAGTTGGTGAATCAGAAATCAAGCAGGTGGGAAAGTTTGAATGTCACCCCGCTG 960
Db 901 ACACGAGTTGGTGAATCAGAAATCAAGCAGGTGGGAAAGTTTGAATGTCACCCCGCTG 960
Qy 961 TGATCGGTGACATGCAAGGACACGCCAACCATGGAATTCGTGGTGAAGTGCCCACT 1020
Db 961 TGATCGGTGACATGCAAGGACACGCCAACCATGGAATTCGTGGTGAAGTGCCCACT 1020
Qy 1021 TGGAGGAGAAACAAGTGTCTCCAAAGAGACATGTTAGGTAAGCAGGTCTTTGACCAAG 1080
Db 1021 TGGAGGAGAAACAAGTGTCTCCAAAGAGACATGTTAGGTAAGCAGGTCTTTGACCAAG 1080
Qy 1081 ATGAACACAGCTGGTCAAGATAAGGCCATTTGCTAGTAACTTTTGGCCATGATGCAAAAG 1140
Db 1081 ATGAACACAGCTGGTCAAGATAAGGCCATTTGCTAGTAACTTTTGGCCATGATGCAAAAG 1140
Qy 1141 GGCATCTCTCCAAAGAGAAACCGTCAAGCCAAACACAAACAGCGGAAACGCTTTA 1200
Db 1141 GGCATCTCTCCAAAGAGAAACCGTCAAGCCAAACACAAACAGCGGAAACGCTTTA 1200
Qy 1201 AGTCAGCTGTAAGAGACACCTTTGTACGTGGACTTCAGTACGTGGGTGGAAATGACT 1260
Db 1201 AGTCAGCTGTAAGAGACACCTTTGTACGTGGACTTCAGTACGTGGGTGGAAATGACT 1260
Qy 1261 GGAATGTGGCTCCCGGGGTATCAGCCTTTTACTGCGAGAGAAATGCCCTTTTCTC 1320
Db 1261 GGAATGTGGCTCCCGGGGTATCAGCCTTTTACTGCGAGAGAAATGCCCTTTTCTC 1320
Qy 1321 TGGCTGATCATCTGAATCTCAATATCATGATGTCATGTTGAGACGTTGGTCAACTCTGTTA 1380
Db 1321 TGGCTGATCATCTGAATCTCAATATCATGATGTCATGTTGAGACGTTGGTCAACTCTGTTA 1380
Qy 1381 ACTCTAGATCTCTTAAGCATGCTGTGTCGCGACAGAACTCAGTGTCTCTCGATGCTGT 1440
Db 1381 ACTCTAGATCTCTTAAGCATGCTGTGTCGCGACAGAACTCAGTGTCTCTCGATGCTGT 1440
Qy 1441 ACCTTGACGAGAAATGAAAAGTTGTATTAAGAACTATCAGGACATGTTGTGGAGGGTT 1500
Db 1441 ACCTTGACGAGAAATGAAAAGTTGTATTAAGAACTATCAGGACATGTTGTGGAGGGTT 1500
Qy 1501 GTGGGTGCTGTAGTACAGCAAAATTAATACATAAATATATATA 1547
Db 1501 GTGGGTGCTGTAGTACAGCAAAATTAATACATAAATATATATA 1547

RESULT 12

US-10-917-265-1
; Sequence 1, Application US/10917265
; Publication No. US20050136042A1
; GENERAL INFORMATION:
; APPLICANT: BETZ, OLIVER B.
; APPLICANT: BETZ, VOLKER M.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TISSUE REPAIR
; FILE REFERENCE: BMW-004.01
; CURRENT APPLICATION NUMBER: US/10/917,265
; CURRENT FILING DATE: 2004-08-11
; PRIOR APPLICATION NUMBER: 60/494,484
; PRIOR FILING DATE: 2003-08-12
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 1
; LENGTH: 1547

; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-917-265-1

Query Match 100.0%; Score 1547; DB 9; Length 1547;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1547; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGACTTCTTGAACTTGCAGGAGAAATACTTGGCACAACCCCACTTTTGGCGCGGTGCTT 60
Db 1 GGGGACTTCTTGAACTTGCAGGAGAAATACTTGGCACAACCCCACTTTTGGCGCGGTGCTT 60
Qy 61 TGCCCCAGCGAGCTGCTTCCGACATCTCCAGCCCCCAGCCCTCCACTCTCTCGGCT 120
Db 61 TGCCCCAGCGAGCTGCTTCCGACATCTCCAGCCCCCAGCCCTCCACTCTCTCGGCT 120
Qy 121 TGCCCGACACTGAGACCTGTTCCAGCGTGAAGAGAGACTGCGCGCGGCAACCCGG 180
Db 121 TGCCCGACACTGAGACCTGTTCCAGCGTGAAGAGAGACTGCGCGCGGCAACCCGG 180
Qy 181 GAGAGGAGGAGGCAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 240
Db 181 GAGAGGAGGAGGCAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 240
Qy 241 AGAGTTTTTCCATGTGACCGCTCTTTCAATGAGACGTGTCCCGGCTCTCTTAGACGA 300
Db 241 AGAGTTTTTCCATGTGACCGCTCTTTCAATGAGACGTGTCCCGGCTCTCTTAGACGA 300
Qy 301 CTGCGGTCTCTTAAAGGTCCAGCATGTTGGTGGCGCGGACCCCGCTGTCTTCTAGCGTTGCTGC 360
Db 301 CTGCGGTCTCTTAAAGGTCCAGCATGTTGGTGGCGCGGACCCCGCTGTCTTCTAGCGTTGCTGC 360
Qy 361 TTCCCGAGTCTCTTGGGCGCGCGCTGGCTGTGTTCCGAGCTTGGGCGCGAGAGT 420
Db 361 TTCCCGAGTCTCTTGGGCGCGCGCTGGCTGTGTTCCGAGCTTGGGCGCGAGAGT 420
Qy 421 TCGGCGGCGGTGCTGCGGCGCGCGCTCATCCAGCCCTCTGACGAGTCTCAGCGAGT 480
Db 421 TCGGCGGCGGTGCTGCGGCGCGCGCTCATCCAGCCCTCTGACGAGTCTCAGCGAGT 480
Qy 481 TCAGATTGCGGCTGCTCAGCATGTTCCGCTGAAACAGAGACCCACCCAGCAGGAGCG 540
Db 481 TCAGATTGCGGCTGCTCAGCATGTTCCGCTGAAACAGAGACCCACCCAGCAGGAGCG 540
Qy 541 CCGTGTGCCCCCTACATCTAGACCTGTATCGAGGCACTCAGGTGAGCGGGCTCAC 600
Db 541 CCGTGTGCCCCCTACATCTAGACCTGTATCGAGGCACTCAGGTGAGCGGGCTCAC 600
Qy 601 CCGCCCCAGACCCCGGTTGGAGGGGCGAGCGGAGCCAACTGTGCGCAGCTTCC 660
Db 601 CCGCCCCAGACCCCGGTTGGAGGGGCGAGCGGAGCCAACTGTGCGCAGCTTCC 660
Qy 661 ACCATGAAGAATCTTTGGAAGAACTACAGAAACGAGTGGGAAACAACTCCAGGATTTCT 720
Db 661 ACCATGAAGAATCTTTGGAAGAACTACAGAAACGAGTGGGAAACAACTCCAGGATTTCT 720
Qy 721 TCTTTAATTTAAGTTCTATCCCAAGGAGTTTATCCTCAGCAGAGCTTCAGGTTT 780
Db 721 TCTTTAATTTAAGTTCTATCCCAAGGAGTTTATCCTCAGCAGAGCTTCAGGTTT 780
Qy 781 TCCGAGAACAGATGCAAGATGCTTTAGGAAACAATAGCAGTTTCCATCACCGAATTAATA 840
Db 781 TCCGAGAACAGATGCAAGATGCTTTAGGAAACAATAGCAGTTTCCATCACCGAATTAATA 840
Qy 841 TTTATGAATCATATAAACCTGCAACAGCCCACTCGAAATTCCTCGTGCAGCAGCTTTTGG 900
Db 841 TTTATGAATCATATAAACCTGCAACAGCCCACTCGAAATTCCTCGTGCAGCAGCTTTTGG 900
Qy 901 ACACGAGTTGGTGAATCAGAAATCAAGCAGGTGGGAAAGTTTGAATGTCACCCCGCTG 960
Db 901 ACACGAGTTGGTGAATCAGAAATCAAGCAGGTGGGAAAGTTTGAATGTCACCCCGCTG 960
Qy 961 TGATCGGTGACTGCAAGGACACGCCAACCATGGAATTCGTGGTGAAGTGCCCACT 1020
Db 961 TGATCGGTGACTGCAAGGACACGCCAACCATGGAATTCGTGGTGAAGTGCCCACT 1020

Db 1201 AGTCAGCTGTAAAGAGACACCCCTTTGTACGTGGACTTCAGTGACGTGGGTGGAATGACT 1260
Qy 1261 GGATTGTGGCTCCCGGGGGTATCAGCGCTTTTACTGCGCAGGAGAAATGCCCTTTTCCCTC 1320
Db 1261 GGATTGTGGCTCCCGGGGGTATCAGCGCTTTTACTGCGCAGGAGAAATGCCCTTTTCCCTC 1320
Qy 1321 TGGCTGATCATCTGAATCCCACTAATCATGCGCATTTGTTACAGACGTGTCGAACCTCTGTTA 1380
Db 1321 TGGCTGATCATCTGAATCCCACTAATCATGCGCATTTGTTACAGACGTGTCGAACCTCTGTTA 1380
Qy 1381 ACTCTAAGATTCCTAAGGCATGCTGTGTCCGACAGAACTCAGTGTCTATCTCGATGCTGT 1440
Db 1381 ACTCTAAGATTCCTAAGGCATGCTGTGTCCGACAGAACTCAGTGTCTATCTCGATGCTGT 1440
Qy 1441 ACCTTGACGAGAAATGAAAGTGTGTTAAAGAACTATCAGGACATGTTGTGAGGGTT 1500
Db 1441 ACCTTGACGAGAAATGAAAGTGTGTTAAAGAACTATCAGGACATGTTGTGAGGGTT 1500
Qy 1501 GTGGGTGTCGTAGTACAGCAAAATTAATAATACATAATATATATATA 1547
Db 1501 GTGGGTGTCGTAGTACAGCAAAATTAATAATACATAATATATATATA 1547

RESULT 14
US-09-804-625-3
; Sequence 3, Application US/09804625
; Publication No. US20030049826A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Elizabeth A.
; Rosen, Vicki A.
; Wozney, John M.
; TITLE OF INVENTION: No. US20030049826A1el BMP Products
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESS: LEGAL AFFAIRS, GENETICS INSTITUTE, INC.
; STREET: 87 CAMBRIDGE PARK DRIVE
; CITY: CAMBRIDGE
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/804,625
; FILING DATE: 09-Mar-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/925,779
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Kapinos, Ellen J.
; REGISTRATION NUMBER: 32,245
; REFERENCE/DOCKET NUMBER: 5160C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-876-1170
; TELEFAX: 617-876-5851
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1607 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo Sapiens
; CELL TYPE: Osteosarcoma Cell Line
; CELL LINE: U-2OS

IMMEDIATE SOURCE:
LIBRARY: U2OS cDNA in Lambda GT10
CLONE: Lambda U2OS-39
POSITION IN GENOME:
UNITS: bp
FEATURE:
NAME/KEY: CDS
LOCATION: 356..1546
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 1202..1543
FEATURE:
NAME/KEY: mRNA
LOCATION: 14..1607
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 356..424
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-804-625-3
Query Match 100.0%; Score 1547; DB 3; Length 1607;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1547; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GGGGACTTCTTTGAACTTTGCAGGGAGAAATACTTGCACACCCCACTTTTGGCGCGGTGCTT 60
Db 33 GGGGACTTCTTTGAACTTTGCAGGGAGAAATACTTGCACACCCCACTTTTGGCGCGGTGCTT 92
Qy 61 TGCCCCAGCGGAGCTGCTTTCGCCATCTCCGAGCCCCACCGCCCTTCACTTCTCGGCCT 120
Db 93 TGCCCCAGCGGAGCTGCTTTCGCCATCTCCGAGCCCCACCGCCCTTCACTTCTCGGCCT 152
Qy 121 TGCCCCAGCTGAGACGCTGTTCCGACGTGAAAAGAGAGACTGCGGCGCGGACCCGG 180
Db 153 TGCCCCAGCTGAGACGCTGTTCCGACGTGAAAAGAGAGACTGCGGCGCGGACCCGG 212
Qy 181 GAGAGGAGGAGGCAAGAAAGAAACGACATTCGTCCTTCGCCAGGTCTTTCAGCTTTCGACC 240
Db 213 GAGAGGAGGAGGCAAGAAAGAAACGACATTCGTCCTTCGCCAGGTCTTTCAGCTTTCGACC 272
Qy 241 AGAGTTTTTCCATGTGGACGCTCTTTTCAATGGACGTGTCCCGCGTCTTCTTAGACGGA 300
Db 273 AGAGTTTTTCCATGTGGACGCTCTTTTCAATGGACGTGTCCCGCGTCTTCTTAGACGGA 332
Qy 301 CTGGGCTCTCTAAAGTTCAGACATGCTGCGCGGAGACCCGCTGCTTCTTAGCGTTCGTC 360
Db 333 CTGGGCTCTCTAAAGTTCAGACATGCTGCGCGGAGACCCGCTGCTTCTTAGCGTTCGTC 392
Qy 361 TTCCCCAGGTCTCTCTGGCGCGCGGCTGCGCTGCGCTGCGTTCGCGAGCTGGCGCGGAGAGT 420
Db 393 TTCCCCAGGTCTCTCTGGCGCGCGGCTGCGCTGCGCTGCGTTCGCGAGCTGGCGCGGAGAGT 452
Qy 421 TCGGCGCGCGCTGCTCGGGCGCGCCCTCATCCAGCCCTCTGACAGGTCTCTGAGCGAGT 480
Db 453 TCGGCGCGCGCTGCTCGGGCGCGCCCTCATCCAGCCCTCTGACAGGTCTCTGAGCGAGT 512
Qy 481 TCAGTTTGGCGCTGCTCAGCATGTTGGGCTGAAAAGAGAGACCCACCCAGCAGCGGACG 540
Db 513 TCAGTTTGGCGCTGCTCAGCATGTTGGGCTGAAAAGAGAGACCCACCCAGCAGCGGACG 572
Qy 541 CCGTGGTGGCCCCCTCATCTAGACCTGTATCGCAGGCACTCAGGTTCAGCGCGGTTCAC 600
Db 573 CCGTGGTGGCCCCCTCATCTAGACCTGTATCGCAGGCACTCAGGTTCAGCGCGGTTCAC 632
Qy 601 CCGCCCCAGACCCCGGTTGGAGGGGACGACCGCGAGCCAAACATGTGGCGAGCTTCC 660
Db 633 CCGCCCCAGACCCCGGTTGGAGGGGACGACCGCGAGCCAAACATGTGGCGAGCTTCC 692
Qy 661 ACCATGAGAAATCTTTGGAAGAACTACACAGAAAGAGTGGGAACAAACCGGAGATTCT 720
Db 693 ACCATGAGAAATCTTTGGAAGAACTACACAGAAAGAGTGGGAACAAACCGGAGATTCT 752
Qy 721 TCTTTAATTTAAGTTTCTATCCCGAGGAGGTTTATCAGCTCAGCAGAGCTTCAGGTTT 780

Db 753 TCTTTAAATTAAGTTCTATCCCCAGGAGGTTTATCACTCAGCAGAGCTTCAGGTTT 812
Qy 781 TCCGAGACAGATGCAAGATGCTTTAGGAAACAATAGCAGTTTCCATCACCAGATTATA 840
Db 813 TCCGAGAACAGATGCAAGATGCTTTAGGAAACAATAGCAGTTTCCATCACCAGATTATA 872
Qy 841 TTTATGAATCATAAACCTGCAACAGCAGCAACTCGAAATTCGCCGTGACACAGACTTTGG 900
Db 873 TTTATGAATCATAAACCTGCAACAGCAGCAACTCGAAATTCGCCGTGACACAGACTTTGG 932
Qy 901 ACACAGGTTGGTGAATCAGATGCAAGCAGAGTGGGAAAGTTTGTATGTACCCCGCTG 960
Db 933 ACACAGGTTGGTGAATCAGATGCAAGCAGAGTGGGAAAGTTTGTATGTACCCCGCTG 992
Qy 961 TGATGCGGTGACTGCAAGGAGCAGCAGCAACCAACCATGGAATTCGTGGTGAAGTGCCCACT 1020
Db 993 TGATGCGGTGACTGCAAGGAGCAGCAGCAACCAACCATGGAATTCGTGGTGAAGTGCCCACT 1052
Qy 1021 TGGAGGAGAAACAAGGTGCTCCAGAGACATGTTAGGATAAGCAGGTCTTTTGACCAAG 1080
Db 1053 TGGAGGAGAAACAAGGTGCTCCAGAGACATGTTAGGATAAGCAGGTCTTTTGACCAAG 1112
Qy 1081 ATGAACACAGCTGTCACAGATAGGCCATTTGCTAGTAACTTTTGGCCATGATGGAAG 1140
Db 1113 ATGAACACAGCTGTCACAGATAGGCCATTTGCTAGTAACTTTTGGCCATGATGGAAG 1172
Qy 1141 GGCATCCTCTCCAAAAGAGAAACGTCAGCCAAACACACACAGCGGAAGCGCTTA 1200
Db 1173 GGCATCCTCTCCAAAAGAGAAACGTCAGCCAAACACACACAGCGGAAGCGCTTA 1232
Qy 1201 AGTCAGCTGTAAGACACACCTTTGTAGTGGACTTCAGTGACGTGGGTGGATGACT 1260
Db 1233 AGTCAGCTGTAAGACACACCTTTGTAGTGGACTTCAGTGACGTGGGTGGATGACT 1292
Qy 1261 GGATTTGGCTCCCCGGGGTATACGCTTTTACTGCCAGGAAATGCCCTTTTCCTC 1320
Db 1293 GGATTTGGCTCCCCGGGGTATACGCTTTTACTGCCAGGAAATGCCCTTTTCCTC 1352
Qy 1321 TGGCTGATCTGTAAGTCCACTAATCATGCTGATGCTTTCAGCGTGGTCACTCTGTTA 1380
Db 1353 TGGCTGATCTGTAAGTCCACTAATCATGCTGATGCTTTCAGCGTGGTCACTCTGTTA 1412
Qy 1381 ACTCTAAGATCTTAAGCATGCTGCTGCCAGACAGAACTCAGTCTATCTCGATGCTG 1440
Db 1413 ACTCTAAGATCTTAAGCATGCTGCTGCCAGACAGAACTCAGTCTATCTCGATGCTG 1472
Qy 1441 ACCTTGACGAGATGAAAGTTGTATTAAAGAACTATCAGGACATGTTGTGGAGGTT 1500
Db 1473 ACCTTGACGAGATGAAAGTTGTATTAAAGAACTATCAGGACATGTTGTGGAGGTT 1532
Qy 1501 GTGGGTGCTGTAGTACAGCAAAATTAATACATAAATATATATA 1547
Db 1533 GTGGGTGCTGTAGTACAGCAAAATTAATACATAAATATATATA 1579

RESULT 15
US-10-397-214-3
; Sequence 3, Application US/10397214
; Publication No. US20040009916A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Elizabeth A.
; APPLICANT: Rosen, Vicki A.
; APPLICANT: Wozney, John M.
; TITLE OF INVENTION: No. US20040009916A1e1 BMP Products
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESS: LEGAL AFFAIRS, GENETICS INSTITUTE, INC.
; STREET: 87 CAMBRIDGE PARK DRIVE
; CITY: CAMBRIDGE
; STATE: MA
; COUNTRY: USA
; ZIP: 02140

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/10/397,214
FILING DATE: 27-MARCH-2003
CLASSIFICATION:
PRIOR APPLICATION DATA: US/07/721,847A
FILING DATE: 14-JUN-1991
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Kapinos, Ellen J.
REGISTRATION NUMBER: 32,245
REFERENCE/DOCKET NUMBER: 5160C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-876-1170
TELEFAX: 617-876-5851
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1607 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo Sapiens
CELL TYPE: Osteosarcoma Cell Line
CELL LINE: U-20S
IMMEDIATE SOURCE:
LIBRARY: U20S cDNA in Lambda GT10
CLONE: Lambda U20S-39
POSITION IN GENOME:
UNITS: bp
FEATURE:
NAME/KEY: CDS
LOCATION: 356..1546
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 1202..1543
FEATURE:
NAME/KEY: mRNA
LOCATION: 14..1607
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 356..424
US-10-397-214-3

Query Match 100.0%; Score 1547; DB 6; Length 1607;
Best Local Similarity 100.0%; Pred. No; 0;
Matches 1547; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GGGGACTTCTTGAACCTTGCAGGAGATAAATCTTGGCACCACCTTTTGGCGCGGTGCTT 60
Db 33 GGGGACTTCTTGAACCTTGCAGGAGATAAATCTTGGCACCACCTTTTGGCGCGGTGCTT 92
Qy 61 TGCCCCAGCGAGCGCTGCTTCCGCACTCTCCGAGGCCCAACCGCCCTTCCACTCTCGGCT 120
Db 93 TGCCCCAGCGAGCGCTGCTTCCGCACTCTCCGAGGCCCAACCGCCCTTCCACTCTCGGCT 152
Qy 121 TGCCCCAGCATGTAGACGCTGTTCCAGCGTGAAGAGAGACTGCGCGCGCGGACCCGG 180
Db 153 TGCCCCAGCATGTAGACGCTGTTCCAGCGTGAAGAGAGACTGCGCGCGCGGACCCGG 212
Qy 181 GAGAAGGAGGAGGCAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 240
Db 213 GAGAAGGAGGAGGCAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 272
Qy 241 AGAGTTTTTCCATGTGGACGCTCTTTCAATGAGAGTGTGTCCCGCGGTGCTTCTTAGACGGA 300

Db 273 AGAGTTTTCATGTGAGAGCTCTTTCAATGAGCGTGTCCCGGTGCTTCTTAGACGGA 332
Qy 301 CTGCGGTCTCTAAAGGTGCAACATGTTGGCCGGGACCCCGTGTCTTCTAGCGTTGCTGC 360
Db 333 CTGCGGTCTCTAAAGGTGCAACATGTTGGCCGGGACCCCGTGTCTTCTAGCGTTGCTGC 392
Qy 361 TTCCCCAGGTCTCTTGGCGGCGGCTGAGCTTCCGGAGCTGGCCGCGAGGAAGT 420
Db 393 TTCCCCAGGTCTCTTGGCGGCGGCTGAGCTTCCGGAGCTGGCCGCGAGGAAGT 452
Qy 421 TCGCGGCGGCTCTGTCGCGGCGGCTCTCATCCAGCCCTCTGACGAGCTCTGAGCGAGT 480
Db 453 TCGCGGCGGCTCTGTCGCGGCGGCTGAGCTTCCGGAGCTGGCCGCGAGGAAGT 512
Qy 481 TCGAGTTGCGGCTCTGACAGATGTTGCGGCTGAAACAGAGACCCACCCAGCAGGGAAG 540
Db 513 TCGAGTTGCGGCTCTGACAGATGTTGCGGCTGAAACAGAGACCCACCCAGCAGGGAAG 572
Qy 541 CCGTGTGCCCCCTACATGCTAGACCTGTATCGCAGGCACTCAGGTCAGGCGGGCTCAC 600
Db 573 CCGTGTGCCCCCTACATGCTAGACCTGTATCGCAGGCACTCAGGTCAGGCGGGCTCAC 632
Qy 601 CCGCCCCAGACACCGGTTGGAGAGGCGAGCCAGCCAGCCAACTGTGCGCAGCTTCC 660
Db 633 CCGCCCCAGACACCGGTTGGAGAGGCGAGCCAGCCAGCCAACTGTGCGCAGCTTCC 692
Qy 661 ACCATGAAGAATCTTTTGAAGAACTTACAGAAACGAGTGGGAAACAAACCCGAGATCT 720
Db 693 ACCATGAAGAATCTTTTGAAGAACTTACAGAAACGAGTGGGAAACAAACCCGAGATCT 752
Qy 721 TCTTTAATTTAAGTTCTATCCCGAGGAGGTTTATCACCTCAGCAGAGCTTCAGGTTT 780
Db 753 TCTTTAATTTAAGTTCTATCCCGAGGAGGTTTATCACCTCAGCAGAGCTTCAGGTTT 812
Qy 781 TCCGAGACAGATGCAAGATGCTTTAGGAAACAATAGCAGTTTCCATCACCAGAAATTAATA 840
Db 813 TCCGAGACAGATGCAAGATGCTTTAGGAAACAATAGCAGTTTCCATCACCAGAAATTAATA 872
Qy 841 TTTATGAATAATCAATAAACCTGCAACAGCCAACTCGAAATTCGCCGTGACCAAGCTTTTGG 900
Db 873 TTTATGAATAATCAATAAACCTGCAACAGCCAACTCGAAATTCGCCGTGACCAAGCTTTTGG 932
Qy 901 ACACAGGTTGGTGAATCAGAACTCAGAGCTGCGGAAAGTTTGTGATGTCACCCCGCTG 960
Db 933 ACACAGGTTGGTGAATCAGAACTCAGAGCTGCGGAAAGTTTGTGATGTCACCCCGCTG 992
Qy 961 TGATCGGTGACCTGCAAGGAGACACGCCAACCATGGATTCGTGTGGAAGTGGCCCACT 1020
Db 993 TGATCGGTGACCTGCAAGGAGACACGCCAACCATGGATTCGTGTGGAAGTGGCCCACT 1052
Qy 1021 TGGAGGAGAAACAAGGTGCTTCCAGAGACATGTTAGGATAAGCAGGTCTTTTGACCAAG 1080
Db 1053 TGGAGGAGAAACAAGGTGCTTCCAGAGACATGTTAGGATAAGCAGGTCTTTTGACCAAG 1112
Qy 1081 ATGAACACAGCTGCTCAGATAGGCCATTTGTAGTAACTTTTGGCCATGATGGAAG 1140
Db 1113 ATGAACACAGCTGCTCAGATAGGCCATTTGTAGTAACTTTTGGCCATGATGGAAG 1172
Qy 1141 GGCAATCTCTCCACAAAGAGAGAAAACGTCAAGCCAAACACAAACAGCGGAAACGCCCTTA 1200
Db 1173 GGCAATCTCTCCACAAAGAGAGAAAACGTCAAGCCAAACACAAACAGCGGAAACGCCCTTA 1232
Qy 1201 AGTCAGCTGTAAGAGACACCCCTTTGTACGTGGACTTTCAGTGAAGTGGGGTGAATGACT 1260
Db 1233 AGTCAGCTGTAAGAGACACCCCTTTGTACGTGGACTTTCAGTGAAGTGGGGTGAATGACT 1292
Qy 1261 GGATTTGGCTCCCCCGGGTATCAGCCTTTTACTGCGAGAGATGCCCTTTTCTC 1320
Db 1293 GGATTTGGCTCCCCCGGGTATCAGCCTTTTACTGCGAGAGATGCCCTTTTCTC 1352
Qy 1321 TGGCTGATCATCTGAACCTCCAACTAATCATGCAATGTTGTCAGACGTTGGTCAACTCTGTTA 1380

Db 1353 TGGCTGATCATCTGAACCTCCAACTCAATCATGCCATTGTTCAGACGTTGGTCAACTCTGTTA 1412
Qy 1381 ACTCTAAGATTCTTAAGGCATGCTGTGTCGCCGACAGAACTCAGTGTCTATCTCGATGCTGT 1440
Db 1413 ACTCTAAGATTCTTAAGGCATGCTGTGTCGCCGACAGAACTCAGTGTCTATCTCGATGCTGT 1472
Qy 1441 ACCTTGACGAGAATGAAAAGGTTGTATTAAAGAACTATCAGGACATGTTGTGGAGGTTT 1500
Db 1473 ACCTTGACGAGAATGAAAAGGTTGTATTAAAGAACTATCAGGACATGTTGTGGAGGTTT 1532
Qy 1501 GTGGGTGTCGTAGTACAGCAAAATTAATAACATAAATATATATA 1547
Db 1533 GTGGGTGTCGTAGTACAGCAAAATTAATAACATAAATATATATA 1579

Search completed: January 10, 2006, 23:43:18
Job time : 929 secs

| Query Match | 100.0%; | Score 1547; | DB 6; | Length 1547; |
|-----------------------|-----------------|---|-----------|--------------|
| Best Local Similarity | 100.0%; | Pred. No. 0; | | |
| Matches 1547; | Conservative 0; | Mismatches 0; | Indels 0; | Gaps 0; |
| Qy | 1 | GGGGACCTTCTTGAACCTTGCAGGGGAGAATAACTTGGCACCCCACTTTTGGCGCGGTGCCTT | 60 | |
| Db | 1 | GGGGACCTTCTTGAACCTTGCAGGGGAGAATAACTTGGCACCCCACTTTTGGCGCGGTGCCTT | 60 | |
| Qy | 61 | TGCCCCAGCGAGCGCTCTTTCGCCCATCTTCGAGGCCCAACCGCCCTCCACTCTCTCGGCT | 120 | |
| Db | 61 | TGCCCCAGCGAGCGCTCTTTCGCCCATCTTCGAGGCCCAACCGCCCTCCACTCTCTCGGCT | 120 | |
| Qy | 121 | TGCCCGACACTGAGACGCTGTTCCAGCGTGAAGAAGAGAGACTGCGCGCGCGGCACCCGG | 180 | |
| Db | 121 | TGCCCGACACTGAGACGCTGTTCCAGCGTGAAGAAGAGAGACTGCGCGCGCGGCACCCGG | 180 | |
| Qy | 181 | GAGAAAGGAGGAGGCAAAAGAAACGGACATTCGGTCTTTTGGGCCAGAGTCTTTTGACC | 240 | |
| Db | 181 | GAGAAAGGAGGAGGCAAAAGAAACGGACATTCGGTCTTTTGGGCCAGAGTCTTTTGACC | 240 | |
| Qy | 241 | AGAGTTTTTCATGTGGACGCTCTTTCAATGGACGTGTCCCGCGTCTCTTTAGACCGGA | 300 | |
| Db | 241 | AGAGTTTTTCATGTGGACGCTCTTTCAATGGACGTGTCCCGCGTCTCTTTAGACCGGA | 300 | |

Qy 301 CTGCGGTCTCTAAAGTTCGACCATGTGTGGCGGGACCCCGTGTCTTCTAGCGTGTCTGC 360
Db 301 CTGCGGTCTCTAAAGTTCGACCATGTGTGGCGGGACCCCGTGTCTTCTAGCGTGTCTGC 360
Qy 361 TTCCCCAGGTCTCTCTGGGCGGCGGCTGGCCCTCTGTTCCGGAGCTGGGCGCAGGAGT 420
Db 361 TTCCCCAGGTCTCTCTGGGCGGCGGCTGGCCCTCTGTTCCGGAGCTGGGCGCAGGAGT 420
Qy 421 TCGCGGGCGGTCTGTCGGGCGGCGGCTCATCCAGCCCTCTGACGAGTCTCTGAGCGAGT 480
Db 421 TCGCGGGCGGTCTGTCGGGCGGCGGCTCATCCAGCCCTCTGACGAGTCTCTGAGCGAGT 480
Qy 481 TCGAGTTCCGCGTCTGACGATGTTCCGCTGAAACAGAGACCCACCCCGCAGCGAGC 540
Db 481 TCGAGTTCCGCGTCTGACGATGTTCCGCGCTGAAACAGAGACCCACCCCGCAGCGAGC 540
Qy 541 CCGTGGTCCCGCTTACATGCTAGACCTGTATCGCAGCACTCAGGTCTCAGCGCGGCTCAC 600
Db 541 CCGTGGTCCCGCTTACATGCTAGACCTGTATCGCAGCACTCAGGTCTCAGCGCGGCTCAC 600
Qy 601 CCGCCACAGACCCCGTTGGAGGGCAGCCAGCCAGCCAACTGTGCGCAGCTTCC 660
Db 601 CCGCCACAGACCCCGTTGGAGGGCAGCCAGCCAGCCAACTGTGCGCAGCTTCC 660
Qy 661 ACCATGAAGATCTTTGGAAGATACACAGAAACGAGTGGGAAACAAACCCGGAGATCT 720
Db 661 ACCATGAAGATCTTTGGAAGATACACAGAAACGAGTGGGAAACAAACCCGGAGATCT 720
Qy 721 TCTTTAATTTAAGTTCTATCCCGAGGAGTTTATCACCTCAGCAGAGCTTCAGGTTT 780
Db 721 TCTTTAATTTAAGTTCTATCCCGAGGAGTTTATCACCTCAGCAGAGCTTCAGGTTT 780
Qy 781 TCCGAGAACAGATGCAAGATCTTTAGGAAACAATAGCAGTTTCCATCACCGAATTAATA 840
Db 781 TCCGAGAACAGATGCAAGATCTTTAGGAAACAATAGCAGTTTCCATCACCGAATTAATA 840
Qy 841 TTTATGAATCATATAAACCTGCAAGCACTGAAATTCCTGTCGACGAGCTTTGG 900
Db 841 TTTATGAATCATATAAACCTGCAAGCACTGAAATTCCTGTCGACGAGCTTTGG 900
Qy 901 ACACGAGTTGCTGAATCAGAAATCAAGCAGTGGGAAAGTTTGTATGTACACCCCGCTG 960
Db 901 ACACGAGTTGCTGAATCAGAAATCAAGCAGTGGGAAAGTTTGTATGTACACCCCGCTG 960
Qy 961 TGATGCGGTGACTGCAAGGAGACCGCAACCATGGAATTCGTGGAAGTGCCCACT 1020
Db 961 TGATGCGGTGACTGCAAGGAGACCGCAACCATGGAATTCGTGGAAGTGCCCACT 1020
Qy 1021 TGGAGGAGAAACAGGTGTCTCCAAGAGACATGTTAGGATAAGCAGGTCTTTGACCCAG 1080
Db 1021 TGGAGGAGAAACAGGTGTCTCCAAGAGACATGTTAGGATAAGCAGGTCTTTGACCCAG 1080
Qy 1081 ATGAACACAGCTGGTTCAGATAAGGCGCATTTAGTAACTTTTGGCCATGATGAAAG 1140
Db 1081 ATGAACACAGCTGGTTCAGATAAGGCGCATTTAGTAACTTTTGGCCATGATGAAAG 1140
Qy 1141 GGCATCTCTCCACAAAAGAGAAAACGTCAAGCCAAACACAAACAGCGGAAACGCCTTA 1200
Db 1141 GGCATCTCTCCACAAAAGAGAAAACGTCAAGCCAAACACAAACAGCGGAAACGCCTTA 1200
Qy 1201 AGTCAGCTGTGAAGAGACACCTTTGTACGTGGACCTTCAGTGAGCTGGGGTGGAAATGACT 1260
Db 1201 AGTCAGCTGTGAAGAGACACCTTTGTACGTGGACCTTCAGTGAGCTGGGGTGGAAATGACT 1260
Qy 1261 GGATTTGGCTCCCGGGGTATCAGCGCTTTTACTGCCACGAGAAATGCCCTTTTCTC 1320
Db 1261 GGATTTGGCTCCCGGGGTATCAGCGCTTTTACTGCCACGAGAAATGCCCTTTTCTC 1320
Qy 1321 TGGCTGATCATCTGAACCTCAATAATCATGCAATGTTTTCAGACGTTGCTCAACTCTGTTA 1380
Db 1321 TGGCTGATCATCTGAACCTCAATAATCATGCAATGTTTTCAGACGTTGCTCAACTCTGTTA 1380

Qy 1381 ACTCTAAGATTCCTAAGCATGCTGTGCCGACAGAACTCAGTGTCTATCTCGATGCTGT 1440
Db 1381 ACTCTAAGATTCCTAAGCATGCTGTGCCGACAGAACTCAGTGTCTATCTCGATGCTGT 1440
Qy 1441 ACCTTGACGAGATGAAAAGTGTGTTATTAAGAACTATCAGGACATGTTGTGAGGGTT 1500
Db 1441 ACCTTGACGAGATGAAAAGTGTGTTATTAAGAACTATCAGGACATGTTGTGAGGGTT 1500
Qy 1501 GTGGGTCTCGCTAGTAGCAGCAAAATTAATAACATAATAATATATATA 1547
Db 1501 GTGGGTCTCGCTAGTAGCAGCAAAATTAATAACATAATAATATATATA 1547

RESULT 2
US-11-051-568-4
; Sequence 4, Application US/11051568
; Publication No. US20050255141A1
; GENERAL INFORMATION:
; APPLICANT: OPPERMAN, HERMANN
; OZKAYNAK, ENGIN
; KUBERASAMPATH, THANGAVEL
; RUEGER, DAVID C.
; PANG, ROY H.L.
; TITLE OF INVENTION: OSTEOGENIC DEVICES
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TESTA, HURWITZ & THIBEAULT
; STREET: 125 HIGH STREET
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: U.S.A.
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/051,568
; FILING DATE: 04-Feb-2005
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 10/321,799
; FILING DATE: 17-DEC-2002
; APPLICATION NUMBER: US 09/148,925
; FILING DATE: 8-SEP-1998
; APPLICATION NUMBER: US 08/449,699
; FILING DATE: 24-MAY-1995
; APPLICATION NUMBER: US 08/147,023
; FILING DATE: 1-NOV-1993
; APPLICATION NUMBER: US 07/841,646
; FILING DATE: 21-FEB-1992
; APPLICATION NUMBER: US 07/827,052
; FILING DATE: 28-JAN-1992
; APPLICATION NUMBER: US 07/579,865
; FILING DATE: 7-SEP-1990
; APPLICATION NUMBER: US 07/621,849
; FILING DATE: 4-DEC-1990
; APPLICATION NUMBER: US 07/621,988
; FILING DATE: 4-DEC-1990
; APPLICATION NUMBER: US 07/810,560
; FILING DATE: 20-DEC-1991
; APPLICATION NUMBER: US 07/569,920
; FILING DATE: 20-AUG-1990
; APPLICATION NUMBER: US 07/600,024
; FILING DATE: 18-OCT-1990
; APPLICATION NUMBER: US 07/599,543
; FILING DATE: 18-OCT-1990
; APPLICATION NUMBER: US 07/616,374
; FILING DATE: 21-NOV-1990
; APPLICATION NUMBER: US 07/483,913
; FILING DATE: 22-FEB-1990
; APPLICATION NUMBER: US 07/179,406

FILING DATE: 08-APR-1988
APPLICATION NUMBER: US 07/232,630
FILING DATE: 15-AUG-1988
APPLICATION NUMBER: US 07/315,342
FILING DATE: 23-FEB-1989
APPLICATION NUMBER: US 07/660,162
FILING DATE: 22-FEB-1991
APPLICATION NUMBER: US 07/422,699
FILING DATE: 17-OCT-1989
APPLICATION NUMBER: US 07/422,613
FILING DATE: 17-OCT-1989
APPLICATION NUMBER: US 07/422,623
FILING DATE: 17-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: DIANA M. STEEL
REGISTRATION NUMBER: 43,153
REFERENCE/DOCKET NUMBER: STK-001CP6C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/248-7000
TELEFAX: 617/248-7100
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1260 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: HOMO SAPIENS
FEATURE:

NAME/KEY: CDS
LOCATION: 9..1196
OTHER INFORMATION: /function= "OSTEOGENIC PROTEIN"
/product= "CBMP2A"
/note= "CBMP2A (CDNA)"
SEQUENCE DESCRIPTION: SEQ ID NO: 4:

US-11-051-568-4

Query Match 79.3%; Score 1227.2; DB 7; Length 1260;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1229; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

| | | | |
|----|-----|--|-----|
| QY | 316 | GGTCACACATGGTGGCGGACCCGCTGTCTTAGCGTTCCTCCCGAGTCCCTCC | 375 |
| DB | 1 | GGTCACACATGGTGGCGGACCCGCTGTCTTAGCGTTCCTCCCGAGTCCCTCC | 60 |
| QY | 376 | TGGCGGCGCGGCTGGCTCGTTCCGGAGCTGGCGCGAGGAAGTTCCGGCGGCTGT | 435 |
| DB | 61 | TGGCGGCGCGGCTGGCTCGTTCCGGAGCTGGCGCGAGGAAGTTCCGGCGGCTGT | 120 |
| QY | 436 | CGGCGCGGCTCATCCAGCCCTCTGACGAGTCTTGAGCGAGTTCGAGTTGCGGCTGC | 495 |
| DB | 121 | CGGCGCGGCTCATCCAGCCCTCTGACGAGTCTTGAGCGAGTTCGAGTTGCGGCTGC | 180 |
| QY | 496 | TCAGCATGTTGGCTGTGAACAGAGACCCACCCCGAGGAGCGCGTGGTCCCGCT | 555 |
| DB | 181 | TCAGCATGTTGGCTGTGAACAGAGACCCACCCCGAGGAGCGCGTGGTCCCGCT | 240 |
| QY | 556 | ACATGCTAGACCTGTATCGAGGCTCAGGTCAGCGGGCTCACCCCGCCCGAGACACC | 615 |
| DB | 241 | ACATGCTAGACCTGTATCGAGGCTCAGGTCAGCGGGCTCACCCCGCCCGAGACACC | 300 |
| QY | 616 | GTTTGGAGGGGAGCGAGCGGAGCCAACTGTGCGAGTTCACCATGAAGAATCTT | 675 |
| DB | 301 | GTTTGGAGGGGAGCGAGCGGAGCCAACTGTGCGAGTTCACCATGAAGAATCTT | 360 |
| QY | 676 | TGGAAGAATACAGAAAGAGTGGGAAAACACCGGAGATCTCTTTAATTAAGTT | 735 |
| DB | 361 | TGGAAGAATACAGAAAGAGTGGGAAAACACCGGAGATCTCTTTAATTAAGTT | 420 |
| QY | 736 | CTATCCCGAGGAGGTTTATACCTCAGCAGAGCTTCAGGTTTCCGAGAACAGATGC | 795 |

| | | | |
|----|------|---|------|
| DB | 421 | CTATCCCGAGGAGGTTTATACCTCAGCAGAGCTTCAGGTTTCCGAGAACAGATGC | 480 |
| QY | 796 | AAGATGCTTTAGGAAAACAATAGCAGTTTCCATACCGAATTAATTAATTAATTAATTA | 855 |
| DB | 481 | AAGATGCTTTAGGAAAACAATAGCAGTTTCCATACCGAATTAATTAATTAATTAATTA | 540 |
| QY | 856 | AACCTGCAACAGCCAACTCGAAATTTCCCGTGACAGACTTTTGGACACCAAGGTTGGTGA | 915 |
| DB | 541 | AACCTGCAACAGCCAACTCGAAATTTCCCGTGACAGACTTTTGGACACCAAGGTTGGTGA | 600 |
| QY | 916 | ATCAGAAATGCAAGCAGGTGGGAAAAGTTTGTGATGACACCCCGCTGTGATCGGTTGATG | 975 |
| DB | 601 | ATCAGAAATGCAAGCAGGTGGGAAAAGTTTGTGATGACACCCCGCTGTGATCGGTTGATG | 660 |
| QY | 976 | CACAGGACACGCCAAACCATGGAATTCGTGGTGGAGTGGCCCACTTTGAGGAGAACCAAG | 1035 |
| DB | 661 | CACAGGACACGCCAAACCATGGAATTCGTGGTGGAGTGGCCCACTTTGAGGAGAACCAAG | 720 |
| QY | 1036 | GTGTCTCCAAGAGACATGTTAGGATAAGCAGGTCTTTGACCAAGATGAACACAGCTGGT | 1095 |
| DB | 721 | GTGTCTCCAAGAGACATGTTAGGATAAGCAGGTCTTTGACCAAGATGAACACAGCTGGT | 780 |
| QY | 1096 | CACAGATAAGGCCATTTCTAGTAACTTTTGGCCATGATGGAAGGGGATCTCTCTCCACA | 1155 |
| DB | 781 | CACAGATAAGGCCATTTCTAGTAACTTTTGGCCATGATGGAAGGGGATCTCTCTCCACA | 840 |
| QY | 1156 | AAAGAGAAAACGTCAGCCAAACACAAACAGCGGAAACGCTTAAAGTCCAGCTGTAAGA | 1215 |
| DB | 841 | AAAGAGAAAACGTCAGCCAAACACAAACAGCGGAAACGCTTAAAGTCCAGCTGTAAGA | 900 |
| QY | 1216 | GACACCCCTTTGACGTGGACTTCAGTGACGTGGGTGGAAATGACTGGATTGTGGCTCCCC | 1275 |
| DB | 901 | GACACCCCTTTGACGTGGACTTCAGTGACGTGGGTGGAAATGACTGGATTGTGGCTCCCC | 960 |
| QY | 1276 | CGGGGTATCACGCCCTTTTACTGCCACGAGAAATGCCCTTTCTCTGCTGATCATCTGA | 1335 |
| DB | 961 | CGGGGTATCACGCCCTTTTACTGCCACGAGAAATGCCCTTTCTCTGCTGATCATCTGA | 1020 |
| QY | 1336 | ACTCAGTAATCATGCCATTTGTTGACAGCTTGGTGGTAACTCTGTTAACTTAAGATTCCTA | 1395 |
| DB | 1021 | ACTCAGTAATCATGCCATTTGTTGACAGCTTGGTGGTAACTCTGTTAACTTAAGATTCCTA | 1080 |
| QY | 1396 | AGGCATGCTGTGCCCGACAGAACTCAGTGCTATCTCGATGCTGTACCTTGACGAGAAATG | 1455 |
| DB | 1081 | AGGCATGCTGTGCCCGACAGAACTCAGTGCTATCTCGATGCTGTACCTTGACGAGAAATG | 1140 |
| QY | 1456 | AAAAGGTTGTATTAAAGAACTATCAGGACATGTTGTGGAGGGTTGTGGGTGTCGCTAGT | 1515 |
| DB | 1141 | AAAAGGTTGTATTAAAGAACTATCAGGACATGTTGTGGAGGGTTGTGGGTGTCGCTAGT | 1200 |
| QY | 1516 | ACAGCAAAATTAATACATAATATATATATA 1547 | |
| DB | 1201 | ACAGCAAAATTAATACATAATATATATATA 1232 | |

RESULT 3

US-11-136-527-2371
; Sequence 2371, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2371
; LENGTH: 2738


```
;
;
;   REGISTRATION NUMBER: 43,153
;   REFERENCE/POCKET NUMBER: STK-001CP6C3
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 617/248-7000
;   TELEFAX: 617/248-7100
;   INFORMATION FOR SEQ ID NO: 6:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 1788 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: cDNA
;   HYPOTHETICAL: NO
;   ANTI-SENSE: NO
;   ORIGINAL SOURCE:
;   ORGANISM: HOMO SAPIENS
;   TISSUE TYPE: HIPPOCAMPUS
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: 403..1526
;   IDENTIFICATION METHOD: experimental
;   OTHER INFORMATION: /function= "OSTEOGENIC PROTEIN"
;   /product= "CBMP2B"
;   /evidence= EXPERIMENTAL
;   /note= "CBMP2B (CDNA)"
;
;   SEQUENCE DESCRIPTION: SEQ ID NO: 6:
;
US-11-051-568-6

Query Match      24.2%; Score 375; DB 7; Length 1788;
Best Local Similarity 61.0%; Pred. No. 5,7e-98;
Matches 672; Conservative 0; Mismatches 405; Indels 24; Gaps 3;

QY 436 CGGCGCGCCCTCATCCAGCCCTCTGACAGGTCCTGAGAGGATTCGAGAGTTGCGGCTGC 495
DB 527 CGGAGGACGCGGCTCAGGCGAGGCCATGAGCTCCTGCGGGAATTCGAGGCGACATTC 586
QY 496 TCAGCATGTCGGCTGAAACAGAGACCCACCCCGCAGGAGCGCGTGTGCCCCCT 555
DB 587 TGCAGATGTTGGGCTGGCGCGCCCGCAGCCTAGCAAGAGTGCGGTCAATCCGACT 646
QY 556 ACATGCTAGACTGTATCGCAGGCACTCAGGTCTAGCCG--GGCTCACCCGCCAGACCA 613
DB 647 ACATGCGGATCTTTACCGGCTTCAGTCTGGGAGGAGGAGAGACAGATCACAGCA 706
QY 614 CCGGTG-----GAGAGGCGAGCAGCCGAGGCCAACACTGTGGCGAGCTTCCACC 663
DB 707 CTGGTCTTGTAGTATCTGAGCGCCCGGCGCAGCCGCGGCCAACACCGGTGAGGAGCTTCCACC 766
QY 664 ATGAAGATCTTTGGAAGAACTACCAAGAACGAGTGGGAAACCAACCCGGAGATTTCT 723
DB 767 ACGAAGAACATCTGGAGAACATCCAGGACACAGTGAATCTGTCTTTCGTTTCTCT 826
QY 724 TTAATTTAAGTTCTATCCCGCAGGAGGATTTATCACCCTCAGCAGAGCTTCAGGTTTCC 783
DB 827 TTAACCTCAGCAGCATCCTGAGAACGAGGTGATCTCTCTGAGAGCTTCGGCTCTCC 886
QY 784 GAGAACAGATGCAAGATGCTTTAGAAACATAGAGTTTCATCACCAGATTAATATT 843
DB 887 GGGAGCAGTGGACGACGCGGCTGATTGGGAAAGGGGCTTCCACCGTATTAACATTTATG 946
QY 844 ATGAATCATAAACCTGCAACAGCCTACTCGAAATTCGCCGTGACACGAGCTTTGGACA 903
DB 947 AGTTATGAAGCCCCCAGCAAGTGTGCTGGGCACCTCATCACAGCACTACTGGACA 1006
QY 904 CCAGGTTGGTGAATCAGAAATCAGAGTGGGAAAGTTTGTATGTACCCCGCTGTGA 963
DB 1007 CGAGACTGTTCCACCAATGTGACACGTTGGGAACTTTGTATGTAGCCTCGGCTCC 1066
QY 964 TCGGTTGAGCTGCACAGGGAACGCGCAACCATGATGCTGGTGGAAAGTGCCCACTGG 1023
DB 1067 TTCGCTGACCCGGGAGAGGAGCAACTATGGCTAGCCATTGAGGTGACTCACCTCC 1126
QY 1024 AGGAGAACAGGTGTCTCCAGAGACATGTTAGGATAAGCAGGTCTTTGACCACAGATG 1083
```

```
DB 1127 ATCAGACTCGGACCCACAGGCGCAGCATGTGAGGATTAGCCGATCTTACTCAAGGA 1186
QY 1084 AACACAGCTGGTCAACAGATAAGGCCATTTGTAGTAACCTTTTGGCCATGATGGAAGGCG 1143
DB 1187 GTGGAAATGGGCCAGCTCCGCGCCCTCTCTGGTCACTTTTGGCCATGATGGCCGGGCC 1246
QY 1144 ATCTCTCCCAAAAGAGAAAAAGTCAAGCCAAACAAACAGCGGGAAGCGCTT---- 1199
DB 1247 ATGCTTTGACCCGACGCGGAGGGCCAAAGCGTAGCCCTAAGCATCACTCAGCGGGCCA 1306
QY 1200 -----AAGTCCAGCTGTAAGAGACACCCCTTTGTACGTGGACTTCAGTGACGTGGGT 1251
DB 1307 GGAAGAAGAAATAAGAACTGCGGGGCCACTCGCTCTATGTGAACTTCAGGATGTGGCT 1366
QY 1252 GGAATGACTGGATTGTGGCTCCCGCGGGTATCACGCTTTTATGCCCAGGAAATGCC 1311
DB 1367 GGAATGACTGGATTGTGGCCCAACCCAGGCTTACCAGGCTTCTACTGCCATGGGACTGCC 1426
QY 1312 CTTTCTCTGGCTGATCATCTGAATCCCACTAATCATGCGCATTTTTCAGACGTTGGTCA 1371
DB 1427 CTTTCCACTGGCTGACCACTCAACTCAACCAACCATGTCATTTGTGCAGACCCCTGCTCA 1486
QY 1372 ACTCTGTTAACTCTTAAGATTCTTAAGGCATGCTGTGTCGCCAGCAAACTCAGTCTATCT 1431
DB 1487 ATTCTGTCAATTCAAGTATCCCAAGCCTGTGTGTGCCCACTGAACTGAGTGCCATCT 1546
QY 1432 CGATGCTGTACCTTGACGAGAATGAAGAAGTTGTATTAAAGAACTATCAGGACATGGTTG 1491
DB 1547 CCATGCTGTACCTGGATGAGTATGATAAGTGTGTTACTGAAAAATTTATCAGGAGATGGTAG 1606
QY 1492 TGAGAGGTTGTGGGTGCGCT 1512
DB 1607 TAGAGGAGATGTGGGTGCGCT 1627

RESULT 6
US-11-051-568-18
; Sequence 18, Application US/11051568
; Publication No. US20050255141A1
; GENERAL INFORMATION:
; APPLICANT: OPPERMANN, HERMANN
; OZKANAK, ENGIN
; KUBERASAMPATH, THANGAVEL
; RUEBER, DAVID C.
; PANG, ROY H.L.
; TITLE OF INVENTION: OSTEOGENIC DEVICES
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TESTA, HURWITZ & THIBEAULT
; STREET: 125 HIGH STREET
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: U.S.A.
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/051,568
; FILING DATE: 04-Feb-2005
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 10/321,799
; FILING DATE: 17-DEC-2002
; APPLICATION NUMBER: US 09/148,925
; FILING DATE: 8-SEP-1998
; APPLICATION NUMBER: US 08/449,699
; FILING DATE: 24-MAY-1995
; APPLICATION NUMBER: US 08/147,023
; FILING DATE: 1-NOV-1993
```

| | Query Match | 24.1% | Score 372.2 | DB 7 | Length 1586 |
|----|-----------------------|--|-------------------|-----------|-------------|
| | Best Local Similarity | 61.4% | Pred. No. 3.5e-97 | | |
| | Matches 662 | Conservative 0 | Mismatches 393 | Indels 24 | Gaps 3 |
| Qy | 458 | CTCTGACGAGGTCTCTGACGAGGTTTCGAGTTGCGGCTGCTCAGCATATGTCGGCTGGAACA | 517 | | |
| Db | 180 | CCCGGAGAGGCTCTCGGGACTTCGAGGCGACATCTTCGAGATGTTTGGGCTGC | 239 | | |
| Qy | 518 | GAGACCCACCCGACGACGGGACGGCTGTGTGTCCTCCCTACATGCTAGACCTGTATCGCAG | 577 | | |
| Db | 240 | CCGCCCGCAGCTAGCAAGATGCGCTCATTTCCGGACTACATCGGGATCTTTACCGGCT | 299 | | |

```

RESULT 7
US-11-136-527-2142
; Sequence 2142, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes

```

```
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2142
; LENGTH: 1900
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-2142

Query Match      24.0%; Score 371.4; DB 7; Length 1900;
Best Local Similarity 60.5%; Pred. No. 6.5e-97;
Matches 666; Conservative 5; Mismatches 406; Indels 24; Gaps 3;

Qy 436 CGGGCGCCCTCATCCAGCCCTCTGACAGGTCCTGAGCGAGTTGAGTTGGGCTGC 495
Db      |||||
Qy 525 CGGAGGAGCGGCTCAGGCGAGGCCATGAGCTCTGCGGGACTTCGAGCGGACATTC 584
Db      |||||
Qy 496 TCAGCATGTTGGGCTGAAACAGAGACCCACCCAGCAGGAGCGCGTGTGCCCCCT 555
Db      |||||
Qy 585 TGCAGATGTTGGGCTGGCGCGGCTCGCAGCGGCAAGAGCGCGCTCATCCCGGATT 644
Db      |||||
Qy 556 ACATGCTAGACCTGTATCGCAGGCACTCAGTTCAGCGGGCTCACCCGCCACACACC 615
Db      |||||
Qy 645 ACATGAGGATCTTTACCGGCTCCAGTCTGGGAGGAGGAGGAGAGAGCAGAGCCAGG 704
Db      |||||
Qy 616 GGTG-----GAGAGGGCAGCCAGCCAGCAACACTGTGCGCAGCTTCC 660
Db      |||||
Qy 705 GAACCGGCTTGAGTACCCTGAGSCTCTGCCAGCAGGCCAACACTGTGAGGATTCC 764
Db      |||||
Qy 661 ACCATGAAGATCTTTGGAAGAACTACAGAAACGAGTGGGAAACAAACCCGAGATTCT 720
Db      |||||
Qy 765 ATCAGGAAGACATCTGGAGAACATCCCAAGGACCACTGAGAGCTCTGCTTTCTGTTCT 824
Db      |||||
Qy 721 TCTTTAATTTAAGTTCATCCCAAGGAGTTTATCACCTCAGCAGAGCTTCAGGTTT 780
Db      |||||
Qy 825 TCTTTAACCCTCAGCAGCATCCAGAGATGAGGTATCTCTGCGAGAGCTCGGCTAT 884
Db      |||||
Qy 781 TCCGAGAACAGATGCAAGATGCTTTAGGAACAATAGCAGTTTCCATCACCAGATTATA 840
Db      |||||
Qy 885 TTCGGAGCAGGTGGACCCAGGSCCTGACTGGGAACAGGGCTTCCACCGTATACATT 944
Db      |||||
Qy 841 TTTATGAATCATAAACCTGCACAGCCAACTCGAAATTCCTCCGTCGACACGACTTTGG 900
Db      |||||
Qy 945 ATGAGGTATGAAGCCCCCAGCAGAAATGTTGCTGGACACCTCATCACAGCACTACTGG 1004
Db      |||||
Qy 901 ACACAGGTTGGTGAATCAGAAATCAAGCAGGTGGGAAAGTTTGTGATGTACACCCGCTG 960
Db      |||||
Qy 1005 ACACAGACTAGTCCRTCAACATGTGACAGCGTGGGAAACTTTCGATGTGAGCCCTGAG 1064
Db      |||||
Qy 961 TGATGCGGTGACTGCAACAGGACACGCCAACCATGATTCGTTGGTGAAGTGCCCACT 1020
Db      |||||
Qy 1065 TCCTTGATGACCCGGGAAAGCAACCAACTATGGCTGGCCATTGAGTGACTACCC 1124
Db      |||||
Qy 1021 TGGAGGAGAAACAAGGTGTCTCCAAGAGACATGTTAGGATAAGCAGTCTTTGACCAAG 1080
Db      |||||
Qy 1125 TCCACAGACAGCAAGCCACCAAGGCCCAACATGTCAAGATTAGCCGATCGTTACTCAAG 1184
Db      |||||
Qy 1081 ATGAACACAGCTGTCACAGATAGGCCATTTAGTAACTTTTGGCCATGATGGAAG 1140
Db      |||||
Qy 1185 GGAATGGAATTTGGGCCCAACTCCGGCCCCCTCTGGTCAATTTTGGCCACATGGCCGG 1244
Db      |||||
Qy 1141 GGCATCTCTCT---CCACAAAAGAGAAACCTCAAGCCAAACACAAACAGCGGAAACGCC 1197
Db      |||||
Qy 1245 GTCATACCTTGACCGCGGAGGCGCAAGCTAGTCCCAAGCATCAACCCAGCGCTCCA 1304
Db      |||||
Qy 1198 TTAAGTCGAG-----CTGTAAGAGACACCTTTTGTAGCTGGACTTCAGTGACGTGGGT 1251
Db      |||||
Qy 1305 GGAAGAGAAATAAGAACTGCGCGTCCGCTTACGCTGAGATTCAGTGACGTGGGCT 1364
Db      |||||
```

```
Qy 1252 GGAATGACTGATGTGGCTCCCGGGGTATACGCGCTTTTACTGCACGAGAAATGCC 1311
Db      |||||
Qy 1365 GGAATGATTTGATGCTGGCCCGCCWCCAGGCTACCAAGGCTTCTACTGCCACGGGACTGTC 1424
Db      |||||
Qy 1312 CTTTTCTCTGGCTGATCATCTGAATCCCACTAATCATGCGCAATGTTTCAGACGTTGGTCA 1371
Db      |||||
Qy 1425 CTTTTCACTGGCGGCCACCTCAACTCAACCAATCATGCCATTTGTGCAGACCCCTGGTCA 1484
Db      |||||
Qy 1372 ACTCTGTTAACTCTAAGATTTCTTAAGGCATGCTGTGTCGCCGACAGAACTCAGTCTATCT 1431
Db      |||||
Qy 1485 ACTCCGTTAATTTAGCATCCCTAAGGCCTGCTGTGCCACCGAACTGAGCCCAATTT 1544
Db      |||||
Qy 1432 CGATGCTGTACCTTTGACGAGAAATGAAAAGTTGTTATTAAGAACTATCAGGACATGGTTG 1491
Db      |||||
Qy 1545 CCATGTTGTTATCTGGACGAGTACGACAAAGTGGTGTGTAATAAATATCAGGAGATGGTG 1604
Db      |||||
Qy 1492 TGGAGGGTTGTGGGTGTCGCT 1512
Db      |||||
Qy 1605 TGGAGGGGTGCGGATGCCGT 1625
Db      |||||

RESULT 8
US-11-136-527-6238
; Sequence 6238, Application US/11/136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6238
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-6238

Query Match      13.0%; Score 201; DB 7; Length 600;
Best Local Similarity 78.2%; Pred. No. 5.4e-48;
Matches 240; Conservative 1; Mismatches 66; Indels 0; Gaps 0;

Qy 1206 AGCTGTAAGAGACACCTTTTGTACGTGACCTTCAGTGACCGTGGGTGGAATGACTGATT 1265
Db      |||||
Qy 1266 GTGGCTCCCGGGGTATCAGCGCTTTTACTGCCACGAGAAATGCCCTTTTCTCTGGCT 1325
Db      |||||
Qy 79 GTGGCCCCWCCAGGCTACCAAGCCCTTCTACTGCCACGCGGACTGTCCCTTTCCACTGGCG 138
Db      |||||
Qy 1326 GATCATCTGAACCTCCACTAATCATGCCATTTGTTCCAGACGTTGGTCAACTCTGTTAACTCT 1385
Db      |||||
Qy 139 GRCCACCTCAACTCAACCAATCATGCCATTTGTGCAGACCCCTGGTCAACTCGTTAATCT 198
Db      |||||
Qy 1386 AAGATTCCTAAGGCATGCTGTGTCGCCGACAGAACTCAGTGTCTATCTCGATGCTGTACCTT 1445
Db      |||||
Qy 199 AGCATCCCTAAGGCCTGCTGTGTCGCCACCGAACTGAGCGCAATTTCCATGTTGTATCTG 258
Db      |||||
Qy 1446 GACGAGATGAAAGGTTGTTAATAAGAACTATCAGGACATGTTGTGGAGGGTGTGGG 1505
Db      |||||
Qy 259 GACGAGTACGACAGGTGGTGTGTAATAAATTTATCAGGAGATGTTGGTGGAGGGGTGGCGA 318
Db      |||||
Qy 1506 TGTGCT 1512
Db      |||||
Qy 319 TGGCGCT 325
Db      |||||

RESULT 9
US-11-051-568-16
```

Sequence 16, Application US/11051568
Publication No. US20050255141A1
GENERAL INFORMATION:
APPLICANT: OPPERMAN, HERMANN
OZKANAK, ENGIN
KUBERASAMPATH, THANGAVEL
RUEGER, DAVID C.
PANG, ROY H.L.
TITLE OF INVENTION: OSTEOGENIC DEVICES
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: TESTA, HURWITZ & THIBEAULT
STREET: 125 HIGH STREET
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: U.S.A.
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/11/051,568
FILING DATE: 04-Feb-2005
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 10/321,799
FILING DATE: 17-DEC-2002
APPLICATION NUMBER: US 09/148,925
FILING DATE: 8-SEP-1998
APPLICATION NUMBER: US 08/449,699
FILING DATE: 24-MAY-1995
APPLICATION NUMBER: US 08/147,023
FILING DATE: 1-NOV-1993
APPLICATION NUMBER: US 07/841,646
FILING DATE: 21-FEB-1992
APPLICATION NUMBER: US 07/827,052
FILING DATE: 28-JAN-1992
APPLICATION NUMBER: US 07/579,865
FILING DATE: 7-SEP-1990
APPLICATION NUMBER: US 07/621,849
FILING DATE: 4-DEC-1990
APPLICATION NUMBER: US 07/621,988
FILING DATE: 4-DEC-1990
APPLICATION NUMBER: US 07/810,560
FILING DATE: 20-DEC-1991
APPLICATION NUMBER: US 07/569,920
FILING DATE: 20-AUG-1990
APPLICATION NUMBER: US 07/600,024
FILING DATE: 18-OCT-1990
APPLICATION NUMBER: US 07/599,543
FILING DATE: 18-OCT-1990
APPLICATION NUMBER: US 07/616,374
FILING DATE: 21-NOV-1990
APPLICATION NUMBER: US 07/483,913
FILING DATE: 22-FEB-1990
APPLICATION NUMBER: US 07/179,406
FILING DATE: 08-APR-1988
APPLICATION NUMBER: US 07/232,630
FILING DATE: 15-AUG-1988
APPLICATION NUMBER: US 07/315,342
FILING DATE: 23-FEB-1989
APPLICATION NUMBER: US 07/660,162
FILING DATE: 22-FEB-1991
APPLICATION NUMBER: US 07/422,699
FILING DATE: 17-OCT-1989
APPLICATION NUMBER: US 07/422,613
FILING DATE: 17-OCT-1989
APPLICATION NUMBER: US 07/422,623
FILING DATE: 17-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: DIANA M. STEEL

REGISTRATION NUMBER: 43,153
REFERENCE/DOCKET NUMBER: STK-001CP6C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/248-7000
TELEFAX: 617/248-7100
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 525 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: YES
FEATURE:
NAME/KEY: CDS
LOCATION: 1..516
OTHER INFORMATION: /function= "OSTEOGENIC PROTEIN"
/product= "CBMP2B-1"
/note= "CBMP2B-1 - FUSION"
SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-11-051-568-16
Query Match 12.5%; Score 192.8; DB 7; Length 525;
Best Local Similarity 76.6%; Pred. No. 1.2e-45;
Matches 236; Conservative 0; Mismatches 72; Indels 0; Gaps 0;
QY 1206 AGCTGTAAGACACACCCCTTTGTAGTGGACTTCAGTGACGTGGGTGGGATGACCTGGATT 1265
DB 211 AACTGCCGGCGCCACTCGCTCTATGTGACATTCAGCATGTGGGTGGGATGACCTGGATT 270
QY 1266 GTGGCTCCCGGGGTATCACGCCCTTTTACTGCCACGGAGAATGCCCTTTTCTCTGGCT 1325
DB 271 GTGGCCCCACACAGGCTACACAGGCTTCTACTGCCATGCGGAATGCCCTTTCCCGCTAGCG 330
QY 1326 GATCATCTGAATCCACTAATCATGCCATTTGTTGACAGCTTGGTCACTCTGTTAACTCT 1385
DB 331 GATCACTTCAACAGCACCAACACCGCCGTGGTGCAGACCCCTGGTGAACCTCTGTCAACTCC 390
QY 1386 AAGATTCCTAAGGATGCTGTGCCGACAGCACTCAGTGTCTATCTCGATGCTGTACCTT 1445
DB 391 AAGATCCCTAAGGCTTGTGCGTGCCACCGAGCTGTCCGCATCAGCATGCTGTACCTG 450
QY 1446 GACGAGATGAAAGGTTGTATTAAAGAACTATCAGGACATGTTGTGGAGGGTTGTGGG 1505
DB 451 GACGAGATGAGAGGTGTGCTGAGAACTACACGAGAGATGGTAGTAGAGGGCTGCGGC 510
QY 1506 TGTCGCTA 1513
DB 511 TGCGGCTA 518
RESULT 10
US-11-136-527-6467
Sequence 6467, Application US/11136527
Publication No. US20050287570A1
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Mounts, William M
TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
FILE REFERENCE: 031896-041000 (AM101086)
CURRENT APPLICATION NUMBER: US/11/136,527
CURRENT FILING DATE: 2005-05-25
PRIOR APPLICATION NUMBER: US 60/574,294
PRIOR FILING DATE: 2005-05-26
NUMBER OF SEQ ID NOS: 362830
SOFTWARE: PatentIn version 3.2
SEQ ID NO 6467
LENGTH: 1400
TYPE: DNA
ORGANISM: Rattus norvegicus
US-11-136-527-6467
Query Match 10.3%; Score 159.6; DB 7; Length 1400;

Best Local Similarity 81.8%; Pred. No. 7.2e-36;
Matches 180; Conservative 3; Mismatches 37; Indels 0; Gaps 0;
Qy 1324 CTGATCATCTGAACCTCCACTAATCATGCAATGTTTCAGACGTTGGTCAACTCTCTTAACT 1383
Db 1 CTGATCATCTGAACCTCCACCAACCATGTCATAGTCAGACTCTGGTAAACTCTCTGAATT 60
Qy 1384 CTAGATTCCTTAAGGCATGCTGTCTCCGACAGAACTCAGTGTCTATCTCGATGCTGTACC 1443
Db 61 CCAAAATCCCTTAAGGCATGCTGTCTCCCACTAGAGCTTAGCGCAATCTCCATGTTGTACC 120
Qy 1444 TTGACGAGATGAAAAGGTTCTATTAAAGAACTATCAGGACATGTTGTGGAGGTTGTG 1503
Db 121 TAGATGAAGAAAGGTTGTCTTAAAAAACTATCAGGACATGTTGTGGAGGTTGCG 180
Qy 1504 GGTGTGCTAGTACAGCAAAATTAATACATAATATATA 1543
Db 181 GGTGTGCTAGTACAGCAAGAAACAAAWAAAAWAAAAWAA 220

RESULT 11
US-10-816-768-90
; Sequence 90, Application US/10816768
; Publication No. US20050250936A1
; GENERAL INFORMATION:
; APPLICANT: Oppermann, Hermann
; APPLICANT: Tai, Mei-Sheng
; APPLICANT: McCartney, John
; TITLE OF INVENTION: Modified TGF-beta Superfamily Proteins
; FILE REFERENCE: STK-075
; CURRENT APPLICATION NUMBER: US/10/816,768
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: PatentIn version 2.0
; SEQ ID NO 90
; LENGTH: 405
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: H2487
US-10-816-768-90

Query Match 8.0%; Score 124.4; DB 6; Length 405;
Best Local Similarity 64.8%; Pred. No. 5.6e-26;
Matches 201; Conservative 0; Mismatches 106; Indels 3; Gaps 1;
Qy 1208 CTGTAAGAGACACCCCTTTGTACGTGGACTTCAGTGACGTGGGGTGGAAATGACTGTGATTGT 1267
Db 81 CTGTAAGAGACACGAGCTGTATGTACGCTCCGAGACCTGGGCTGGCAGGACTGGATCAT 140
Qy 1268 GGCTCCCCGGGGTATCAGCCCTTTTACTGCCACGGAGAAATGCCCTTTCTCTGGGTGA 1327
Db 141 CGCGCCTTGAAGGCTACGCGCCTTACTGTGAGGGGGAGTGTGCTTCCCTCTGAATC 200
Qy 1328 TCATCTGAATCCTCACTAATCATGTCATGTTTCAGAGCTGTGTCAACTCTGTAACTC--- 1384
Db 201 CTACATGAACGCCACACACAGCCATCTGTCAGACGCTGTGTCCACTTCATCAACCCGGA 260
Qy 1385 TAAGATTCCTTAAGGCATGCTGTGTCCGACAGAACTCAGATGCTATCTCGATGCTGTACCT 1444
Db 261 AACGGTGCCCAAGCCCTGTGTGCGCCCAACGACGCTCAGCGCTATCTCCGCTCTACTT 320
Qy 1445 TGACGAGATGAAGGTTGTATTAAAGAACTATCAGGACATGTTGTGGAGGTTGTGG 1504
Db 321 CGATGACAGCTCCAAACGTCATCCTGAAAGAAATACGAAGACATGTTGTGCGAAGCTTGTGG 380
Qy 1505 GTGTGCGTAG 1514
Db 381 CTGCAGATAG 390

RESULT 12
US-10-131-826A-341

; Sequence 341, Application US/10131826A
; Publication No. US20050245730A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Deenoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary B.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C128
; CURRENT APPLICATION NUMBER: US/10/131,826A
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 341
; LENGTH: 1252
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-131-826A-341

Query Match 8.0%; Score 123.6; DB 6; Length 1252;
Best Local Similarity 60.4%; Pred. No. 1.7e-25;
Matches 204; Conservative 0; Mismatches 134; Indels 0; Gaps 0;
Qy 1199 TAAGTCAGCTGTAAAGAGACACCCCTTTGTACGTGGACTTCAGTGACGCTGGGGTGGAAATGA 1258
Db 845 TAAGAACCTCTGCCACCGCTCACCAGCTATTCACTTAACTTCGGGACCTGGGTTGGCAAA 904
Qy 1259 CTGGATTGTGCTCCCCCGGGTATCAGCGCTTTTACTGCCACGGAGAAATGCCCTTTTCC 1318
Db 905 GTGGATCATTTGCCCGGAGGGGTTTCATGGCAATTTACTGCCATGGAGAGTGTCCCTTCTC 964
Qy 1319 TCTGGCTGATCATCTGAACCTCCCAATATCATGCAATTTTCTGAGAGCTTTGTTGTTCAACTCTGT 1378
Db 965 ACTGACCATCTCTCTCAACAGCTCCCAATTTATGCTTTTTCATGCAAGCCCTGATGATGCCGT 1024
Qy 1379 TAATCTTAAGATTCTTAAGGCATGCTGTGTGCCGACAGAACTCAGTGTGTATCTCGATGCT 1438
Db 1025 TGACCCAGAGATCCCCCGAGGCTGTGTGTATATCCCAAGCTGTCTCCCATTTCCATGCT 1084

Qy 1439 GTACCTTCAGCAGATGAAAGTGTGTTATTAAGAACTATCAGGACATGCTGTGGAGGG 1498
Db 1085 CTACAGGACAAATGATGCAATGTCATCTCAGGACATTTAGACATGTTAGTCATGA 1144
Qy 1499 TTGTGGGTGCTGCTAGTAGCAGCAAAATTAATACATAA 1536
Db 1145 ATGTGGGTGTGGTAGGATGTCAGAAATGGGAATAGAA 1182

RESULT 13

US-11-091-334-1
; Sequence 1, Application US/11091334
; Publication No. US20050244867A1
; GENERAL INFORMATION:
; APPLICANT: Soppet, et al.
; TITLE OF INVENTION: Growth Factor HTER36
; FILE REFERENCE: PF230P1
; CURRENT APPLICATION NUMBER: US/11/091,334
; CURRENT FILING DATE: 2005-03-29
; PRIOR APPLICATION NUMBER: 60/557,393
; PRIOR FILING DATE: 2004-03-30
; PRIOR APPLICATION NUMBER: 10/117,178
; PRIOR FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: 09/357,905
; PRIOR FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: 08/827,336
; PRIOR FILING DATE: 1997-03-26
; PRIOR APPLICATION NUMBER: 60/014,098
; PRIOR FILING DATE: 1996-03-26
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1212
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (41)..(1132)
; OTHER INFORMATION:
US-11-091-334-1

Query Match 7.9%; Score 122; DB 9; Length 1212;
Best Local Similarity 60.1%; Pred. No. 4.8e-25;
Matches 203; Conservative 0; Mismatches 135; Indels 0; Gaps 0;
Qy 1199 TAAGTCAGCTGTAAAGACACACCCTTTGTACGTGACTTCAGTGAGCTGGGGTGAATGA 1258
Db 820 TAAGAACCTCTGCCACCGCTCACGAGCTATTCATTAACCTTCGGGACCTGGGGTTGGCAAA 879
Qy 1259 CTGGAATGTGGCTCCCGGGGTATCAGCCCTTTTACTGCCACGAGAAATGCCCTTTTCC 1318
Db 880 GTGGATCATTTGCCCCCAAGGGGTTCATGGCAATTTACTGCCATGGAGAGTGTCCCTTCTC 939
Qy 1319 TCTGGCTGATCATCTGAACTCCCACTAATCATGCCATTTGTTACAGAGTTGGTCAACTGT 1378
Db 940 ACTGACCATCTCTCAACAGGTCCCAATATGCTTTTCATGCAAGCCCTGATGCGCT 999
Qy 1379 TAACTCTAAGATCTCTAAGGCATGCTGTGTCGCCGACAGAACTCACTGCTATCTCATGCT 1438
Db 1000 TGACCCAGAGATCCCGCCCGCTGTGTGTATCCGCCCAAGCTGTCTCCCATTTCCATGCT 1059
Qy 1439 GTACCTTCAGCAGATGAAAGTGTGTTATTAAGAACTATCAGGACATGCTGTGGAGGG 1498
Db 1060 CTACAGGACAAATATGCAATGTCACTTACGACATTTATGAAGACATGGTAGTCATGA 1119
Qy 1499 TTGTGGGTGCTGCTAGTAGCAGCAAAATTAATACATAA 1536
Db 1120 ATGTGGGTGTGGTAGGATGTCAGAAATGGGAATAGAA 1157

RESULT 14

US-11-136-527-3392
; Sequence 3392, Application US/11136527

; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3392
; LENGTH: 1764
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-3392

Query Match 7.9%; Score 122; DB 7; Length 1764;
Best Local Similarity 64.1%; Pred. No. 5.8e-25;
Matches 195; Conservative 3; Mismatches 103; Indels 3; Gaps 1;
Qy 1209 TGTAAGACACACCCCTTTGTACGTGACTTCAGTGACGTGGGTGGAATGACTGATTTG 1268
Db 316 TGCAAGAGACATGAGCTTTACGTGAGCTTCAGGACCTGGGATGGCAGACWGGATCATC 375
Qy 1269 GCTCCCCGGGGTATCAGCCCTTTTACTGCCACGAGAAATGCCCTTTCTCTGCTGAT 1328
Db 376 GCWCCCAAGGCTAGCTGCCAACTATTGTGACGGAGAGTGTCTCTCTCTCAATGCA 435
Qy 1329 CATCTGAACCTCCACTAATCATGCCATTTGTTACAGAGTTGGTCAACTCTGTTAACTTAAG 1388
Db 436 CACATGATGCCACCAACCCAGCCATTGTACAGACTTTGGTCCACCTTATGAATCCCGAG 495
Qy 1389 ---ATTCTAAGGCATGCTGTGTCGCCGACAGAACTCAGTGTCTATCTGATGCTACCTT 1445
Db 496 TACGTCCCAAAACCATGCTGGCCACCAACCAACTGAATGCCATCTCGGTTCTTTACTTC 555
Qy 1446 GACGAGATGAAAGGTTGTATTAAAGAACTATCAGGACATGTTGTGGAGGTTGTGGG 1505
Db 556 GACGACAACTCCAATGTCATCTTGAANAATACAGGAACATGGTTGTGAGAGCTTGTGGA 615
Qy 1506 TGTC 1509
Db 616 TGTC 619

RESULT 15

US-11-051-568-33
; Sequence 33, Application US/11051568
; Publication No. US20050255141A1
; GENERAL INFORMATION:
; APPLICANT: OPPERMANN, HERMANN
; OZKAYNAK, ENGIN
; KUBERASAMPATH, THANGAVEL
; RUEGER, DAVID C.
; PANG, ROY H. L.
; TITLE OF INVENTION: OSTEOGENIC DEVICES
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TESTA, HURWITZ & THIBEAULT
; STREET: 125 HIGH STREET
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: U.S.A.
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/051,568

FILING DATE: 04-Feb-2005
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 10/321,799
FILING DATE: 17-DEC-2002
APPLICATION NUMBER: US 09/148,925
FILING DATE: 8-SEP-1998
APPLICATION NUMBER: US 08/449,699
FILING DATE: 24-MAY-1995
APPLICATION NUMBER: US 08/147,023
FILING DATE: 1-NOV-1993
APPLICATION NUMBER: US 07/841,646
FILING DATE: 21-FEB-1992
APPLICATION NUMBER: US 07/827,052
FILING DATE: 28-JAN-1992
APPLICATION NUMBER: US 07/579,865
FILING DATE: 7-SEP-1990
APPLICATION NUMBER: US 07/621,849
FILING DATE: 4-DEC-1990
APPLICATION NUMBER: US 07/621,988
FILING DATE: 4-DEC-1990
APPLICATION NUMBER: US 07/810,560
FILING DATE: 20-DEC-1991
APPLICATION NUMBER: US 07/569,920
FILING DATE: 20-AUG-1990
APPLICATION NUMBER: US 07/600,024
FILING DATE: 18-OCT-1990
APPLICATION NUMBER: US 07/599,543
FILING DATE: 18-OCT-1990
APPLICATION NUMBER: US 07/616,374
FILING DATE: 21-NOV-1990
APPLICATION NUMBER: US 07/483,913
FILING DATE: 22-FEB-1990
APPLICATION NUMBER: US 07/179,406
FILING DATE: 08-APR-1988
APPLICATION NUMBER: US 07/232,630
FILING DATE: 15-AUG-1988
APPLICATION NUMBER: US 07/315,342
FILING DATE: 23-FEB-1989
APPLICATION NUMBER: US 07/660,162
FILING DATE: 22-FEB-1991
APPLICATION NUMBER: US 07/422,699
FILING DATE: 17-OCT-1989
APPLICATION NUMBER: US 07/422,613
FILING DATE: 17-OCT-1989
APPLICATION NUMBER: US 07/422,623
FILING DATE: 17-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: DIANA M. STEEL
REGISTRATION NUMBER: 43,153
REFERENCE/DOCKET NUMBER: STK-001CP6C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/248-7000
TELEFAX: 617/248-7100
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 314 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: YES
ANTI-SENSE: NO
FEATURE:

Search completed: January 10, 2006, 23:47:16
Job time : 233 secs

Qy 1240 GTGACGTGGGGTGGGAATGACTGGATTGCTGCCCGGGGTATCACGCCCTTTTACTGCC 1299
Db 32 GCGACGTGGGGTGGGACGACTGGATCATCGCCCCGTCGACTTCGACGCCCTACTACTGCT 91
Qy 1300 ACGGAGAATGCCCTTTTCTCTGGCTGATCATCTGAACTCCCACTAATCATGCCATTGTTTC 1359
Db 92 CCGGAGCTGCCAGTTCCCTCTCGGATCACTTCAACAGGACCAACACGCCCGTGGTGC 151
Qy 1360 AGACGTTGGTCAACTCTGTTAACTC---TAAGATTCTTAAGGCAATGCTGTCCGACAG 1416
Db 152 AGACCTGGTGAACAAACATGAACCCCGCAAGGTACCCAGCCCTGCTGCGTGCACCG 211
Qy 1417 AACTCAGTGTATCTCGATGCTGTACCTTGACGGAATGAAAAGTTGTATTAAAGAACT 1476
Db 212 AGCTGTCCGCCATCAGCATGCTGTACCTGGACGGAATTCACCGTGGTGTGAAGAACT 271
Qy 1477 ATCAGGACATGTTGTGGAGGTTGTGGGTGTCGCTA 1513
Db 272 ACCAGGAGATGACCGTGGTGGGCTGCGGCTGCCGCTA 308

NAME/KEY: misc feature
LOCATION: 1..314
OTHER INFORMATION: /note= "CONSENSUS PROBE"
SEQUENCE DESCRIPTION: SEQ ID NO: 33:

Query Match 7.7%; Score 119; DB 7; Length 314;
Best Local Similarity 66.8%; Pred. No. 1.8e-24;
Matches 185; Conservative 0; Mismatches 89; Indels 3; Gaps 1;

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 10, 2006, 19:43:19 ; Search time 4466 Seconds
(without alignments)

16206.811 Million cell updates/sec

Title: US-10-801-648-1

Perfect score: 1547

Sequence: 1 ggggactcttggaacttgca.....atacataaatatatata 1547

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_est4:*
5: gb_est5:*
6: gb_est6:*
7: gb_est7:*
8: gb_est8:*
9: gb_est9:*
10: gb_est10:*
11: gb_est11:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|----------------------|
| 1 | 1547 | 100.0 | 2394 | 4 | CR618407 full-length |
| 2 | 981.4 | 63.4 | 983 | 10 | AY418812 Homo sapi |
| 3 | 825.8 | 53.4 | 903 | 5 | BX431362 BX431362 |
| 4 | 816.6 | 52.8 | 890 | 5 | BX424086 BX424086 |
| 5 | 763.8 | 49.4 | 977 | 10 | AY418814 Mus muscu |
| 6 | 699.2 | 45.2 | 724 | 8 | CV804617 AGENCOURT |
| 7 | 695 | 44.9 | 711 | 10 | AY418813 Pan trogl |
| 8 | 683.8 | 44.2 | 727 | 5 | BU625617 UI-H-FGI- |
| 9 | 683 | 44.1 | 711 | 7 | CN396138 170004241 |
| 10 | 673.8 | 43.6 | 769 | 8 | CX755622 AGENCOURT |
| 11 | 664.4 | 42.9 | 841 | 8 | DN117475 1117145 M |
| 12 | 644.8 | 41.7 | 830 | 8 | DN117122 1116761 M |
| 13 | 623.6 | 40.3 | 1001 | 5 | BX432994 BX432994 |
| 14 | 619.6 | 40.1 | 666 | 1 | AW339267 xz89f02.x |
| 15 | 607 | 39.2 | 648 | 3 | BM683313 UI-E-EJ1- |
| 16 | 606.4 | 39.2 | 649 | 3 | BQ184625 UI-E-EJ1- |
| 17 | 605.2 | 39.1 | 674 | 3 | BM674840 UI-E-EJ0- |
| 18 | 597 | 38.6 | 642 | 3 | BM929343 UI-E-EJ1- |
| 19 | 585 | 37.8 | 649 | 3 | BQ186599 UI-E-EJ1- |
| 20 | 579.4 | 37.5 | 581 | 3 | BP276858 BP276858 |
| 21 | 558.4 | 36.1 | 715 | 7 | CK940908 4064444 B |
| 22 | 552 | 35.7 | 881 | 5 | BU444424 603213309 |

| | | | | | | | | |
|---|----|-------|------|-----|---|----------|----------|-----------|
| c | 23 | 533 | 34.5 | 548 | 1 | AA488371 | AA488371 | ab39c02.s |
| | 24 | 526 | 34.0 | 526 | 6 | CB132019 | CB132019 | K-EST0182 |
| | 25 | 525.8 | 34.0 | 529 | 3 | BM717570 | BM717570 | UI-E-EJ0- |
| | 26 | 522 | 33.7 | 544 | 1 | AA488503 | AA488503 | ab39c02.r |
| | 27 | 497.2 | 32.1 | 511 | 1 | AI492136 | AI492136 | tg12e01.x |
| | 28 | 497.2 | 32.1 | 632 | 8 | CX593098 | CX593098 | CT020004A |
| | 29 | 497 | 32.1 | 529 | 2 | BF416123 | BF416123 | UI-R-CA0- |
| | 30 | 493.6 | 31.9 | 746 | 7 | CV736172 | CV736172 | 1061.e7.5 |
| | 31 | 484.4 | 31.3 | 521 | 1 | AA190917 | AA190917 | zv23h03.r |
| | 32 | 482.2 | 31.2 | 536 | 1 | AA436230 | AA436230 | zv23h06.r |
| | 33 | 480.4 | 31.1 | 497 | 1 | AA883895 | AA883895 | am26h03.s |
| | 34 | 469.2 | 30.3 | 580 | 2 | BG149658 | BG149658 | nad31h05. |
| | 35 | 469 | 30.3 | 483 | 1 | AI084926 | AI084926 | qf17h06.x |
| | 36 | 467 | 30.2 | 515 | 1 | AA436231 | AA436231 | zv23h06.s |
| | 37 | 465.6 | 30.1 | 628 | 6 | CB422223 | CB422223 | 595306.MA |
| | 38 | 465.6 | 30.1 | 628 | 6 | CB445202 | CB445202 | 696453.MA |
| | 39 | 456.8 | 29.5 | 474 | 1 | AW135750 | AW135750 | UI-H-B11- |
| | 40 | 456.6 | 29.5 | 614 | 9 | AZ655571 | AZ655571 | 1M0530C11 |
| | 41 | 451.2 | 29.2 | 656 | 3 | BI400982 | BI400982 | MI-P-AY1- |
| | 42 | 448 | 29.0 | 831 | 7 | CK792068 | CK792068 | AGENCOURT |
| | 43 | 446.6 | 28.9 | 564 | 6 | CB417831 | CB417831 | 590567.MA |
| | 44 | 440 | 28.4 | 441 | 1 | AA181547 | AA181547 | zp51a05.s |
| | 45 | 439 | 28.4 | 469 | 2 | BF409439 | BF409439 | UI-R-CA1- |

ALIGNMENTS

RESULT 1
CR618407
LOCUS
DEFINITION
full-length cDNA clone CS0DE003YB10 of Placenta of Homo sapiens (human).
ACCESSION
CR618407
VERSION
CR618407.1 GI:50499214
KEYWORDS
HTC; CNSLT_CDNA.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 2394)
AUTHORS
Li,W.B., Gruber,C., Jesse,J. and Polayes,D.
TITLE
Full-length cDNA libraries and normalization
JOURNAL
Unpublished
REMARK
Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Faraday Avenue
REFERENCE
2 (bases 1 to 2394)
AUTHORS
Genoscope.
TITLE
Direct Submission
JOURNAL
Submitted (20-JUL-2004) Genoscope - Centre National de Sequençage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqrefgenoscope.cns.fr)
COMMENT
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
FEATURES
Location/Qualifiers
source
1..2394
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DE003YB10"
/tissue_type="Placenta"
/plasmid="pCMVSPORT_6"

ORIGIN
Query Match 100.0%; Score 1547; DB 4; Length 2394;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1547; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy 1 GGGGACTTCTTGAATCTTCAGGAGATAAATTGCGCACCCACACTTTTGGCGCGGTCCTT 60
Db |
Qy 37 GGGGACTTCTTGAATCTTCAGGAGATAAATTGCGCACCCACACTTTTGGCGCGGTCCTT 96
Db |
Qy 61 TGCCCCAGCGGAGCCTGCTTCCGCACTCTCCGAGCCCAACCGCCCTCCACCTCTCGGCT 120
Db |
Qy 97 TGCCCCAGCGGAGCCTGCTTCCGCACTCTCCGAGCCCAACCGCCCTCCACCTCTCGGCT 156
Qy 121 TGCCCCAGCACTGAGACGCTGTTCCAGCGTGAAGAGAGAGACTGCGCGGCGGCAACCGG 180
Db |
Qy 157 TGCCCCAGCACTGAGACGCTGTTCCAGCGTGAAGAGAGAGACTGCGCGGCGGCAACCGG 216
Qy 181 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
Db |
Qy 217 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 276
Qy 241 AGAGTTTTTCCATGTGAGCGCTCTTTCAATGGAAGCTGTCCTCCGCGGCTCTTCTAGACGGA 300
Db |
Qy 277 AGAGTTTTTCCATGTGAGCGCTCTTTCAATGGAAGCTGTCCTCCGCGGCTCTTCTAGACGGA 336
Qy 301 CTGCGGCTCTCTAAAGGTGCAACATGCTGAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
Db |
Qy 337 CTGCGGCTCTCTAAAGGTGCAACATGCTGAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAG 396
Qy 361 TTCCCCAGGTCCTCTGCGGCGCGGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
Db |
Qy 397 TTCCCCAGGTCCTCTGCGGCGCGGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 456
Qy 421 TCGGCGGCGGCTGCTGCGGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
Db |
Qy 457 TCGGCGGCGGCTGCTGCGGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 516
Qy 481 TCAGAGTTCGGGCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
Db |
Qy 517 TCAGAGTTCGGGCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 576
Qy 541 CCGTGTGTCGCCCTTACATGCTAGACCTGATCCGAGGCTATCCGAGGCTATCCGAGGCTATCC 600
Db |
Qy 577 CCGTGTGTCGCCCTTACATGCTAGACCTGATCCGAGGCTATCCGAGGCTATCCGAGGCTATCC 636
Qy 601 CCGGCCAGACACCGGTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
Db |
Qy 637 CCGGCCAGACACCGGTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 696
Qy 661 ACCATGAAGAACTCTTTGGAAGAACTTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
Db |
Qy 697 ACCATGAAGAACTCTTTGGAAGAACTTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 756
Qy 721 TCTTTAATTTAAGTTCTATCCCGAGGAGGTTTATCAGGCTGAGAGAGAGAGAGAGAGAGAG 780
Db |
Qy 757 TCTTTAATTTAAGTTCTATCCCGAGGAGGTTTATCAGGCTGAGAGAGAGAGAGAGAGAGAG 816
Qy 781 TCCGAGAACAGATGCAAGATGCTTTAGGAACAATAGCAGTTTCCATCAGGAGATTAATA 840
Db |
Qy 817 TCCGAGAACAGATGCAAGATGCTTTAGGAACAATAGCAGTTTCCATCAGGAGATTAATA 876
Qy 841 TTTATGAATCATTAACCTGCAACAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
Db |
Qy 877 TTTATGAATCATTAACCTGCAACAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 936
Qy 901 ACACGAGTTCGTAATCAGAGATGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960
Db |
Qy 937 ACACGAGTTCGTAATCAGAGATGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 996
Qy 961 TGATGCGGTGAGCTGCAACAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
Db |
Qy 997 TGATGCGGTGAGCTGCAACAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1056
Qy 1021 TGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080
Db |
Qy 1057 TGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1116
Qy 1081 ATGAACACAGCTGGTTCACAGATAAGGCCATTTGCTAGTAACCTTTTGGCCATGATGGAAGAG 1140
```

```
Db |
Qy 1117 ATGAACACAGCTGGTTCACAGATAAGGCCATTTGCTAGTAACCTTTTGGCCATGATGGAAGAG 1176
Qy 1141 GGCAATCTCTCCACAAAGAGAGAAAACGTCAGGCAAAACAAACAGCGGAAAACGCTTTA 1200
Db |
Qy 1177 GGCAATCTCTCCACAAAGAGAGAAAACGTCAGGCAAAACAAACAGCGGAAAACGCTTTA 1236
Qy 1201 AGTCAGCTGTAAAGAGACACCCCTTTGTAGTGGACTTCAGTGAGCTGGGGTGGATGACT 1260
Db |
Qy 1237 AGTCAGCTGTAAAGAGACACCCCTTTGTAGTGGACTTCAGTGAGCTGGGGTGGATGACT 1296
Qy 1261 GGATTGTGGCTCCCGCGGGTATCACGCTTTTACTGCGCAGGAGAAATGCCCTTTTCTC 1320
Db |
Qy 1297 GGATTGTGGCTCCCGCGGGTATCACGCTTTTACTGCGCAGGAGAAATGCCCTTTTCTC 1356
Qy 1321 TGGCTGATCATCTGAACCTCCCAATCATGCTGTCATTTGTCAGACGTTGGTCAACTCTGTTA 1380
Db |
Qy 1357 TGGCTGATCATCTGAACCTCCCAATCATGCTGTCATTTGTCAGACGTTGGTCAACTCTGTTA 1416
Qy 1381 ACTCTAAGATCTCTAAGGCAATGCTGTGTCGCGACAGAACTCAGTGCTATCTCGATGCTGT 1440
Db |
Qy 1417 ACTCTAAGATCTCTAAGGCAATGCTGTGTCGCGACAGAACTCAGTGCTATCTCGATGCTGT 1476
Qy 1441 ACCTTGACGAGAAATGAAGAAGTGTGTTAAAGAACTATCAGGACATGCTGTGCGAGGTT 1500
Db |
Qy 1477 ACCTTGACGAGAAATGAAGAAGTGTGTTAAAGAACTATCAGGACATGCTGTGCGAGGTT 1536
Qy 1501 GTGGGTGCTGCTAGTACAGCAAAATTAATAACATAATATATATATA 1547
Db |
Qy 1537 GTGGGTGCTGCTAGTACAGCAAAATTAATAACATAATATATATA 1583

RESULT 2
AY418812 983 bp DNA linear GSS 17-DEC-2003
LOCUS Homo sapiens BMP2 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION AY418812
VERSION AY418812.1 GI:39774772
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 983)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarimal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,P., Murphy,B.,
Ferrera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 983)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarimal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,P., Murphy,B.,
Ferrera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT These sequences were made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
source Location/Qualifiers
1..983
/mol_type="genomic DNA"
/db_xref="taxon:9606"
<1..>983
/gene="BMP2"
/locus_tag="HCM6682"
gene
ORIGIN
```



```

Db      306 TGGACACCAGGTTGGTGAATCAGAAATGCAAGCAGGTGGGAAGTTTGTATGTACACCCCG 365
Qy      958 CTGTGATGCGGTGAGCTGTCACAGGACACGGCAACCATAGATGATTCGTGTGTAAGTGGCCC 1017
Db      366 CTGTGATGCGGTGAGCTGTCACAGGACACGGCAACCATAGATTCGTGTGTAAGTGGCCC 425
Qy      1018 ACTTGGAGGAAACAAAGGTCTCTCCAGAGACATGTTAGGATAAGCAGGTCTTTGACCC 1077
Db      426 ACTTGGAGGAAACAAAGGTCTCTCCAGAGACATGTTAGGATAAGCAGGTCTTTGACCC 485
Qy      1078 AAGATGAACACAGCTGGTGCACAGATAAGGCCATTTAGTAACTTTTGGCCATGATGGAA 1137
Db      486 AAGATGAACACAGCTGGTGCACAGATAAGGCCATTTAGTAACTTTTGGCCATGATGGAA 545
Qy      1138 AAGGCGATCTCTCCACAAAGAGAAAAAGCTCAAGCCAAACACAAACAGCGGAAACGCC 1197
Db      546 AAGGCGATCTCTCCACAAAGAGAAAAAGCTCAAGCCAAACACAAACAGCGGAAACGCC 605
Qy      1198 TTAAGTCCAGCTGTAAAGAGACACCTTTGTACGTGGACTTCAGTGACGTGGGGTGGAAATG 1257
Db      606 TTAAGTCCAGCTGTAAAGAGACACCTTTGTACGTGGACTTCAGTGACGTGGGGTGGAAATG 665
Qy      1258 ACTGATGTGTGGCTCCCGGGGTATCAAGGCTTTTACTGCAAGGAAATGCCCTTTTC 1317
Db      666 ACTGATGTGTGGCTCCCGGGGTATCAAGGCTTTTACTGCAAGGAAATGCCCTTTTC 725
Qy      1318 CTCTGGCTGATCATCTGAACCTCCACTAATCATGCCATTTGTCAGACGTTGTGTCACCTCTG 1377
Db      726 CTCTGGCTGATCATCTGAACCTCCACTAATCATGCCATTTGTCAGACGTTGTGTCACCTCTG 785
Qy      1378 TTAAGTCTTAAGATCTTAAGGCATGCTGTGTCAGACGAACTCAGTGCTATCTCGATGC 1437
Db      786 TTAAGTCTTAAGATCTTAAGGCATGCTGTGTCAGACGAACTCAGTGCTATCTCGATGC 845
Qy      1438 TGTACCTTGACGAGAAATGAAAGGTTGTATTAAGAACT 1476
Db      846 TGTACCTTGACGAGATG-AAAGGTTGTATTAAGAACT 883

```

```

RESULT 4
BX424086
LOCUS   BX424086 Homo sapiens PLACENTA Homo sapiens cDNA clone CS0DE003YB10
DEFINITION 5-PRIME, mRNA sequence.
ACCESSION BX424086
VERSION   BX424086.2  Gi:46951674
KEYWORDS EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens

```

```

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

```

```

REFERENCE
AUTHORS  Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE    Full-length cDNA libraries and normalization
JOURNAL  Unpublished (2001)
COMMENT  On May 13, 2003 this sequence version replaced gi:30659639.
Contact: Genoscope

```

```

Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.

```

```

This sequence belongs to sequence cluster 10041.f
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?c=CS1DE001ZF080QPI&c=10041.f.

```

```

FEATURES
source
1. .890
/mol_type="rRNA"

```

```

/db_xref="taxon:9606"
/clone="CS0DE003YB10"
/tissue_type="PLACENTA"
/clone_lib="Homo sapiens PLACENTA"
/notes="Vector: pCMVSPORT 6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."

```

ORIGIN

```

Query Match      52.8%; Score 816.6; DB 5; Length 890;
Best Local Similarity 97.3%; Pred. No. 4.3e-218;
Matches 832; Conservative 16; Mismatches 2; Gaps 2;

Qy      1 GGGGACTTCTTTGAACTTTCAGGGGAGAAATACTTGGCGACCCCACTTTTGGCGGGTGCCTT 60
Db      37 GGGGACTTCTTTGAACTTTCAGGGGAGAAATACTTGGCGCRCCCACTTTTGGCGGGTGCCTT 96
Qy      61 TGGCCGACGGGAGGCTCTTTCGCCATCTCCGAGCCCCCAGCCGCCCTCCACTCTCTGGGCT 120
Db      97 TGGCCGACGGGAGG-SCCTCTTGGCCATCTCCGAGCCCCCAGCCGCCCTCCACTCTCTGGGCT 155
Qy      121 TGGCCGACACTGAGACGCTGTTCCAGCTGAAAGAGAGACTGCGCGGCGCGCACCCGG 180
Db      156 TGGCCGACACTGAGACGCTGTTCCAGCGTGAAGAGAGACTGCGCGGCGCGCACCCGG 215
Qy      181 GAGAAGAGGAGGCAAAAGAAAGGAAACGGAATTCGTCGTCCTTGGCCAGGTCCTTTGACC 240
Db      216 GAGAAGAGGAGGCAAAAGAAAGGAAACGGAATTCGTCGTCCTTGGCCAGGTCCTTTGACC 275
Qy      241 AGAGTTTTCATGTGACGCTCTTTCAATGGACGTCGTCGCCGCGTCTTCTTAGACGGA 300
Db      276 AGAGTTTTCATGTGACGCTCTTTCAATGGACGTCGTCGCCGCGTCTTCTTAGACGGA 335
Qy      301 CTGCGGTCTCTAAAGGTCGACCATGTGGCGCGGACCCGCTGCTTCTAGCGTTGCTGC 360
Db      336 CTGCGGTCTCTAAAGGTCGACCATGTGGCGCGGACCCGCTGCTTCTAGCGTTGCTGC 395
Qy      361 TTCCCGAGGTCTCTCTCGGCGGCGGCTGCGCTCTGTTTCGCGAGCTGCGGCGCAGGAAGT 420
Db      396 TTCCCGAGGTCTCTCTCGGCGGCGGCTGCGCTCTGTTTCGCGAGCTGCGGCGCAGGAAGT 455
Qy      421 TCGCGGCGGCGTCTGTCGCGCGGCGGCTCATCCAGCCCTCTGACGAGGTCCTGACGCGAGT 480
Db      456 TCGCGGCGGCGTCTGTCGCGCGGCGGCTCATCCAGCCCTCTGACGAGGTCCTGACGCGAGT 515
Qy      481 TCGAGTTTGGGCTCTCTCAGCATGTTTCGCGCTTGAAGACAGAGACCCACCCAGCAGGAGACG 540
Db      516 TCGAGTTTGGGCTCTCTCAGCATGTTTCGCGCTTGAAGACAGAGACCCACCCAGCAGGAGACG 575
Qy      541 CCCTGTTGCCCTTACATGCTAGACCTGTATCCGAGCACTCAGGTCAGCGGGCTCAC 600
Db      576 CCCTGTTGCCCTTACATGCTAGACCTGTATCCGAGCACTCAGGTCAGCGGGCTCAC 635
Qy      601 CCGCCCCAGACCCGCTTGGAGAGGCGCAGCCAGCCGCAACACTGTGCGGAGCTTCC 660
Db      636 CCGCCCCAGACCCGCTTGGAGAGGCGCAGCCAGCCGCAACACTGTGCGGAGCTTCC 695
Qy      661 ACCATGAAGAAATCTTT--GGAAGAACTACTCAAGAAACGAGTGGGAAAAAACAACCCGAGATTC 719
Db      696 ACCATGAAGAAATCTTTTGGGAGAACTACTCAAGAAACGAGTGGGAAAAAACAACCCGAGATTC 755
Qy      720 TTCTTTAATTAAGTCTTATCCCCAGGAGAGTTTATACCTCAGCAGAGCTTCAGGTT 779
Db      756 TTCTTTAATTAAGTCTTATCCCCAGGAGAGTTTATACCTCAGCAGAGCTTCAGGTT 815
Qy      780 TTCCGAGACAGATGCAAGATGCTTTTAGGAAACAAATAGCAGTTTCCATCAGCGAATTAAT 839
Db      816 TTCCGAGACAGATGCAAGAGGCTTTTAGGARAACAATAGCAGTKTCCMTCACCSAAATTAAT 875
Qy      840 ATTTATGAATTCATA 854

```

```

Db      876 ATTTATGAATCATATA 890

RESULT 5
LOCUS   AY418814
DEFINITION Mus musculus BMP2 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.
ACCESSION AY418814
VERSION   AY418814.1 GI:39774774
KEYWORDS GSS.
SOURCE   Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferreria,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE    Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios
JOURNAL  Science 302 (5652), 1960-1963 (2003)
PUBMED   14671302
REFERENCE
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferreria,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE    Direct Submission
JOURNAL  Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
COMMENT  These sequences were made by sequencing genomic exons and ordering them based on alignment.
FEATURES
source   1..977
          /organism="Mus musculus"
          /mol_type="genomic DNA"
          /db_xref="taxon:10090"
          <1..>977
          /gene="BMP2"
          /locus_tag="HCM6682"

ORIGIN

Query Match      49.4%; Score 763.8; DB 10; Length 977;
Best Local Similarity 87.5%; Pred.No. 3.3e-203;
Matches 860; Conservative 0; Mismatches 117; Indels 6; Gaps 2;

Qy      331 CCGGACCCGCTGCTCTTAGCGTGGCTTCCCGCAGTCTCTCTGGCGCGCGCGCTG 390
Db      1 CCGGACCCGCTGCTCTTAGCGTGGCTTCCCGCAGTCTCTCTGGCGCGCGCGCG 60

Qy      391 GCCTCGTTCCGAGTCGCGCGCAGAGAGTTGCGCGCGCGCTGCTGCGCGCGCGCTCAT 450
Db      61 GCCTCATTTCCAGAGTCGCGCGCAGAGAGTTGCGCGCGCGCTGCTGCGCGCGCGCT 117

Qy      451 CCCAGCCTCTGACGAGTCTCTGACGAGTTCGAGTTCGCGTCTGACGATGTCGCGCC 510
Db      118 CCCGCGCTTCGGAAGACGCTCTCAGCGAATTTGAGTTGAGGTCGTCAGCATGTTTGCC 177

Qy      511 TGAAACAGAGACCCACCCCGCAGCGAGCGCGTGCCTCCCTACATGCTAGACCTGT 570
Db      178 TGAAACAGAGACCCACCCCGCAGCGAGCGCGTGCCTCCCTATATGCTAGATCTGT 237

Qy      571 ATFCGAGGCACTCAGTTCAGCGCGGCTCACCAGCGCGCGCGCGCGCGCGCGCGAG 630
Db      238 ACCGCGAGGCACTCAGCGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 297

Qy      631 CCAGCGGAGCGCAACTGTCGCGAGCTTCACCATGAAGATCTTTGGAAGAACTACAG 690
Db      298 CCAGCGCGCGCAACTGTCGCGAGCTTCCTCATCAGGAAGAGCGCGTGGAGGAATCTCCAG 357

```

```

Qy      691 AAACGAGTGGGAAACCAACCCGAGATCTCTTTAAATTTAAGTTCTATCCCAACGAGG 750
Db      358 AGATGAGTGGGAAAGAGCGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 417

Qy      751 AGTTTATCAGCTCAGCAGAGCTTCAGGTTTTCGAGAAACAGATGCAAGATGCTTTAGAA 810
Db      418 AGTTTCTCAGATCTGCGAAGTCCAGATCTTTCCGAGAAACAGATGCAAGATGCTTTAGAA 477

Qy      811 ACAATAGCAGTTTCCATCAGCGAATTAATATTTATGAATCATATAAATCTGCAACAGCCA 870
Db      478 AC---AGTAGTTTCAGCAGCAGCAATTAATATTTATGAATTAATAAGCTGCGAGCGCA 534

Qy      871 ACTCAAAATCCCGTGACAGACTTTTGGACACAGAGTTGGTGAATCAGAAATGCAAGCA 930
Db      535 ACTTGAATTTCTGTGACCAAGACTATTGGACACCCAGGTTAGTGAATCAGAAACACAAGTC 594

Qy      931 GGTGGAAAGTTTGTATGTCAACCCCGCTGTGATGCGGTGGACTGCACAGGACAGCGCA 990
Db      595 AGTGGAGAGCTTCGACGCTCAACCCCGCTGTGATGCGGTGGACCAACAGGAGACACCA 654

Qy      991 ACCATGGAATTCGTGTGAAGTGGCCCACTTTGGAGGAGAAACAGGTGTCTCTCAAGAGAC 1050
Db      655 ACCATGGGTTTGTGTGAAGTGGCCCACTTTAGAGGAGAACCCAGGTGTCTCTCAAGAGAC 714

Qy      1051 ATGTTAGGATAAGCAGAGTCTTTTGACCAAGATGAACACAGCTGGTTCACAGATAAGGCCAT 1110
Db      715 ATGTGAGGATTAGCAGAGTCTTTTGACCAAGATGAACACAGCTGGTTCACAGATAAGGCCAT 774

Qy      1111 TGCTAGTAACCTTTGGCCATGATGAAAGGGCATCTCTTCCACAAAAGAGAAACAGTC 1170
Db      775 TGCTAGTGACTTTTGGACATGATGAAAGGACATCCGCTCCACAAACGAGAAACAGTC 834

Qy      1171 AAGCCAAACACAAACAGCGGAAACCCCTTAAGTCCAGCTGTAAAGAGACACCCCTTTGTAGC 1230
Db      835 AAGCCAAACACAAACAGCGGAGCGCTCAAGTCCAGCTGCAGAGACACCCCTTTGTATG 894

Qy      1231 TGGACTTCAGTGACGTGGGGTGGAAATGACTGGATTTGGCTCCCCCGGGGTATCACGCT 1290
Db      895 TGGACTTCAGTGATGTGGGGTGGAAATGACTGGATTTGGCTCCCCCGGGGTATCATGCT 954

Qy      1291 TTTACTGCCACGAGAAATGCCCT 1313
Db      955 TTTACTGCCATGGGGAGTGTCT 977

RESULT 6
CV804617 724 bp mRNA linear EST 15-NOV-2004
AGENCY 36361580 NIH MGC 280 Homo sapiens cDNA clone
IMAGE:7503800 5', mRNA sequence.
ACCESSION CV804617
VERSION CV804617.1 GI:55747583
KEYWORDS EST.
ORGANISM Homo sapiens (human)
SOURCE Homo sapiens
REFERENCE 1 (bases 1 to 724)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-remail.nih.gov
Tissue Procurement: Meri Firpo
cDNA Library Preparation: Express Genomics
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

```

```

http://image.llnl.gov
Plate: L1AM15873 row: h column: 06
High quality sequence stop: 598.
Location/Qualifiers
1. 724
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clones="IMAGE:7503800"
/tissue_type="pluripotent cell line derived from
blastocyst inner cell mass"
/lab_host="DH10B"
/clone_lib="NIH MGC 280"
/note="Organ: Blastocyst; Vector: pExpress-1; Site_1:
EcorV; Site_2: NotI; RNA obtained from pluripotent cell
line derived from blastocyst inner cell mass (cell line
HSP-6, NIH Registry designation UC06. Positive for OCT4
expression by rtPCR, positive for SSEA-3, SSEA-4,
Tra-1-81, Tra-1-60 by immunofluorescence. Negative for
SSEA-1 by immunofluorescence Passage 62. cDNA was primed
using oligo-dt primer:
5'-PGACTGTTAGATCGGAGCGCGGCC(T)25-3' and cloned into
the EcorV/NotI sites of pExpress-1. Size-selection >1.25
kb resulted in an average insert size of 1.8 kb. This
primary library is non-normalized (normalized primary
library is NIH_MGC 281) and was constructed by Express
Genomics (Frederick, MD). Note: this is a Mammalian Gene
Collection library."

ORIGIN
Query Match 45.2%; Score 699.2; DB 8; Length 724;
Best Local Similarity 98.8%; Pred. No. 4.7e-105;
Matches 715; Conservative 0; Mismatches 8; Indels 1; Gaps 1;

Qy 576 AGGCACTCAGGTGACCGGGCTCACCCGCCAGACACCGGTTGGAGGCGCAGCCAGC 635
Db 1 AGGCACTCGGTGACCGGGCTCACCCGCCAGACACCGGTTGGAGGCGCAGCCAGC 60

Qy 636 CGAGCCAACTGTGGCGAGCTTCACCATGAAGAATCTTTGGAAGAACTACCGAAGACG 695
Db 61 CGAGCCAACTGTGGCGAGCTTCACCATGAAGAATCTTTGGAAGAACTACCGAAGACG 120

Qy 696 AGTGGGAAAACACCGGAGATCTCTTTAAATTTAGTTCTATCCCGAGGAGGTTT 755
Db 121 AGTGGGAAAACACCGGAGATCTCTTTAAATTTAGTTCTATCCCGAGGAGGTTT 180

Qy 756 ATCACTCAGCAGAGCTTCAGGTTTCCGAGAACAGATGCAAGATGCTTTAGGAAAACAT 815
Db 181 ATCACTCAGCAGAGCTTCAGGTTTCCGAGAACAGATGCAAGATGCTTTAGGAAAACAT 240

Qy 816 AGCAGTTTCCATCACCAGATTAATTTATGAATATATAAACTGCAACAGCCAACTCG 875
Db 241 AGCAGTTTCCATCACCAGATTAATTTATGAATATATAAACTGCAACAGCCAACTCG 300

Qy 876 AAATTCCTCCGTCACAGACTTTTCGACACAGGTTGGTGAATCAGATGCAAGCAGGTGG 935
Db 301 AAATTCCTCCGTCACAGACTTTTGGACACAGGTTGGTGAATCAGATGCAAGCAGGTGG 360

Qy 936 GAAAGTTTGTGATGTCAACCCCGCTGTGATCGGTGGACTGCAACAGGGACAGCCAACTAT 995
Db 361 GAAAGTTTGTGATGTCAACCCCGCTGTGATCGGTGGACTGCAACAGGGACAGCCAACTAT 420

Qy 996 GGATTCGTGGTGGAGTGCCCATCTTGGAGGAGAAAACAAAGTGTCTCCAGAGACATGTT 1055
Db 421 GGATTCGTGGTGGAGTGCCCATCTTGGAGGAGAAAACAAAGTGTCTCCAGAGACATGTT 480

Qy 1056 AGGATAGCAGCTCTTTGCACCAAGATGAACACAGCTGGTCCACAGATTAAGCCATTGCTA 1115
Db 481 AGGATAGCAGCTCTTTGCACCAAGATGAACACAGCTGGTCCACAGATTAAGCCATTGCTA 540

Qy 1116 GTAACTTTTGGCCCATGATGGAAGGGGATCTCTTCCCAAAAGAGAAAACGTCAGGCC 1175
Db 541 GTAACTTTTGGCCCATGATGGAAGGGGATCTCTTCCCAAAAGAGAAAACGTCAGGCC 600

```

```

Qy 1176 AAACACAAACACGCGAAACGCTTAAGTCCAGCTGTAAAGAGACACCCCTTTGTACGTGAC 1235
Db 601 AAACACAAACACGCGAAACGCTTTAAGTCCAGCTGTAAAGAGACACCCCTTTGTACGTGAC 660

Qy 1236 TTCACTGACGCTGGGTGGAAATGACTGGATTGTGCTCCCCCGGGTATCACGCCCTTTTAC 1295
Db 661 TTCACTGACGCTGGGTGGAAATGACGGATTGTGCTCCCCCGGGG-ATCAGCCCTTTTAC 719

Qy 1296 TGCC 1299
Db 720 TGCC 723

RESULT 7
AY418813 711 bp DNA linear GSS 17-DEC-2003
LOCUS Pan troglodytes BMP2 gene, VIRTUAL TRANSCRIPT, partial sequence,
DEFINITION genomic survey sequence.
ACCESSION AY418813
VERSION AY418813.1 GI:39774773
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Pan.
REFERENCE 1 (bases 1 to 711)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarimal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 711)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarimal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT These sequences were made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
source
1..711
Location/Qualifiers
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
<1..>711
/gene="BMP2"
/locus_tag="HCM6682"

gene

ORIGIN
Query Match 44.9%; Score 695; DB 10; Length 711;
Best Local Similarity 98.2%; Pred. No. 7.1e-184;
Matches 698; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Qy 670 AATCTTTGGAGAACTACCGAAGAGTTTATCACTCAGCAGAGCTTCAGGTTTTCGAGAAC 729
Db 1 AATCTTTGGAGAACTACCGAAGAGTTTATCACTCAGCAGAGCTTCAGGTTTTCGAGAAC 60

Qy 730 TAAGTTCTATCCCCCAGGAGGTTTATCACTCAGCAGAGCTTCAGGTTTTCGAGAAC 789
Db 61 TAAGTTCTATCCCCCAGGAGGTTTATCACTCAGCAGAGCTTCAGGTTTTCGAGAAC 120

Qy 790 AGATGCAAGATGCTTTTAGGAAAACAAATAGCAGTTTCCATCACCGAATTAATATTATGAAA 849
Db 121 AGATGCGAGATGCTTTTAGGAAAACAAATAGCAGTTTCCATCACCGAATTAATATTATGAAA 180

Qy 850 TCATAAAACCTGCAACAGCCCAACTCGAAATTTCCCGGTGACCAGACTTTTGACACACAGGT 909

```



```

|||||
181 TCATAAAACCTGCAACAGCACTCGAAATCCCGTGACCAAGCTTTGGACACAGGT 240
|||
910 TGGTGAATCAGATCGAAGCAGGTGGGAAGTTTGTATGTACCCCGCTGTGATCGCGT 969
|||
241 TGGTGAATCAGATCGAAGCAGGTGGGAAGTTTGTATGTACCCCGCTGTGATCGCGT 300
|||
970 GCACTGACAGGACACGACCAACCACTGGATTCTGTGTGAAGTGGCCCACTTGGAGGAGA 1029
|||
301 GCACTGACAGGACACGACCAACCACTGGATTCTGTGTGAAGTGGCCCACTTGGAGGAGA 360
|||
1030 AACAGGTCTCTCAAGAGACATGTTAGGATAAGCAGGTCTTTGGACCAAGATGAACACA 1089
|||
361 AACAGGTCTCTCAAGAGACATGTTAGGATAAGCAGGTCTTTGGACCAAGATGAACACA 420
|||
1090 GCTGGTACAGATAGGCCATTTGTAGTAACTTTTGGCCATGATGGAAAGGCGATCTTC 1149
|||
421 GCTGGTACAGATAGGCCATTTGTAGTAACTTTTGGCCATGATGGAAAGGCGATCTTC 480
|||
1150 TCACAAAAGAGAAAACGTCAGCCAAACACAAACAGCGGAAACGCCCTTAAGTCCAGCT 1209
|||
481 TCACAAAAGAGAAAACGTCAGCCAAACACAAACAGCGGAAACGCCCTTAAGTCCAGCT 540
|||
1210 GTAAGAGACACCTTTGTAGTGGACTTCAGTGACGTGGGGTGGAAATGATCGATTGTGG 1269
|||
541 GTAAGAGACACCTTTGTAGTGGACTTCAGTGACGTGGGGTGGAAATGATCGATTGTGG 600
|||
1270 CTCCTCCCGGGTATCAGCGCTTTTACTGACAGGAGATGCCCTTTTCTCTGGCTGATC 1329
|||
601 CTCCTCCCGGGTATCAGCGCTTTTACTGACAGGAGATGCCCTTTTCTCTGGCTGATC 660
|||
1330 ATCTGAACCTCACTAATCATGCACTGTTTTCAGACGTTGGTCAACTCTGTTA 1380
|||
661 ATCTGAACCTCACTAATCATGCACTGTTTTCAGACGTTGGTCAACTCTGTTA 711
|||

```

```

RESULT 8
BU625617/c
LOCUS
DEFINITION
  BU625617 727 bp mRNA linear EST 23-SEP-2002
  UI-H-FGI-bgn-b-18-0-UI.61 NCI_CGAP FGI Homo sapiens cDNA clone
  UI-H-FGI-bgn-b-18-0-UI 3', mRNA sequence.
ACCESSION
  BU625617
VERSION
  BU625617.1 GI:23291832
KEYWORDS
  EST.
SOURCE
  Homo sapiens (human)
ORGANISM
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
  Homnidae; Homo.
1 (bases 1 to 727)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: James Martin
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@uiowa.edu
The following repetitive elements were found in this cDNA
sequence: 1-27, >POLY A#simple repeat (matched complement) 31-61,
>(TA)n#simple repeat (matched complement)
Seq primer: M13 FORWARD
POLYA=Yes.
Location/Qualifiers
  1..727
    /organism="Homo sapiens"
    /mol_type="mRNA"
    /db_xref="taxon:9606"
    /clone="UI-H-FGI-bgn-b-18-0-UI"
FEATURES
  source

```

```

/tissue_type="Cell lines"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI_CGAP_FGI"
/notes="Organ: Enchondroma; Vector: p7773-Pac (Pharmacia)
with a modified polylinker; Site 1: EcoR I; Site 2: Not I;
NCI CGAP FGI is a normalized cDNA library obtained from a
pool of mRNA from 2 cell lines from Enchondroma tissues.
The library was constructed according to Bonaldo, Lennon
and Soares, Genome Research, 6:791-806, 1996. First strand
cDNA synthesis was primed with an oligo-dT primer
containing a Not I site. Double stranded cDNA was ligated
to an EcoR I adaptor, digested with Not I, and cloned
directionally into p7773-Pac vector. The oligonucleotide
used to prime the synthesis of first-strand cDNA contains
a library tag sequence that is located between the Not I
site and the (dT)18 tail. The sequence tag for this
library is CGGTCACTC. The cell lines were provided by Dr.
James Martin from the University of Iowa.
TAG_TISSUE=Enchondroma cell line (Mix of EN1 and EN2)
TAG_LIB=UI-H-FGI
TAG_SEQ=CGGTCACTC"

```

ORIGIN

```

Query Match      44.2%; Score 683.8; DB 5; Length 727;
Best Local Similarity 99.6%; Pred. No. 1e-180;
Matches 585; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      860 TGCACAGCCAACTCGAAATTCCTCCGTGACACAGACTTTTGGACACACAGGTGGTGAATCA 919
DB      727 TGCACAGCCAACTCGAAATTCCTCCGTGACACAGACTTTTGGACACACAGGTGGTGAATCA 668

QY      920 GAATGACAGCAGGTGGGAAGTTTGTATGTACACCCCGCTGTGATCGCGTGGACGACACA 979
DB      667 GAATGACAGCAGGTGGGAAGTTTGTATGTACACCCCGCTGTGATCGCGTGGACGACACA 608

QY      980 GGGACACGCCCAACCATGATTCGTGTGGAAGTGGCCCACTTGGAGGAGAAACAAGGTGT 1039
DB      607 GGGACACGCCCAACCATGATTCGTGTGGAAGTGGCCCACTTGGAGGAGAAACAAGGTGT 548

QY      1040 CTCCAAGAGACATGTTAGGATAAGCAGTCTTTTGACCAAGATGAACACAGCTGTGTACA 1099
DB      547 CTCCAAGAGACATGTTAGGATAAGCAGTCTTTTGACCAAGATGAACACAGCTGTGTACA 488

QY      1100 GATAAGGCCATTCGTAGTAACTTTTGGCCATGATGGAAAGGGCATCTCTCCACAAAG 1159
DB      487 GATAAGGCCATTCGTAGTAACTTTTGGCCATGATGGAAAGGGCATCTCTCCACAAAG 428

QY      1160 AGAAAAAGCTCAAGCCAAACACAAACAGCGGAAACGCCCTTAAGTCCAGCTGTAAAGACA 1219
DB      427 AGAAAAAGCTCAAGCCAAACACAAACAGCGGAAACGCCCTTAAGTCCAGCTGTAAAGACA 368

QY      1220 CCTTTGTAGCTGGACATTCAGTGACGTGGGGTGGAAATGACGTGGATGTGGCTCCCGCGG 1279
DB      367 CCTTTGTAGCTGGACATTCAGTGACGTGGGGTGGAAATGACGTGGATGTGGCTCCCGCGG 308

QY      1280 GTATCAGCGCTTTTACTGCGCAGGAATGCCCTTTCTCTGGCTGATCATCTGACATC 1339
DB      307 GTATCAGCGCTTTTACTGCGCAGGAATGCCCTTTCTCTGGCTGATCATCTGACATC 248

QY      1340 CACTAATCATGCAATTTGTTTCAGACGCTGTGTCAACTCTGTAACTCTAAGATTCCTAAGGC 1399
DB      247 CACTAATCATGCAATTTGTTTCAGACGCTGTGTCAACTCTGTAACTCTAAGATTCCTAAGGC 188

QY      1400 ATGCTGTGTCCCGACAGAACTCAGTGTCTATCTCGATGCTGTACCTTGGACGAGAATAA 1459
DB      187 ATGCTGTGTCCCGACAGAACTCAGTGTCTATCTCGATGCTGTACCTTGGACGAGAATAA 128

QY      1460 GGTGTATTAAGAACTATCAGGACATGGTTGTGAGGGTTGTGGGTTCGCTAGTACAG 1519
DB      127 GGTGTATTAAGAACTATCAGGACATGGTTGTGAGGGTTGTGGGTTCGCTAGTACAG 68

QY      1520 CAAAATTAATACATAATATATATATA 1547

```

```
|||||
67 CAAATTAATACATAAATATATATA 40

Db
CN396138
LOCUS
DEFINITION 1700424182561 GRN_BB Homo sapiens linear mRNA 711 bp EST 16-MAY-2004
ACCESSION CN396138
VERSION CN396138.1 GI:47383733
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
Bradenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J.,
Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R.,
Lebkowski, J. and Stanton, L.W.
Transcriptome characterization elucidates signaling networks that
control human ES cell growth and differentiation
Nat. Biotechnol. 22 (6), 707-716 (2004)
15146197
Contact: Bradenberger R
Regenerative Medicine
Geron Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760
Email: rbradenberger@geron.com
Insert Length: 711 Std Error: 0.00.
Location/Qualifiers
1..711
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="embryonic stem cells, embryoid bodies
derived from H1, H7 and H9 cells"
/clone_lib="GRN_BB"
/notes="oligo dr primed, full-length enriched cDNA library
from embryoid body outgrowths derived from hES cell lines
H1 (p32), H7 (p29), and H9 (p26) maintained in feeder-free
conditions."

FEATURES
source
1..711

ORIGIN
Query Match 44.1%; Score 683; DB 7; Length 711;
Best Local Similarity 99.3%; Pred. No. 1.7e-180;
Matches 686; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

246 TTTTCCATGTGGACGCTCTTTCAATGGACGTGTCCCGCGTCTCTTAGACGACTGCG 305
18 TTTTCTCTGTGGACGCTCTTTCAATGGACGTGTCCCGCGTCTCTTAGACGACTGCG 77
306 GTCTCTCTAAAGTCGACCATGTGTGCGGGACCGCTGTCTCTTAGGCTTCTGCTTCCC 365
78 GTCTCTCTAAAGTCGACCATGTGTGCGGGACCGCTGTCTCTTAGGCTTCTGCTTCCC 137
366 CAGGTCTCTCTGGGCGGCGGCTGTCTCTCGGAGCTGGGCGCGAGGAAGTTGCGG 425
138 CAGGTCTCTCTGGGCGGCGGCTGTCTCTCGGAGCTGGGCGCGAGGAAGTTGCGG 197
426 CGGGGCTGTGGGCGGCGGCTCTATCCAGCCCTCTGACGAGGTCTGAGCGAGTTGAG 485
198 CGGGGCTGTGGGCGGCGGCTCTATCCAGCCCTCTGACGAGGTCTTTAGCGAGTTGAG 257
486 TTGGCGGTGTCTCAGCATGTCTGGCTGAAACAGAGACCCACCCAGCAGGAGCGCGTG 545
258 TTGGCGGTGTCTCAGCATGTCTGGCTGAAACAGAGACCCACCCAGCAGGAGCGCGTG 317
546 GTGCCCCCTACATGCTAGACTGTATCGCAGGCACTCAGGTACGCGGGCTCACCGGCC 605
318 GTGCCCCCTACATGCTAGACTGTATCGCAGGCACTCAGGTACGCGGGCTCACCGGCC 377
```

SSEA-1 by immunofluorescence. Passage 35. This line is a subclone of the parental line; the parental line was subcloned to remove aneuploid cells). cDNA was primed using oligo-dT primer.
5'-pGACTAGTCTTCTAGATCGGAGCGCGCC(T)25-3' and cloned into the EcoRV/NotI sites of pExpress-1. Size selection >1.25 kb resulted in an average insert size of 1.82 kb. This primary library is normalized (non-normalized primary library is NIH MGC 278) and was constructed by Express Genomics (Frederick, MD). Note: this is a Mammalian Gene Collection library."

ORIGIN

| | | | | | | | |
|-----------------------|--------|--------------|-----------|------------|-----|--------|------|
| Query Match | 43.6%; | Score | 673.8; | DB | 8; | Length | 769; |
| Best Local Similarity | 96.0%; | Pred. No. | 6.7e-178; | | | | |
| Matches | 723; | Conservative | 0; | Mismatches | 27; | Indels | 3; |
| Gaps | 3; | | | | | | |

Qy 131 TGAGACGCTGTTCCAGCGTGAAGAGAGAGACTGCGCGCGCGCACCCGGGAGAGAGG 190
Db 1 TGAGACGCTGTTCCAGCGTGAAGAGAGAGACTGCGCGCGCGCACCCGGGAGAGAGG 60
Qy 191 AGGCAAGAAAGAGACGACATTCGCTCTTGGCCAGGTCCTTTGACAGAGTTTTC 250
Db 61 AGGCAAGAAAGAGACGACATTCGCTCTTGGCCAGGTCCTTTGACAGAGTTTTC 120
Qy 251 CATGTGGACGCTCTTCAATGACGCTGTCGCCGCGTGTCTTTCAGACGACTGCGGTCTC 310
Db 121 CATGTGGACGCTCTTCAATGACGCTGTCGCCGCGTGTCTTTCAGACGACTGCGGTCTC 180
Qy 311 CTAAGAGTCACATGTTGGCGGACCGCTGTCTTTCAGGTTGCTGCTTCCCGAGGT 370
Db 181 CTAAGAGTCACATGTTGGCGGACCGCTGTCTTTCAGGTTGCTGCTTCCCGAGGT 240
Qy 371 CCTCTCTGGCGCGCGCTGGCTGTCTTTCAGGTTGCTGCTTTCAGGTTGCTGCTTCCCGCGC 430
Db 241 CCTCTCTGGCGCGCGCTGGCTGTCTTTCAGGTTGCTGCTTTCAGGTTGCTGCTTCCCGCGC 300
Qy 431 GTCGTGGCGCGCGCTCATCCAGCTCTCAGCAGGTCCTGAGCAGTTTTCAGTTGCTG 490
Db 301 GTCGTGGCGCGCGCTCATCCAGCTCTCAGCAGGTCCTGAGCAGTTTTCAGTTGCTG 360
Qy 491 GCTGCTCAGCATGTTGGCGCTGAAGACAGAGACCCAGCAGGAGCGCGTGGTGC 550
Db 361 GCTGCTCAGCATGTTGGCGCTGAAGACAGAGACCCAGCAGGAGCGCGTGGTGC 420
Qy 551 CCCCTACATGCTAGACCTGTATGCGAGGCACTCAGTACGCGGCTCAGCCGCCCGAGA 610
Db 421 CCCCTACATGCTAGACCTGTATGCGAGGCACTCAGTACGCGGCTCAGCCGCCCGAGA 480
Qy 611 CCACCGTTGGAGAGGCGAGCGAGCGGACCACTGTGCGAGCTTCCACCATGAGA 670
Db 481 CCACCGTTGGAGAGGCGAGCGAGCGGACCACTGTGCGAGCTTCCACCATGAGA 540
Qy 671 ATCTTTGGAAGAACTACCAAGAACAGTGGGAAACCAACCCGGAGATCTCTTTAAAT 730
Db 541 ATCTTTGGAAGAACTACCAAGAACAGTGGGAAACCAACCCGGAGATCTCTTTAAAT 599
Qy 731 AAGTTCTTATCCCGAGGAGGTTTATCCTCAGCAGAGCTTTCAGGTTTCCGAGACA 790
Db 600 AAGTTCTTATCCCGAGGAGGTTTATCCTCAGCAGAGCTTTCAGGTTTCCGAGACA 659
Qy 791 GATGGAAGATGCTTTAGGAAACATAGAGGTTTCCATCAGGATTAATATTATGAAT 850
Db 660 AATGCGAGATGCTTTCCGAAACATAGAGGTTTCCATC-CCACATACTATTATTGGAAT 718
Qy 851 CATAAACCTGCAACAGCAGCACTCGAAATTTCC 883
Db 719 CAT-TAACCTGCTACCAACCACTTGATTTCC 750

RESULT 11

DN117475/c

LOCUS

DN117475 841 bp mRNA linear EST 15-FEB-2005

DEFINITION

1117145 MARC 4PTG Sus scrofa cDNA 3', mRNA sequence.

ACCESSION

DN117475

DN117475.1 GI:59811735

VERSION

EST.

KEYWORDS

Sus scrofa (pig)

SOURCE

Sus scrofa

ORGANISM

Sus

1 (bases 1 to 841)

Smith,T.P.L., Fekking,B.A., Ford,J.J., Vallet,J.L., Wise,T.A.,

Noneman,D.J., Wray,J.B. and Keele,J.W.

Porcine EST collection using a normalized library constructed from

embryos representing early developmental stages

Unpublished (2003)

Contact: Smith TPL

USDA, ARS, US Meat Animal Research Center

PO Box 166, Clay Center, NE 68933-0166, USA

Tel: 402 762 4366

Fax: 402 762 4390

Email: smith@mail.marc.usda.gov

Single pass sequencing. Bases called with phred v0.020425.c and

trimmed with the aid of the trim_alt option. Vector identified with

cross_match v0.990329.

Plate: HHY8017 row: A column: 20

Seq primer: TAGAAGCACAGTCGAG.

Location/Qualifiers

1..841

/organism="Sus scrofa"

/mol_type="mRNA"

/db_xref="taxon:9823"

/tissue_type="pooled"

/lab_host="DH10B"

/clone_lib="MARC 4PTG"

/note="Vector: pCDNA3.1; Site: 1: EcoRI; Site 2: NotI;

Library made with combined RNA from day-10, day-13,

day-15, day-25, and day-30 whole embryos."

FEATURES

source

ORIGIN

| | | | | | | | |
|-----------------------|--------|--------------|---------|------------|-----|--------|------|
| Query Match | 42.9%; | Score | 664.4; | DB | 8; | Length | 841; |
| Best Local Similarity | 88.2%; | Pred. No. | 3e-175; | | | | |
| Matches | 733; | Conservative | 0; | Mismatches | 97; | Indels | 1; |
| Gaps | 1; | | | | | | |

Qy 718 TCTCTTTAAATTTAAGTTCTATCCCGAGGAGGTTTATCACTCAGCAGAGCTTCAGG 777
Db 841 TTTTCTTTAAATTTAAGTTCTATCCCGAGGAGGTTTATCACTCAGCAGAGCTTCAGG 782
Qy 778 TTTTCCGAGAACAGATGCAAGATGCTTTAGGAAACAATAGCAGTTTCCATCACCGAATTA 837
Db 781 TCTTCCGGAACAGACACAGGAGACTTTGGATTAACAGTAGCAGTTTCCATCACCGAATTA 722
Qy 838 ATATTATGAATATCAATAAACTGCAACAGCACTCGAAATTCCTCCGTGACCACTTT 897
Db 721 ATATTATGAATATCAATAAACTGCAACAGCACTCGAAATTCCTCCGTGACCACTTT 662
Qy 898 TGGACACAGGTTGCTGTAATCAGATGCAAGCAGTGGGAAAGTTTTCATGTCACTCCG 957
Db 661 TGGACACAGGTTGCTGTAATCAGATGCAAGCAGTGGGAAAGTTTTCATGTCACTCCG 502
Qy 958 CTGTGATCGGTGGAGTCTGCACAGGAGCACGCCAACCATGGATTCGTGGTGAAGTGGCC 1017
Db 601 CTGTGATCGGTGGAGTCTGCACAGGAGTCCGCCAACCATGGATTCGTGGTGAAGTGGCC 542
Qy 1018 ACTTGGAGGAGAACACAGGTGCTCCAAGAGCATGTTAGGATAGCAGGCTTTTGACCC 1077
Db 541 ACCCGAGGAGACAGCCCGAGGTCTCCAAGAGCATGTTAGGATAGCAGGCTTTTGACCC 482
Qy 1078 AAGATGAACACAGCTGCTCAGATGAAGCCATTCCTAGTACTTTTGGCCATGATGAA 1137
Db 481 AAGATGAACACAGCTGCTCAGATGAAGCCATTCCTAGTACTTTTGGCCATGATGAA 422
Qy 1138 AAGGCGATCTCTCCACAAAAGAGAAAAACGTCAGGCCAAAACACAAAACAGCGGAAACGCC 1197

| | | | |
|----|------|--|------|
| Db | 421 | AAGGACACCCCTCTCTGCACAAAGGGAAGCGTCAAGCAAAACA | 362 |
| Qy | 1198 | TTAAGTCCAGCTGTAAAGAGACACCCCTTTGTACGTGGACCTT | 1257 |
| Db | 361 | TGAATCCAGCTGCAAGAGACACCCCTTTGTACGTGGACCTT | 302 |
| Qy | 1258 | ACTGGATTGGGCTCCCCCGGGGTATCAGCCCTTTTACTGCGC | 1317 |
| Db | 301 | ACTGGATCGTAGCCCCCCCGGGGTATCATGCTTTTACTGCGC | 242 |
| Qy | 1318 | CTCTGGGCTGATCATCTGAACTCCACTAATCATGCGATTTGT | 1377 |
| Db | 241 | CCCTGGGCTGATCACTCTGAATCTCCAGAACTCAGCCATCGT | 182 |
| Qy | 1378 | TTAACTCTAAGATTCTTAAGGCATGCTGTGTGCCGACAGAACT | 1437 |
| Db | 181 | TTAACTCTAAGATCCCAAGGCGTGCTGTGTGCCACAGAACT | 122 |
| Qy | 1438 | TGTAACCTTGACGAGAATGAAAGGTTGTTATTAAGAAGACTAT | 1497 |
| Db | 121 | TGTAACCTTGACGAGAACGAAAGGTGGTATTAAAGAACTACC | 62 |
| Qy | 1498 | GTTGTGGGTGTCCGTAGTACAGCAAAAT-TAAATACATAAATAT | 1547 |
| Db | 61 | GTTGTGGGTGTGTTTAGCACAGCAAAATAAAAAATAATATATA | 11 |

RESULT 12
DN117122
LOCUS DN117122 830 bp mRNA linear EST 15-FEB-2005
DEFINITION 1116761 MARC 4PTG Sus scrofa cDNA 5', mRNA sequence.

| | |
|-----------|---|
| ACCESSION | DN117122 |
| VERSION | DN117122.1 |
| KEYWORDS | GI:59811382 |
| SOURCE | EST. |
| ORGANISM | Sus scrofa (pig) |
| | Sus scrofa |
| | Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; |
| | Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae; |
| | Sus. |
| REFERENCE | 1 (bases 1 to 830) |
| AUTHORS | Smith,T.P.L., Preking,B.A., Ford,J.J., Vallet,J.L., Wise,T.A., Nonneman,D.J., Wray,J.E. and Keele,J.W. |
| TITLE | Porcine EST collection using a normalized library constructed from embryos representing early developmental stages |
| JOURNAL | Unpublished (2003) |
| COMMENT | Contact: Smith TPL |

| FEATURES | SOURCE |
|--|--|
| 1. High Accuracy: The model achieves a high accuracy rate, consistently performing well across various datasets and tasks. | 1. High Accuracy: The model achieves a high accuracy rate, consistently performing well across various datasets and tasks. |
| 2. Scalability: The model is designed to scale efficiently, handling large volumes of data and complex tasks without significant performance degradation. | 2. Scalability: The model is designed to scale efficiently, handling large volumes of data and complex tasks without significant performance degradation. |
| 3. Interpretability: The model's decisions are transparent and explainable, allowing users to understand the underlying factors influencing the results. | 3. Interpretability: The model's decisions are transparent and explainable, allowing users to understand the underlying factors influencing the results. |
| 4. Robustness: The model is highly robust, maintaining stable performance even in the presence of noisy or incomplete data. | 4. Robustness: The model is highly robust, maintaining stable performance even in the presence of noisy or incomplete data. |
| 5. Efficiency: The model is optimized for fast execution, ensuring timely results and minimizing resource consumption. | 5. Efficiency: The model is optimized for fast execution, ensuring timely results and minimizing resource consumption. |

```

/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/tissue_type="pooled"
/lab_host="DH10B"
/clone_lib="MARC 4P1G"
/notes="vector: pCDNA3.1; Site 1: EcoRI; Site 2: NotI;
Library made with combined RNA from day-10, day-13,
day-15, day-25, and day-30 whole embryos."

```

RESULT 13
BX432994/c

| LOCUS | DEFINITION | 1001 bp | mRNA | linear | EST |
|----------|------------|----------|-----------------------|-------------------------------------|-------------|
| LOC25547 | | BX432994 | Homo sapiens PLACENTA | Homo sapiens CDNA clone CSODE03YB10 | 04-MAY-2004 |
| | | BX432994 | 3-PRIME. | mRNA sequence. | |

ACCESSION
BX432994

VERSION
BX432994.2 GI:47009598

KEYWORDS
SOURCE
ORGANISM

REFERENCE

1 (bases 1 to 1001)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
TITLE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.

| | | | | |
|--|----|-----|---|-----|
| | Qy | 140 | GTTCCTCCAGCGTGAAGAAGAGAGACTGCGCGCGCGGCACCCGGGAGAGAGAGGAGCAAAAGA | 199 |
| | Db | 1 | GTTCCTCTGCGTGCGGAGAGGAACTGCCCGGCGCACCCGGGAGGAGAGAGGAGGAGCGGA | 60 |
| | Qy | 200 | AAAGGAAACGACAATTGGTTCTTTGGCGCAGGTCCTTTTGACCAGAG-TTTTTTCATGTGGA | 258 |
| | Db | 61 | A---GGAAGGGAACCCGGTCCCCTGTGCCAGGTCCTTCAGTCAGAGCTTTTTCATGTGGA | 117 |
| | Qy | 259 | CGCTCTTTCAATGGAAGTGTCCCCCGGCGTCTTCTTAGACGGACTGCGGCTCTCTCAAAGGT | 318 |
| | Db | 118 | GGCTCTTTCAATGGAAGTGTCCCCCGGCGTCTTCTTAGACGGTCTGCGGTCTCTCAAAGGT | 177 |
| | Qy | 319 | GGAACATGTGTGGCCGGGAACCCGCTGTCTTCTTAGGTTGTCTTCCCGCAGGTCTCTCTGG | 378 |
| | Db | 178 | GGAACATGTGTGGCCGGGAACCCGCTGTCTTCTTAGGTTGTCTTCCCGCAGGTCTCTCTGG | 237 |
| | Qy | 379 | GCGGCGCGGCTGCGCTCTGTTTCCGAGCTGSGGCGCAGGAAGTTTCGCGCGGCGTCTGTCG | 438 |
| | Db | 238 | GCGGCGGCGCGAACCTCATTTCCGAGTGGGCCGGAAGATTC---GCGCGTCTACTG | 294 |
| | Qy | 439 | GCGCGCCCTCATCCAGCCCTCTGACAGGTCCTTGACGAGTTTCGAGTTTCGGCTCTCTCA | 498 |
| | Db | 295 | GCCTCTCTCTTCCAGCCCTCGGACGAGTCCTCAGCGAGTTTGTAGTTTGGGCTGCTCA | 354 |
| | Qy | 499 | GCATGTTCCGCTGAACACAGAGACCCACCCCGACGAGGAGCGCGTGTGCCCCCTACA | 558 |
| | Db | 355 | GCATGTTCCGCTGGAAGACAGAGACCCACCCCGACGAGGAGCGCGTGTGCCCCCTACA | 414 |
| | Qy | 559 | TGCTAGACCTGTATCGCAGGCACTCAGGTCAGCGCGGCTCACCGCGCCACAGACACCGGT | 618 |
| | Db | 415 | TGCTGACCTGTATCCGCGGACATTCGGTTCAGCAGGCGGCTGCCCCGGACACCGGC | 474 |
| | Qy | 619 | TGAGAGGGGAGCCAGCCCGAGCCAACATGTGCGCAGTTCACCAATGAAGAATCTTTGG | 678 |
| | Db | 475 | TGAGAGGGGAGCCAGCTTGGCCCAACACCGTGGCAGCTTCACCAACAGGAATCTTTGG | 534 |
| | Qy | 679 | AAGAACTACAGAAAACGAGTGGGAACAACCCGGAGATTCCTCTTAATTTTAAGTTCTA | 738 |
| | Db | 535 | AAGAACTGCCAGAAATGAGTGGAAAAACAACCCGGCGCTTCCTCTTAATTTTAAC TTCG | 594 |
| | Qy | 739 | TCCCCACGGAGGAGTTTATCACTCTCAGCAGAGCTTCAGGTTTTCGAGAACAGATGCAAG | 798 |
| | Db | 595 | TCCCCACCGAGGAGTTTATCACTCTCAGCAGAACTTCAGGCTTCGGGAACAGACACAGG | 654 |
| | Qy | 799 | ATGCTTTAGAAAACAATAGCAGTTTCCATCAACGAAATTAAATATTATGAAATCATAAAAC | 858 |
| | Db | 655 | AGACTTTGGATTAACAGTAGCAGTTTCCATCACCGAAATTAAATATTATGAAATCATCAAAC | 714 |
| | Qy | 859 | CTGCAACAGCCAACCTCGAAATTCGCCGTGACCAAGCTTTTGGACACACAGGTTGGTCAATC | 918 |
| | Db | 715 | CTGCAACAGCCAACCTCAAGTTCCCGTGACCAAGCTTTTGGACACACAGGTTGGTCAATC | 774 |
| | Qy | 919 | AGAATCAAGCAGGTCGGAAAGTTTGTATGTCAACCCCGCTGTGATGCGGTGSACT | 974 |
| | Db | 775 | CGAATGCAAGCAGGTCGGAGAGCTTCGAGSTCAACCCCGCTGTGATGCGGTGSACT | 830 |

BX432994 1001 bp mRNA linear EST 04-MAY-2004
 BX432994 Homo sapiens PLACENTA Homo sapiens cDNA clone CS0DE003YB10
 3-PRIME. mRNA sequence.

BX432994
BX432994.2 GI:47009598

KEYWORDS
SOURCE
ORGANISM

REFERENCE

1 (bases 1 to 1001)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
TITLE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.

JOURNAL
COMMENT

Unpublished (2001)
On May 15, 2003 this sequence version replaced gi:30781178.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
This sequence belongs to sequence cluster 10041.f
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CS0BAI008ZG11_CS00759_1&c=10041.f.

FEATURES
source

Location/Qualifiers
1..1001
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DE003YB10"
/tissue_type="PLACENTA"
/clone_lib="Homo sapiens PLACENTA"
/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."

ORIGIN

Query Match 40.3%; Score 623.6; DB 5; Length 1001;
Best Local Similarity 93.1%; Pred. No. 9.7e-164;
Matches 707; Conservative 0; Mismatches 45; Indels 7; Gaps 5;

QY 794 GCAAGATGCTTTAGGAAACAATAGCAGTTTCCATCCGGAATTAATATTATGAATCAT 853
DB 1001 GCAAAATTTTAAAGGAACAATAGACAGTTTCTCTCCCGGAATTATATTTATGAATCAAT 942
QY 854 AAAACTGACAGGCAACTCGAATT--CCCGTGACAGACTTTTGAC--ACCAGGT 909
DB 941 AAACTTGCACACGACAACTGGAATTTCCCGGTGACAGCTTTTGGCCACCACAGGT 882
QY 910 TGGTCAATCAGAACTCAAGCAGTGGGAAAGTTTGTATGTC-ACCCCGCTGTGTATGCG 968
DB 881 TGTTAATCAAAATCAAAAGAGTGGGAAAGTTTGTATGTCACCCCGCTGTGTATGCG 822
QY 969 TGGACTGCACAGGACAGCCCAACCATGGATTGCTGGTGGAGTGGCCCACTTGGAGGAG 1028
DB 821 TGGACTGCACAGGAAACAGCCCAACCATGGATTGCTGGTGGAGTGGCCCACTT-GAGGAG 763
QY 1029 AAACAAGGTGCTCAAGGACATGTTAGGATAAGCAGTCTTTGCAACCAAGATGAACAC 1088
DB 762 AAACAAGGTGCTCAAGGAAACATGTTAGGATAAGCAGTCT-TNGCACCAGATGAACAC 704
QY 1089 AGCTGTCACAGATAGGCAATTGCTAGTAACCTTTTGGCCATGATGGAAAGGCGATCCT 1148
DB 703 AGCTGTCACAGATAGGCAATTGCTAGTAACCTTTTGGCCATGATGGAAAGGCGATCCT 644
QY 1149 CTCACAAAGAGAAACAGTCAAGCACAACCAACAGCGGAAACGCGCTTAAGTCCAGC 1208
DB 643 CTCACAAAGAGAAACAGTCAAGCACAACCAACAGCGGAAACGCGCTTAAGTCCAGC 584
QY 1209 TGTAAAGACACCTTTGTACGTGACCTTCAGTGACGTGGGTGGAAATGACTGGATTGTG 1268
DB 583 TGTAAAGACACCTTTGTACGTGACCTTCAGTGACGTGGGTGGAAATGACTGGATTGTG 524
QY 1269 GCTCCCGGGGTATCACGCTTTTACTGACGAGGATGCCCTTTTCCCTCTGCTGCTGAT 1328
DB 523 GCTCCCGGGGTATCACGCTTTTACTGACGAGGATGCCCTTTTCCCTCTGCTGCTGAT 464
QY 1329 CATCTGAATCCCACTAATCATGCCATTTGTTACAGAGTTGGTCAACTCTGTTAACTCTAAG 1388
DB 463 CATCTGAATCCCACTAATCATGCCATTTGTTACAGAGTTGGTCAACTCTGTTAACTCTAAG 404

QY 1389 ATTCTAAGGCATGCTGTGTCGCCGACGAACTCAGTGTCTATCTCGATGCTGTACCTTCAC 1448
DB 403 ATTCTAAGGCATGCTGTGTCGCCGACGAACTCAGTGTCTATCTCGATGCTGTACCTTCAC 344
QY 1449 GAGAAATGAAAGGTTGTATTAAAGAACTATCAGGACATGTTGTGTGGAGGTTGTGGGTGT 1508
DB 343 GAGAAATGAAAGGTTGTATTAAAGAACTATCAGGACATGTTGTGTGGAGGTTGTGGGTGT 284
QY 1509 CGCTAGTACACAAAATTAATACATATAATATATATA 1547
DB 283 CGCTAGTACACAAAATTAATACATATAATATATA 245

RESULT 14
AW33267/c

LOCUS AW33267 666 bp mRNA linear EST 31-JAN-2000
DEFINITION xz89f02.x1 NCI CGAP Lu24 Homo sapiens cDNA clone IMAGE:2871387 3',
similar to gb:M22485 BONE MORPHOGENETIC PROTEIN 2 PRECURSOR
(HUMAN);, mRNA sequence.

ACCESSION AW33267 GI:5835926

VERSION EST.

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1 (bases 1 to 666)

1 NCI CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgsab@remail.nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: M. Bento Soares, Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www.bio.llnl.gov/bbrp/image/image.html

Seq primer: -40UP from Gibco

High quality sequence stop: 455.

FEATURES

source

1..666
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2871387"
/tissue_type="carcinoid"
/lab_host="DH10B"
/clone_lib="NCI CGAP Lu24"

/note="Organ: lung; Vector: pVT3D-Pac (Pharmacia) with a
modified polylinker; Plasmid DNA from the normalized
library NCI CGAP Lu5 was prepared, and ss circles were
made in vitro. Following HAP purification, this DNA was
used as tracer in a subtractive hybridization reaction.
The driver was PCR-amplified cDNAs from a pool of 5,000
clones made from the same library (cloneID8
1414920-1417991 and 1520904-1522439). Subtraction by Bento
Soares and M. Fatima Bonaldo."

ORIGIN

Query Match 40.1%; Score 619.6; DB 1; Length 666;
Best Local Similarity 97.7%; Pred. No. 1.2e-162;
Matches 639; Conservative 0; Mismatches 14; Indels 1; Gaps 1;

QY 894 CTTTGGACACAGGTTGGTGAATCAGAAATGCAACAGGTGGGAAAGTTTGTATGATCTACC 953
DB 666 CTTTGGACACAGGTTGGTGAATCAGAAATGCAACAGGTGGGAAAGTTTGTATGATCTACC 607

Qy 954 CCGCTGTGATGCGTGGACTGCACAGGACACGCCAACCATGATTCGTGCGAAGTG 1013
Db |||||
Qy 606 CCGCTGTG-ATGCGGTGACTAGCAGGACACGCCAACCATGATTCGTGCGTAAAGTG 548
Db |||||
Qy 1014 GCCCATTGGAGGAGAAACAAGGTGTCTCCAAAGAGACATGTTAGGATAAGCAGGTCTTTG 1073
Db |||||
Qy 547 GCCCATTGGAGTAGAACAAGGTGTCTCCAAAGAGACATGTTAGGATAAGCAGGTCTTTG 488
Db |||||
Qy 1074 CACCAAGATGAACACAGCTGTGTACAGATAGGCCATGCTAGTAACATTTTGGCCATGAT 1133
Db |||||
Qy 487 CACCAAGATGAACACAGCTGTGTACAGATAGGCCATGCTAGTAACATTTTGGCCATGAT 428
Db |||||
Qy 1134 GGAAGAGGATCTCTCCACAAAGAGAGAAACGTCAGGCAACACAAACACGCGGAAA 1193
Db |||||
Qy 427 GGAAGAGGATCTCTCCACAAAGAGAGAAACGTCAGGCAACACAAACACGCGGAAA 368
Db |||||
Qy 1194 CGCCTTAAGTCCAGCTGTGAAGAGACACCCCTTTGTACGTGGACTTCAGTGACGTGGGGTGG 1253
Db |||||
Qy 367 CGCCTTAAGTCCAGCTGTGAAGAGACACCCCTTTGTACGTGGACTTCAGTGACGTGGGGTGG 308
Db |||||
Qy 1254 AATGACTGGATGTGGCTCCCGGGGTATCACGCCCTTTTACTGCCACGGAGATGCCCT 1313
Db |||||
Qy 307 AATGACTGGATGTGGCTCCCGGGGTATCACGCCCTTTTACTGCCACGGAGATGCCCT 248
Db |||||
Qy 1314 TTTCCTCTGGCTGATCATCTGAATCCACTCAATCATGCTCATGTTTCAGAGCTTGGTCAAC 1373
Db |||||
Qy 247 TTTCCTCTGGCTGATCATCTGAATCCACTCAATCATGCTCATGTTTCAGAGCTTGGTCAAC 188
Db |||||
Qy 1374 TCTGTTAACTCTAAGATTCCTAAGGCATGCTGTGTCCGACAGAACTCAGTGCTATCTCG 1433
Db |||||
Qy 187 TCTGTTAACTCTAAGATTCCTAAGGCATGCTGTGTCCGACAGAACTCAGTGCTATCTCG 128
Db |||||
Qy 1434 ATGCTGACCTTGACGAGAAAGAAAGTTGTATTAAGAACTATCAGGACATGTTGTG 1493
Db |||||
Qy 127 ATGCTGACCTTGACGAGAAAGAAAGTTGTATTAAGAACTATCAGGACATGTTGTG 68
Db |||||
Qy 1494 GAGGGTGTGGGTGTCGCTAGTACAGCAAAATTAATACATATATATATA 1547
Db |||||
Qy 67 GAGGGTGTGGGTGTCGCTAGTACAGCCAAATTAATACATATATATATA 14
Db |||||

RESULT 15
BM683313/c
LOCUS BM683313 648 bp mRNA linear EST 27-FEB-2002
DEFINITION UI-E-EJ1-aje-m-21-0-UI.s1 UI-E-EJ1 Homo sapiens cDNA clone
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
ACCESSION BM683313
VERSION BM683313.1 GI:18993209
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 648)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)
JOURNAL 889548
PUBMED
COMMENT Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: bento-soares@uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.reagen.com).

The following repetitive elements were found in this cDNA
sequence: 22-52,>(TA)n#Simple_repeat (matched complement)
Seq primer: M13 Forward
POLYA=Yes.
FEATURES
Location/Qualifiers
1..648
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-E-EJ1-aje-m-21-0-UI"
/tissue_type="fetal eye, lens, eye anterior segment,
optic nerve, retina, Retina Foveal and Macular, RPE and
Choroid"
/dev_stage="fetal and adult"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/clone_lib="UI-E-EJ1"
/note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a
modified polylinker; Site 1: EcoR I; Site 2: Not I;
UI-E-EJ1 is a subcloned cDNA library constructed
according to Bonaldo, Lennon and Soares, Genome Research,
6:791-806, 1996. First strand cDNA synthesis was primed
with an oligo-dT primer containing a Not I site. Double
stranded cDNA was ligated to an EcoR I adaptor, digested
with Not I, and cloned directionally into pT7T3-Pac
vector. The oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tags for this library are: fetal eyes,
AGATCAAGA; lens, CGATTAGCA; eye anterior segment,
AATGCCCAT; optic nerve, CCATTAAGTG; retina, CCGCG;
Foveal and Macular, GTCC; RPE and Choroid, ACCTA. This
library was created for the program, Gene Discovery in the
Visual system, supported by National Eye Institute (NEI).
TAG TISSUE=human fetal eyes
TAG LIB=UI-E-EJ1
TAG_SEQ=AGATCAAGA"

ORIGIN

Query Match 39.2%; Score 607; DB 3; Length 648;
Best Local Similarity 99.7%; Pred. No. 4.2e-159;
Matches 607; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 939 AGTTTTCATGTCACCCCGCTGTGATCGGTGGACTGCACAGGACACGCCAACCATGGA 998
Db |||||
Qy 639 AGTTTTCATGTCACCCCGCTGTGATCGGTGGACTGCACAGGACACGCCAACCATGGA 580
Db |||||
Qy 999 TTCTGTGTGGAAGTGGCCCACTTGGAGGAGAAACAAGGTGTCTCCAAAGACATGTTAGG 1058
Db |||||
Qy 579 TTCTGTGTGGAAGTGGCCCACTTGGAGGAGAAACAAGGTGTCTCCAAAGACATGTTAGG 520
Db |||||
Qy 1059 ATAAGCAGGTCTTTGCAACCAAGATGAACACAGCTGGTCAAGATAAGGCCATTTGCTAGTA 1118
Db |||||
Qy 519 ATAAGCAGGTCTTTGCAACCAAGATGAACACAGCTGGTCAAGATAAGGCCATTTGCTAGTA 460
Db |||||
Qy 1119 ACTTTTGGCCATGATGAAAGGGCATCTCTCCAAAGAGAGAAACGTCAGAGCCAAA 1178
Db |||||
Qy 459 ACTTTTGGCCATGATGAAAGGGCATCTCTCCAAAGAGAGAAACGTCAGAGCCAAA 400
Db |||||
Qy 1179 CACAAACAGCGGAAACGCCCTTAAGTCCAGCTGTGAAGAGACACCCCTTTGTAGTGGACTTC 1238
Db |||||
Qy 399 CACAAACAGCGGAAACGCCCTTAAGTCCAGCTGTGAAGAGACACCCCTTTGTAGTGGACTTC 340
Db |||||
Qy 1239 AGTCAGCTGGGTGGAATGACTGGAATGTGGCTCCCGGGGGTATCAGCGCTTTTACTGTC 1298
Db |||||
Qy 339 AGTCAGCTGGGTGGAATGACTGGAATGTGGCTCCCGGGGGTATCAGCGCTTTTACTGTC 280
Db |||||
Qy 1299 CACGAGAAATGCCCTTTTCTCTCGCTCATCTGAACTCCACTTAATCATGCCATCTT 1358
Db |||||
Qy 279 CACGAGAAATGCCCTTTTCTCTCGCTCATCTGAACTCCACTTAATCATGCCATCTT 220
Db |||||
Qy 1359 CAGAGTTGGTCAACTCTGTAACTCTAAGATTCTTAAGGATGCTGTGTCGCCAGAGAA 1418
Db |||||
Qy 219 CAGAGTTGGTCAACTCTGTAACTCTTAAGATTCTTAAGGATGCTGTGTCGCCAGAGAA 160
Db |||||

```
QY 1419 CTCAGTGTATCTCGATGCTGTACCTTGACGAGAAATGAAAAGGTTGTATTAAAGAACTAT 1478
    |||||
Db 159 CTCAGTGTATCTCGATGCTGTACCTTGACGAGAAATGAAAAGGTTGTATTAAAGAACTAT 100
    |||||
QY 1479 CAGGACATGGTTGTGGAGGGTTGTGGGTGTCGCTAGTACAGCAAAATTAATAACATAAAT 1538
    |||||
Db 99 CAGGACATGGTTGTGGAGGGTTGTGGGTGTCGCTAGTACAGCAAAATTAATAACATAAAT 40
    |||||
QY 1539 ATATATATA 1547
    |||||
Db 39 ATATATATA 31
    |||||
```

Search completed: January 10, 2006, 23:23:52
Job time : 4473 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: January 10, 2006, 23:24:00 ; Search time 4449 Seconds
(without alignments)
5059.565 Million cell updates/sec

Title: US-10-801-648-2

Perfect score: 2098

Sequence: 1 MVAGTRCILLALLPQVLGG.....NEKVLKNYQDMVVGCGCR 396

Scoring table: BLOSUM62

Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+_{p2n}.model -DEV=xlh
-Q=/cgm2_1/USPTO.spool/US10801648/runat_09012006_143119_14760/app_query.fasta_1.583
-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPECL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFWT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10801648 @CGN_1_1_3360@runat_09012006_143119_14760 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOC=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl.*

1: gb_ba.*
2: gb_in.*
3: gb_env.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pr.*
9: gb_ro.*
10: gb_sts.*
11: gb_sy.*
12: gb_un.*
13: gb_vi.*
14: gb_hg.*
15: gb_pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|--------------------|
| 1 | 2098 | 100.0 | 1215 | 6 | BD124160 Treatment |
| 2 | 2098 | 100.0 | 1547 | 6 | CQ875282 Sequence |
| 3 | 2098 | 100.0 | 1547 | 6 | CS031823 Sequence |

| | | | | | | |
|----|--------|-------|-------|---|------------|---------------------|
| 4 | 2098 | 100.0 | 1547 | 6 | CS040775 | CS040775 Sequence |
| 5 | 2098 | 100.0 | 1547 | 6 | I78455 | I78455 Sequence 2 |
| 6 | 2098 | 100.0 | 1547 | 6 | AX775087 | AX775087 Sequence |
| 7 | 2098 | 100.0 | 1547 | 8 | HUMBMP2A | M22489 Human bone |
| 8 | 2098 | 100.0 | 1581 | 6 | CS038212 | CS038212 Sequence |
| 9 | 2098 | 100.0 | 1607 | 6 | ARI57708 | ARI57708 Sequence |
| 10 | 2098 | 100.0 | 3526 | 6 | AR447458 | AR447458 Sequence |
| 11 | 2095 | 99.9 | 1607 | 6 | AR031482 | AR031482 Sequence |
| 12 | 2095 | 99.9 | 1607 | 6 | AR130859 | AR130859 Sequence |
| 13 | 2095 | 99.9 | 1607 | 6 | AR353792 | AR353792 Sequence |
| 14 | 2092 | 99.7 | 1260 | 6 | AR075478 | AR075478 Sequence |
| 15 | 2092 | 99.7 | 1260 | 6 | I15550 | I15550 Sequence 4 |
| 16 | 2092 | 99.7 | 1260 | 6 | I83779 | I83779 Sequence 4 |
| 17 | 2092 | 99.7 | 1260 | 6 | AR308031 | AR308031 Sequence |
| 18 | 2092 | 99.7 | 1260 | 6 | AR350343 | AR350343 Sequence |
| 19 | 2092 | 99.7 | 1607 | 6 | I08630 | I08630 Sequence 32 |
| 20 | 2092 | 99.7 | 2041 | 8 | BC069214 | BC069214 Homo sapi |
| 21 | 2092 | 99.7 | 2154 | 6 | CS031821 | CS031821 Sequence |
| 22 | 2092 | 99.7 | 2154 | 6 | CS040773 | CS040773 Sequence |
| 23 | 2092 | 99.7 | 2154 | 6 | AX201366 | AX201366 Sequence |
| 24 | 2084 | 99.3 | 1547 | 6 | CQ728408 | CQ728408 Sequence |
| 25 | 2043.5 | 97.4 | 1314 | 6 | BD003258 | BD003258 P-Selecti |
| 26 | 2022.5 | 96.4 | 2148 | 4 | AF041421 | AF041421 Oryctolag |
| 27 | 1948 | 92.9 | 2540 | 9 | BC100344 | BC100344 Mus muscu |
| 28 | 1943 | 92.6 | 2502 | 4 | DSPBMP2 | AJ001817 Dama sp. |
| 29 | 1932.5 | 92.1 | 1258 | 9 | RATMORPH2A | L20678 Rat bone mo |
| 30 | 1932.5 | 92.1 | 1275 | 9 | RNBMP2 | Z25868 R.norvegicu |
| 31 | 1796.5 | 85.6 | 1233 | 6 | I62380 | I62380 Sequence 27 |
| 32 | 1796.5 | 85.6 | 1233 | 6 | AR492773 | AR492773 Sequence |
| 33 | 1687 | 80.4 | 1179 | 5 | AY237249 | AY237249 Gallus ga |
| 34 | 1565 | 74.6 | 2093 | 5 | XLBMP2 | X55031 X. laevis m |
| 35 | 1562 | 74.5 | 2366 | 5 | XLBMP27 | X63424 X.laevius mR |
| 36 | 1554 | 74.1 | 2643 | 5 | CR484833 | CR484833 Xenopus t |
| 37 | 1542 | 73.5 | 1992 | 6 | XLBMP222 | X63425 X.laevius mR |
| 38 | 1542 | 73.5 | 1992 | 6 | E03670 | E03670 DNA sequenc |
| 39 | 1542 | 73.5 | 1992 | 6 | I66400 | I66400 Sequence 6 |
| 40 | 1540 | 73.4 | 2630 | 5 | BC100164 | BC100164 Xenopus 1 |
| 41 | 1532.5 | 73.0 | 1120 | 5 | GGBMP2 | W75914 G.gallus mR |
| 42 | 1530 | 72.9 | 1940 | 5 | BC092021 | BC092021 Xenopus 1 |
| 43 | 1511 | 72.0 | 14759 | 6 | CQ876148 | CQ876148 Sequence |
| 44 | 1511 | 72.0 | 14759 | 6 | CQ877130 | CQ877130 Sequence |
| 45 | 1511 | 72.0 | 14759 | 6 | CQ880078 | CQ880078 Sequence |

ALIGNMENTS

| RESULT 1 | BD124160 | 1215 bp | DNA | linear | PAT 18-SEP-2002 |
|------------|--|--|-----|-----------|-----------------|
| LOCUS | BD124160 | Treatment of bone loss with osteoblastoma precursor cells. | | | |
| DEFINITION | BD124160 | | | | |
| ACCESSION | BD124160 | | | | |
| VERSION | BD124160.1 | GI:23219105 | | | |
| KEYWORDS | JP 2002502822-A/13. | | | | |
| SOURCE | synthetic construct | | | | |
| ORGANISM | other sequences: artificial sequences. | | | | |
| REFERENCE | 1 (bases 1 to 1215) | | | | |
| AUTHORS | Hollinger,J.O., Win,S.R., Edmondo,P. and Wang,S.S. | | | | |
| TITLE | Treatment of bone loss with osteoblastoma precursor cells | | | | |
| JOURNAL | Patent: JP 2002502822-A 13 29-JAN-2002; | | | | |
| COMMENT | OREGON HEALTH SCIENCES UNIVERSITY | | | | |
| | OS Artificial Sequence | | | | |
| | PN JP 2002502822-A/13 | | | | |
| | PD 29-JAN-2002 | | | | |
| | PF 10-FEB-1999 | JP 2000530221 | | | |
| | PP 10-FEB-1998 | US 60/074240,12-FEB-1998 | US | 60/074451 | PI |
| | JEFFREY O HOLLINGER, SHELLEY R WIN, FRANK EDMONDO, SHU SI WANG | | | | PC |
| | A61K35/12, A61B17/56, A61F2/38, A61K9/00, A61K38/22, A61L27/00, PC | | | | |
| | A61L29/00 | | | | |
| | PC A61P19/00, A61P19/10, C07K14/51, C12N5/10, C12N15/09, A61K37/24, PC | | | | |
| | C12N5/00, | | | | |
| | PC C12N15/00 | | | | |
| | CC Description of Artificial Sequence: KS-hBMP-2 plasmid FH | | | | Key |

```
FT source Location/Qualifiers
FT 1..1215 /organism='Artificial Sequence'
FEATURES
  source
    1..1215
    /organism='synthetic construct'
    /mol_type='genomic DNA'
    /db_xref='taxon:32630'
ORIGIN
Alignment Scores:
Pred. No.: 1.38e-135 Length: 1215
Score: 2098.00 Matches: 396
Percent Similarity: 100.00% Conservativeness: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-10-801-648-2 (1-396) x BD124160 (1-1215)
Qy 1 MetValAlaGlyThrArgCysLeuLeuAlaLeuLeuProGlnValLeuLeuGlyGly 20
Db 17 ATGGTGGCGGAGCCCGCTTCTTAGCGTTGCTCTTCCAGGTCCTCTCGGGCGGC 76
Qy 21 AlaAlaGlyLeuValProGluLeuGlyArgGlyPheAlaAlaSerSerGlyArg 40
Db 77 GCGGCTGGCCCTCGTTCCGGAGCTGGCGCGCAGGAAGTTCCGCGCGCGCTGTCGGGCGGC 136
Qy 41 ProSerSerGlnProSerAspGluValLeuSerGluPheGluLeuLeuArgLeuSerMet 60
Db 137 CCTCATCCAGCCCTCTGACGAGGTCCTGACGAGTTCGAGTTGCGGCTGCTCAGCATG 196
Qy 61 PheGlyLeuLysGlnArgProThrProSerArgAspAlaValValProProTyMetLeu 80
Db 197 TTCGCGCTGAAACAGAGACCCACCCAGCAGGAGCGCGTGTGCCCTACATGCTA 256
Qy 81 AspLeuTyArgArgHisSerGlyGlnProGlySerProAlaProAspHisArgLeuGlu 100
Db 257 GACCTGTATCCAGGCACTTCAGGTGAGCGCGGCTCACCCCGCCAGACCCAGCGGTGGAG 316
Qy 101 ArgAlaAlaSerArgAlaAsnThrValArgSerPheHisHisGluGluSerLeuGluGlu 120
Db 317 AGGCGAGCCAGCCGAGCCAACTGTGCGAGCTTCCACCATGAGATCTTTGGAGAA 376
Qy 121 LeuProGluThrSerGlyLysThrThrArgArgPhePheAsnLeuSerSerIlePro 140
Db 377 CTACCAAGACGAGTGGGAAACACCCGAGATCTTCTTTAATTTAAGTTCTATCCCC 436
Qy 141 ThrGluGluPheIleThrSerAlaGluLeuGlnValPheArgGluGlnMetGlnAspAla 160
Db 437 ACGGAGGAGTTTATCACCTCAGCAGAGCTTCAGGTTTCCGAGAACAGATGCAAGATGCT 496
Qy 161 LeuGlyAsnAsnSerSerPheHisArgIleAsnIleTyGluIleLeuLysProAla 180
Db 497 TTAGGAACATAGCAGTTTCCATCCAGCATTAATTTATGAAATCATTAACCTGCA 556
Qy 181 ThrAlaAsnSerLysPheProValThrArgLeuLeuAspThrArgLeuValAsnGlnAsn 200
Db 557 ACAGCAACTCGAATTCCTCCGTCACACAGCTTTTGGACACAGGTTGGTGAATCAGAA 616
Qy 201 AlaSerArgTyrGluSerPheAspValThrProAlaValMetArgTyrThrAlaGlnGly 220
Db 617 GCAAGCAGTGGGAAAGTTTGTATGTCACTCCCGCTGTGATGCGGTGGACTGCACAGGA 676
Qy 221 HisAlaAsnHisGlyPheValValGluValAlaHisLeuGluGluLysGlnGlyValSer 240
Db 677 CACGCCAACCATGGATTCTGTGGTGAAGTGGCCCACTTGGAGGAACAACAGGTGTCTCC 736
Qy 241 LysArgHisValArgIleSerArgSerLeuHisGlnAspGluHisSerTyrSerGlnIle 260
Db 737 AAGACATGTTAGGATTAAGCAGGTCTTTGACCAAGATGAACACAGCTGTCTCAGATA 796
Qy 261 ArgProLeuLeuValThrPheGlyHisAspGlyLysGlyHisProLeuHisLysArgGlu 280
Db 977 AGCCATTGCTAGTAACCTTTTGGCCATGATGAAAAGGCGATCTCTCCACAAAGAGAA 856
Qy 281 LysArgGlnAlaLysHisLysGlnArgLysArgLeuLysSerSerCysLysArgHisPro 300
Db 857 AACGTCAGCCAAACACAAACAGCGGAAACGCTTAAGTCCAGCTGTAAGAGACACCCCT 916
Qy 301 LeuTyrValAspPheSerAspValGlyTyrAsnAspTrpIleValAlaProProGlyTyr 320
Db 917 TTGTACGTGACTTCACTGACGTGGGTGGAATGACTGGATTTGTGGTCCCGGGGTAT 976
Qy 321 HisAlaPheTyCysHisGlyGluCysProPheProLeuAlaAspHisLeuAsnSerThr 340
Db 977 CACGCTTTTACTCCACGAGAAATGCCCTTTCTCTGCTGATCATCTGAATCCACT 1036
Qy 341 AsnHisAlaIleValGlnThrLeuValAsnSerValAsnSerLysIleProLysAlaCys 360
Db 1037 AATCATGCCATTGTTTCAGAGCTTGTCACTCTGTTAACTCTAAGATTCTTAAGGCAATG 1096
Qy 361 CysValProThrGluLeuSerAlaIleSerMetLeuTyrLeuAspGluAsnGluLysVal 380
Db 1097 TGTGTCCCGACAGAACTCAGTGTCTATCTCGATGCTGTACCTTGACGAGAAATGAAAAGTT 1156
Qy 381 ValLeuLysAsnTyrGlnAspMetValValGluGlyCysGlyCysArg 396
Db 1157 GTATTAAAGAACTATACAGGACATGTTGTGAGGTTGTGGGTGTGCG 1204
RESULT 2
LOCUS CQ875282 1547 bp DNA linear PAT 27-SEP-2004
DEFINITION Sequence 25 from Patent WO2004076613.
ACCESSION CQ875282
VERSION CQ875282.1 GI:52748370
KEYWORDS Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1
AUTHORS Herr,A., Hinzmann,B., Dahl,E., Staub,E., Pilarsky,C. and Specht,T.
TITLE Human nucleic acid sequences from carcinomas of the bladder
JOURNAL Patent: WO 2004076613-A 25 10-SEP-2004;
Herr, Alexander (DE); Hinzmann, Bernd (DE); Dahl, Edgar (DE);
Staub, Elke (DE); Pilarsky, Christian (DE); Specht, Thomas (DE)
FEATURES
  Location/Qualifiers
    source
      1..1547
      /organism='Homo sapiens'
      /mol_type='unassigned DNA'
      /db_xref='taxon:9606'
ORIGIN
Alignment Scores:
Pred. No.: 1.84e-135 Length: 1547
Score: 2098.00 Matches: 396
Percent Similarity: 100.00% Conservativeness: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-10-801-648-2 (1-396) x CQ875282 (1-1547)
Qy 1 MetValAlaGlyThrArgCysLeuLeuAlaLeuLeuProGlnValLeuLeuGlyGly 20
Db 324 ATGGTGGCGGAGCCCGCTTCTTAGCGTTGCTCTTCCAGGTCCTCTCGGGCGGC 383
Qy 21 AlaAlaGlyLeuValProGluLeuGlyArgArgLysPheAlaAlaSerSerGlyArg 40
Db 384 GCGGCTGGCTCTGTTCCGAGCTGGCGCGCAGGAAGTTCCGCGCGCGCTCTCGGGCGGC 443
Qy 41 ProSerSerGlnProSerAspGluValLeuSerGluPheGluLeuArgLeuLeuSerMet 60
Db 444 CCTCATCCAGCCCTCTGACGAGGTCCTGAGCGAGTTCGAGTTGCGGCTGCTCAGCATG 503
```

QY 61 PheGlyLeuLysGlnArgProThrProSerArgAspAlaValValProProTyrMetLeu 80
 DB 504 TTCGGCCTGAAACAGAGACCCACCCAGCAGGAGCGGTGCTCCCTACATGCTA 563
 QY 81 AspLeuTyrArgArgHisSerGlyGlnProGlySerProAlaProAspHisArgLeuGlu 100
 DB 564 GACCTGTATCGAGGCACTCAGGTGAGCGGCTCAGCGGCCAGAGACCGGTTGGAG 623
 QY 101 ArgAlaAlaSerArgAlaAsnThrValArgSerPheHisHisGluGluSerLeuGlu 120
 DB 624 AGGCGAGCCAGCGAGCAACTGTGCGAGCTTCCACCAATGAAGAATCTTTGGAAGAA 683
 QY 121 LeuProGluThrSerGlyLysThrThrArgArgPhePheAsnLeuSerSerIlePro 140
 DB 684 CTACAGAAACGAGTGGGAAACACCCGGAGATCTCTTTAAATTAAGTTCTATCCCC 743
 QY 141 ThrGluGluPheIleThrSerAlaGluLeuGlnValPheArgGluGlnMetGlnAspAla 160
 DB 744 ACGGAGGAGTTTATCACCTCAGCAGAGCTTCAGGTTTCCGAGAACAGATGCAATGCT 803
 QY 161 LeuGlyAsnAsnSerSerPheHisHisArgIleAsnIleTyrGluIleIleIleProAla 180
 DB 804 TTAGGAAACAATAGCAGTTTCATCACCAGATTAATATTTATGAATCATAAACCTGCA 863
 QY 181 ThrAlaAsnSerLysPheProValThrArgLeuLeuAspThrArgLeuValAsnGlnAsn 200
 DB 864 ACAGCCAACTCGAAATTCCTGTCAGCAGATCTTTGGACACAGGTTGGTGAATCAGAT 923
 QY 201 AlaSerArgTTPGluSerPheAspValThrProAlaValMetArgTTPThrAlaGlnGly 220
 DB 924 GCAAGCAGGTGGGAAAGTTTGTATGTCTACCCCGCTGTGTATGCGGTGACATGACAGGGA 983
 QY 221 HisAlaAsnHisGlyPheValValGluValAlaHisLeuGluGluLysGlnGlyValSer 240
 DB 984 CACGCCAACCACTAGATTCGTGTGAGAGTGGCCCTCTGGAGGAGAAACAAGGTCTCTCC 1043
 QY 241 LysArgHisValArgIleSerArgSerLeuHisGlnAspGluHisSerTTPSerGlnIle 260
 DB 1044 AAGAGACATGTAGATAGCAGGTCTTTGACCAAGATGAACAGCTGTGTACAGATA 1103
 QY 261 ArgProLeuLeuValThrPheGlyHisAspGlyLysGlyHisProLeuHisLysArgGlu 280
 DB 1104 AGGCCATTTGCTAGTAACCTTTGGCCATGATGAAAGGCACTCTCCACAAAAGAGAA 1163
 QY 281 LysArgGlnAlaLysHisGlnArgLysArgLeuLysSerSerCysLysArgHisPro 300
 DB 1164 AAACGTCAAGCCAAACACAAACAGCGGAAACGCCCTTAAAGTCCAGCTGTAAGAGACACCT 1223
 QY 301 LeuTyrValAspPheSerAspValGlyTTPAsnAspTTPileValAlaProProGlyTyr 320
 DB 1224 TTGTACGTGGACTTCAGTGACGTGGGTGGGAATGACTGGATTTGTGCTCCCGGGGTAT 1283
 QY 321 HisAlaPheTyrCysHisGlyGluCysProPheProLeuAlaAspHisLeuAsnSerThr 340
 DB 1284 CACGCTTTTACTGCGCAGGAGATGCGCTTTCTCTGCTGATCATCTGAATCCACT 1343
 QY 341 AsnHisAlaIleValGlnThrLeuValAsnSerValAsnSerLysIleProLysAlaCys 360
 DB 1344 AATCATGCCATTTGTCAGACGTGGTCAACTCTGTTAACCTCTTAAGATTCCTTAAGGCATGC 1403
 QY 361 CysValProThrGluLeuSerAlaIleSerMetLeuTyrLeuAspGluAsnGluLysVal 380
 DB 1404 TGTGTCCCGACAGAACTCATGCTATCTCGATGCTGTACCTTGACAGATGAGAAAGTTT 1463
 QY 381 ValLeuLysAsnTyrGlnAspMetValValGluGlyCysGlyCysArg 396
 DB 1464 GTATTAAAGAACTATCAGGACATGTTGTGGAGGTTGTGGGTGTCGC 1511
 RESULT 3
 CS031823
 LOCUS
 DEFINITION Sequence 1329 from Patent WO2005016962. linear PAT 10-MAR-2005

ACCESSION CS031823
 VERSION CS031823.1 GI:60731673
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 MAMMALIA; EUTHERIA; EUARCHONTOLIRES; PRIMATES; CATARRHINI;
 HOMINIDAE; HOMO.
 REFERENCE
 AUTHORS Abbas A., Clark H., Ouyang W., Williams M.P., Wood W.I. and Wu, T.D.
 TITLE Compositions and methods for the treatment of immune related diseases
 JOURNAL Patent: WO 2005016962-A 1329 24-FEB-2005;
 Genentech, Inc. (US)
 FEATURES
 source 1..1547
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"
 ORIGIN
 Alignment Scores: 1.84e-135 Length: 1547
 Pred. No.: 2098.00 Matches: 396
 Score: 2098.00
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0
 US-10-801-648-2 (1-396) x CS031823 (1-1547)
 QY 1 MetValAlaGlyThrArgCysLeuLeuAlaLeuLeuLeuProGlnValLeuLeuGly 20
 DB 324 ATGTGGCGGGAGCCCGTGTCTTCTAGCTGTGCTTCCCGAGTCTCTCTGGGGGC 383
 QY 21 AlaAlaGlyLeuValProGluLeuGlyArgArgLysPheAlaAlaAsnSerGlyArg 40
 DB 384 GCGGCTGCTCGTTCGGAGCTGGCGCGCAGGAAGTTCCGGCGCGCTGCTCGGCGCGC 443
 QY 41 ProSerSerGlnProSerAspGluValLeuSerGluPheGluLeuArgLeuSerMet 60
 DB 444 CCTCATCCCCAGCCCTCTGACGAGTCTGACGAGTTCGAGTTCGGCTGCTCAGCATG 503
 QY 61 PheGlyLeuLysGlnArgProThrProSerArgAspAlaValValProProTyrMetLeu 80
 DB 504 TTGGCCTGAAACAGAGACCCACCCAGCAGGAGCGGTGCTGCCCTACATGCTA 563
 QY 81 AspLeuTyrArgArgHisSerGlyGlnProGlySerProAlaProAspHisArgLeuGlu 100
 DB 564 GACCTGTATCGAGGCACTCAGGTGAGCGGCTCAGCGGCCAGAGACCGGTTGGAG 623
 QY 101 ArgAlaAlaSerArgAlaAsnThrValArgSerPheHisHisGluGluSerLeuGlu 120
 DB 624 AGGCGAGCCAGCGAGCAACTGTGCGAGCTTCCACCAATGAAGAATCTTTGGAAGAA 683
 QY 121 LeuProGluThrSerGlyLysThrThrArgArgPhePheAsnLeuSerSerIlePro 140
 DB 684 CTACAGAAACGAGTGGGAAACACCCGGAGATCTCTTTAAATTAAGTTCTATCCCC 743
 QY 141 ThrGluGluPheIleThrSerAlaGluLeuGlnValPheArgGluGlnMetGlnAspAla 160
 DB 744 ACGGAGGAGTTTATCACCTCAGCAGAGCTTCAGGTTTCCGAGAACAGATGCAATGCT 803
 QY 161 LeuGlyAsnAsnSerSerPheHisHisArgIleAsnIleTyrGluIleIleIleProAla 180
 DB 804 TTAGGAAACAATAGCAGTTTCATCACCAGATTAATATTTATGAATCATAAACCTGCA 863
 QY 181 ThrAlaAsnSerLysPheProValThrArgLeuLeuAspThrArgLeuValAsnGlnAsn 200
 DB 864 ACAGCCAACTCGAAATTCCTGTCAGCAGATCTTTGGACACAGGTTGGTGAATCAGAT 923
 QY 201 AlaSerArgTTPGluSerPheAspValThrProAlaValMetArgTTPThrAlaGlnGly 220

| | | | | | | |
|---|---|--|------|--|--|--|
| Qy | 181 | ThrAlaAsnSerIysPheProValThrArgLeuLeuAspThrArgLeuValAsnGlnAsn | 200 | | | |
| Db | 864 | ACAGCCAACTCGAAATTCCTCCGTCGACAGACTTTTGGACACAGGTTGGTGAATCAGAAAT | 923 | | | |
| Qy | 201 | AlaSerArgTyrGlnSerPheAspValThrProAlaValMetArgTyrThrAlaGlnGly | 220 | | | |
| Db | 924 | GCAGCAGGTGGGAAGATTTTGTACACCCCGCTGTGATGCGGTGGACTGCACAGGGA | 983 | | | |
| Qy | 221 | HisAlaAsnHisGlyPheValValGluValAlaHisLeuGluGluLysGlnGlyValSer | 240 | | | |
| Db | 984 | CAGCCCAACCATGATTGCTGGTGGAGTGGCCCACTTGGAGGAGAAACAAGGTGTCTCC | 1043 | | | |
| Qy | 241 | LysArgHisValArgIleSerArgSerLeuHisGlnAspGluHisSerTrpSerGlnIle | 260 | | | |
| Db | 1044 | AAGAGACATGTTAGGATAAGCAGGTCTTTTGCACCAAGATGAACACAGCTGGTCACAGATA | 1103 | | | |
| Qy | 261 | ArgProLeuLeuValThrPheGlyHisAspGlyLysGlyHisProLeuHisLysArgGlu | 280 | | | |
| Db | 1104 | AGCCCATTCGTAGTAACATTTTGCCCATGATGGAAGAGGCGATCCTCTCCACAAAGAGAA | 1163 | | | |
| Qy | 281 | LysArgGlnAlaLysHisLysGlnArgLysArgLeuLysSerSerCysLysArgHisPro | 300 | | | |
| Db | 1164 | AAACGTCAGCCAAACACAAACAGCGGAAACGCCCTTAAAGTCCAGCTGTAAGACACACCT | 1223 | | | |
| Qy | 301 | LeuTyrValAspPheSerAspValGlyTrpAsnAspTrpIleValAlaProProGlyTyr | 320 | | | |
| Db | 1224 | TTGTAGCTGCACTTCAGTGACGTGGGGTGGAAATGCACTGGATTTGTGGCTCCCCGGGGTAT | 1283 | | | |
| Qy | 321 | HisAlaPheTyrCysHisGlyGluCysProPheProLeuAlaAspHisLeuAsnSerThr | 340 | | | |
| Db | 1284 | CAGCCCTTTTACTGCCACGAGAGATCCCTTTTTCCTCGCTGATCATCTGAACCTCACT | 1343 | | | |
| Qy | 341 | AsnHisAlaIleValGlnThrLeuValAsnSerValAsnSerLysIleProLysAlaCys | 360 | | | |
| Db | 1344 | AATCATGCCATTGTCAGACGTTGGTCACTCTGTAACTCTAAGATTCCTAAGGCATGC | 1403 | | | |
| Qy | 361 | CysValProThrGlnLeuSerAlaIleSerMetLeuTyrLeuAspGluAsnGluLysVal | 380 | | | |
| Db | 1404 | TGTGTCGCCAGACAACTCAGTGCTATCTCGATGCTGTACCTTCAGCAGAGAATGAAAGGTT | 1463 | | | |
| Qy | 381 | ValLeuLysAsnTyrGlnAspMetValValGluGlyCysGlyCysArg | 396 | | | |
| Db | 1464 | GTATTAAAGAACTATCAGACATGTTGTGGAGGGTTGTGGGTGTCGC | 1511 | | | |
| RESULT 6 | | | | | | |
| AX775087 | | | | | | |
| LOCUS | AX775087 1547 bp DNA linear PAT 09-JUL-2003 | | | | | |
| DEFINITION | Sequence 403 from Patent WO03038129. | | | | | |
| ACCESSION | AX775087 | | | | | |
| VERSION | AX775087.1 GI:32486603 | | | | | |
| KEYWORDS | | | | | | |
| SOURCE | Homo sapiens (human) | | | | | |
| ORGANISM | Homo sapiens | | | | | |
| Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | | | | |
| Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; | | | | | | |
| Hominidae; Homo. | | | | | | |
| REFERENCE | 1. | | | | | |
| AUTHORS | Raponi, M. | | | | | |
| TITLE | Methods for assessing and treating leukemia | | | | | |
| JOURNAL | Patent: WO 03038129-A 403 08-MAY-2003; | | | | | |
| Ortho-Clinical Diagnostics, Inc. (US) | | | | | | |
| FEATURES | Location/Qualifiers | | | | | |
| source | 1..1547 | | | | | |
| /organism="Homo sapiens" | | | | | | |
| /mol_type="unassigned DNA" | | | | | | |
| /db_xref="taxon:9606" | | | | | | |
| ORIGIN | | | | | | |
| Alignment Scores: | | | | | | |
| Pred. No.: | 1,846-135 | Length: | 1547 | | | |
| Score: | 2098.00 | Matches: | 396 | | | |
| Percent Similarity: | 100.00% | Conservative: | 0 | | | |
| Best Local Similarity: | 100.00% | Mismatches: | 0 | | | |

```

Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-10-801-648-2 (1-396) x AX775087 (1-1547)

Qy 1 MetValAlaGlyThrArgCysLeuLeuAlaLeuLeuProGlnValLeuLeuGlyGly 20
Db 324 ATGGTGGCGGACCCCGCTGCTCTTCTAGCGTGTGCTTCCCGAGTCTCTCTGGGCGG 383
Qy 21 AlaAlaGlyLeuValProGluLeuGlyArgArgLysPheAlaAlaLaSerSerGlyArg 40
Db 384 GCGGCTGGCCCTCGTTCCGAGCTGGCGCGCAGGAAGTTCCGCGCGGCGTCTCGCGCGCG 443
Qy 41 ProSerSerGlnProSerAspGluValLeuSerGluPheGluLeuArgLeuLeuSerMet 60
Db 444 CCCTCATCCCCAGCCCTCTGACGAGGTCTGACGAGTTCGAGTTCGCGCTGCTCAGCATG 503
Qy 61 PheGlyLeuLysGlnArgProThrProSerArgAspAlaValProProTyMetLeu 80
Db 504 TTCGGCTGAACAGAGACCCACCCCGCAGCAGGACGCCGTGGTGGCCCCCTACATGCTA 563
Qy 81 AspLeuTyArgArgHisSerGlyGlnProGlySerProAlaProAspHisArgLeuGlu 100
Db 564 GACCTGTATCGCAGCACTCAGGTTCAGCGCGGCTCACCGCGCCAGACACCGGTGGAG 623
Qy 101 ArgAlaLaSerArgAlaAsnThrValArgSerPheHisHisGluGluSerLeuGluGlu 120
Db 624 AGGGCAGCAGCCCGCAGCAACACACTGTGCGCAGCTTCACCAATGAAGAACTCTTCGAAGA 683
Qy 121 LeuProGluThrSerGlyLysThrThrArgArgPhePheAsnLeuSerSerIlePro 140
Db 684 CTACAGAAACGAGTGGGAAACACACCGGAGATCTCTTAAATTAAGTTCATATCCCC 743
Qy 141 ThrGluGluPheIleThrSerAlaGluLeuGlnValPheArgGluGlnMetGlnAspAla 160
Db 744 ACGGAGGAGTTATCACCTCAGCAGAGCTTCAGGTTTCCGAGAACAGATCAAGATGCT 803
Qy 161 LeuGlyAsnAsnSerSerPheHisHisArgIleAsnIleTyGluIleLysProAla 180
Db 804 TTAGAAACAAATAGCAGTTCCATCACCAGAAATTAATATTATGAATAATCATAAACCTGCA 863
Qy 181 ThrAlaAsnSerLysPheProValThrArgLeuLeuAspThrArgLeuValAsnGlnAsn 200
Db 864 ACAGCCAACTCGAAATTCCTCGTACCAGACTTTTGGACACACAGTGGTGAATCAGAT 923
Qy 201 AlaSerArgTrpGluSerPheAspValThrProAlaValMetArgTrpThrAlaGlnGly 220
Db 924 GCAAGCAGGTGGGAAAGTTTGTATGTACACCCCGCTGTGATGCGGTGACCTGCACAGGA 983
Qy 221 HisAlaAsnHisGlyPheValValGluValAlaHisLeuGluGluLysGlnGlyValSer 240
Db 984 CACGCCAACCAACATGATTCGTGGTGAAGTGGCCCACTTGGAGGAGAAACAGGTTGTCTCC 1043
Qy 241 LysArgHisValArgIleSerArgSerLeuHisGlnAspGluHisSerTrpSerGlnIle 260
Db 1044 AAGAGACATGTTAGATAAGCAGTCTTTGACCAAGATGACACAGCTGTGTACAGATA 1103
Qy 261 ArgProLeuLeuValThrPheGlyHisAspGlyLysGlyHisProLeuHisLysArgGlu 280
Db 1104 AGGCCATTTGCTAGTAACCTTTTGGCCATGATGGAAGAGGCACTCTCTCCACAAAGAGAA 1163
Qy 281 LysArgGlnAlaLysHisLysGluArgLysArgLeuLysSerSerCysLysArgHisPro 300
Db 1164 AAACGTCAAGCCAAACACAAACAGCGGAAACGCTTAAAGTCCAGCTGTAAAGACACCCCT 1223
Qy 301 LeuTyValAspPheSerAspValGlyTrpAsnAspTrpIleValAlaProProGlyTyTr 320
Db 1224 TTGTACGTGGACTTCAGTGAAGTGGGTGGAAATGACTGGATTTGGCTTCCCCCGGGGTAT 1283
Qy 321 HisAlaPheTyCysHisGlyGluCysProPheProLeuAlaAspHisLeuAsnSerThr 340
Db 1284 CACGCCCTTTACTGCGCAGGAGATGCCCTTTTCTCTGGCTGATCATCTCAACTCCACT 1343

```

341 AsnHisAlaIleValGlnThrLeuValAsnSerValAsnSerLysLysIleProLysAlaCys 360
1344 ATCATGCCATTGTTTCAGACGTGGTCACTCTGTTAACTCTAGATTCCTTAAGCATGC 1403
361 CysValProThrGluLeuSerAlaIleSerMetLeuTyTrLeuAspGluAsnGluLysVal 380
1404 TGTGTCCCGACAGAACTCAGTGCTATCTCGATGCTGTACCTTGACGAGATGAAGAAGTT 1463
381 ValLeuLysAsnTyTrGlnAspMetValValGluGlyCysGlyCysArg 396
1464 GTATTAAAGAACTATCAGGACATGTTGTGGAGGTTGTGGTGTCTGC 1511

RESULT 7
HUMBMP2A 1547 bp mRNA linear PRI 31-OCT-1994
LOCUS Human bone morphogenetic protein 2A (BMP-2A) mRNA.
DEFINITION M22489
ACCESSION M22489
VERSION 1
KEYWORDS bone morphogenetic protein.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (sites)
AUTHORS Wozney,J.M., Rosen,V., Celeste,A.J., Mitsock,L.M., Whitters,M.J.,
Kriz,R.W., Hewick,R.M. and Wang,E.A.
TITLE Novel regulators of bone formation: molecular clones and activities
JOURNAL Science 242 (4885), 1528-1534 (1988)
PUBMED 3201241
REFERENCE 2 (bases 1 to 1547)
AUTHORS Wozney,J.M., Rosen,V., Celeste,A.J., Mitsock,L.M., Whitters,M.J.,
Kriz,R.W., Hewick,R.M. and Wang,E.A.
JOURNAL Unpublished (1989)
COMMENT Original source text: Human osteosarcoma cell line U-2 OS, cDNA to
mRNA, clone hBMP-2A.
[1] sites.
Draft entry by and computer readable copy of sequence [1] kindly
submitted by R.W. Kriz 10-FEB-1989.

FEATURES
source
1. .1547
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/map="20"
gene
1. .1547
/gene="BMP2"
324. .1514
/notes="bone morphogenetic protein 2A"
/codon_start=1
/protein_id="AAA51834.1"
/db_xref="GI:179502"
/db_xref="GDB:G00-125-204"
/tranlations="MVAGTRCLALLPVLQVLLGGAAGLVPGLRRKFAAASSGRPSQ
PSDEVSEFELRLSMPEGLKORPSPSDAVVPVMDLYRHSQPGSPADPHLELA
ASRANTVSRFHHEESLEELPETSCKTRRFFNLSSIPTEFTISALQVREQMDA
LGNSSPHHINIYELIKPATANSKPPVTRLLDRLVNQNASWESFDVTPAVNRWTA
QKHAHGFVVEVAHLEKQSVKRHYRISRLHQDEHSWSQIRPLLVTFHGDGKHPL
HKEKRAKHQRKRLKSSCKRHPLYVDFSDGVNDWIVAPPGHYFCHGECFPFLA
DHLNSTHAIQTLLVNSVNSKIPKACCVPTLSAISMLYLDENEKVVLYKNVQDMVVEG
CGCR"

ORIGIN
Alignment Scores:
Pred. No.: 1,84e-135 Length: 1547
Score: 2098.00 Matches: 396
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 8 Gaps: 0
US-10-801-648-2 (1-396) x HUMBMP2A (1-1547)

QY 1 MetValAlaGlyThrArgCysLeuLeuAlaLeuLeuLeuProGlnValLeuLeuGlyGly 20
 Db 324 ATGTGGCGCGGACCGCTGCTTCTAGCTTGTCTTCTCCCGAGTCTCTCTGGCGCGC 383
 QY 21 AlaAlaGlyLeuValProGlnLeuGlyArgArgLysPheAlaAlaSerSerGlyArg 40
 Db 384 GCGGCTGGCTGCTTCCGAGCTGGCGCGCAGGAGTTCCGGCGCGCTGCTGGCGCGC 443
 QY 41 ProSerSerGlnProSerAspGluValLeuSerGluPheGluLeuArgLeuLeuSerMet 60
 Db 444 CCTCATCCAGCCCTCTGACAGAGTCTGACGAGTTCGAGTTCGAGTTCGAGTTCGAGT 503
 QY 61 PheGlyLeuLysGlnArgProThrProSerArgAspAlaValProProProThrMetLeu 80
 Db 504 TTGGCGCTGGAACAGAGACCCACCCAGCAGGAGCGCGTGGTGGTGGTGGTGGTGGT 563
 QY 81 AspLeuTyrArgArgHisSerGlyGlnProGlySerProAlaProAspHisArgLeuGlu 100
 Db 564 GACCTGTATCGCAGGCACTCAGGTCCAGCGCGCTCAGCGCGCGCCAGACCCAGCGGTGGAG 623
 QY 101 ArgAlaAlaSerArgAlaAsnThrValArgSerPheHisGluGluSerLeuGluGlu 120
 Db 624 AGGGCAGCGCAGCGCAGCAACTGTCGCGCAGTTCACCATGAAGAATCTTTTGAAGAA 683
 QY 121 LeuProGluThrSerGlyLysThrThrArgArgPhePheAsnLeuSerSerilePro 140
 Db 684 CTACAGAAACGAGTGGGAAACACACCGGAGATCTCTCTTTAAATTTAAGTTCTATATCCC 743
 QY 141 ThrGluGluPheIleThrSerAlaGluLeuGlnValPheArgGluGlnMetGlnAspAla 160
 Db 744 ACGGAGGAGTTTATCACCTCAGCAGAGCTTCAAGTTTCCGAGAACAGATGCAAGTGT 803
 QY 161 LeuGlyAsnAsnSerSerPheHisArgIleAsnIleTyrGluIleIleLysProAla 180
 Db 804 TTAGGAAACAAATAGCAGTTTCCATCACCGAATTAATATTATGAATCATATAAACCCTGCA 863
 QY 181 ThrAlaAsnSerLysPheProValThrArgLeuLeuAspThrArgLeuValAsnGlnAsn 200
 Db 864 ACAGCCAACTCGAAATTCCTCCGTGACAGACTTTTGGACACAGGTTGGTGAATCAGAA 923
 QY 201 AlaSerArgTyrGluSerPheAspValThrProAlaValMetArgTyrThrAlaGlnGly 220
 Db 924 GCAACGAGTGGGAAAGTTTGTATGTACCCCGCTGTGTATGCGTGGACTGCACAGGA 983
 QY 221 HisAlaAsnHisGlyPheValValGluValAlaHisLeuGluGluLysGlnGlyValSer 240
 Db 984 CACGCCAACCATGGATTCGTGGTGAAGTGGCCACTTGGAGGAGAAACAAGGTGTCTCC 1043
 QY 241 LysArgHisValArgIleSerArgSerLeuHisGlnAspGluHisSerTyrSerGlnIle 260
 Db 1044 AAGACACATGTTAGGATTAAGCAGGTCTTTGGACCAAGATGAACACAGCTGGTGCACAGATA 1103
 QY 261 ArgProLeuLeuValThrPheGlyHisAspGlyLysGlyHisProLeuHisLysArgGlu 280
 Db 1104 AGGCCATGCTAGTAATCTTTTGGCCATGATGAAAGGCGATCTCTCCACAAAGAGANA 1163
 QY 281 LysArgGlnAlaLysHisLysGlnArgLysArgLeuLysSerSerCysLysArgHisPro 300
 Db 1164 AAACGTCAGCCAAACACACACAGCGGAAACGCCCTTAAGTCCAGCTGTAAGAGACACCT 1223
 QY 301 LeuTyrValAspPheSerAspValGlyTyrAsnAspTyrIleValAlaProProGlyTyr 320
 Db 1224 TTGTAGCTGGACTTCAGTGACGTGGGTGGAAATGATGAGTGGTGGTGGTGGTGGTGGT 1283
 QY 321 HisAlaPheTyrCysHisGlyGluCysProPheProLeuAlaAspHisLeuAsnSerThr 340
 Db 1284 CAGGCTTTTACTGCGCAGGAGAAATGCCCTTTTCTCTGGCTGATCACTGAACTCCACT 1343
 QY 341 AsnHisAlaIleValGlnThrLeuValAsnSerValAsnSerLysIleProLysAlaCys 360
 Db 1344 ATCATGCCATGTTTCAGAGGTTGGTCACTCTGTGTAATCTCTAAGATCTCTAAGGCATGC 1403

QY 361 CysValProThrGluLeuSerAlaIleSerMetLeuTyrLeuAspGluAsnGluLysVal 380
 Db 1404 TGTGTCCGACAGAACTCAGTGTCTATCTCGATCTGTGTACCTTGACGAGATGAAGGTT 1463
 QY 381 ValLeuLysAsnTyrGlnAspMetValValGluGlyCysGlyCysArg 396
 Db 1464 GTATTAAAGAACTATCAGGACATGTTGTGGAGGTTGTGGGTGTGCG 1511
 RESULT 8
 CS038212 1581 bp DNA linear PAT 10-MAR-2005
 LOCUS Sequence 10 from Patent WO2005016368.
 DEFINITION CS038212
 ACCESSION CS038212
 VERSION CS038212.1 GI:60734760
 KEYWORDS Homo sapiens (human)
 SOURCE
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Homo.
 REFERENCE
 1 Sfeir,C., Campbell,P., Jadowiec,J.A. and Kumta,P.
 TITLE Method of inducing biomineralization, method of inducing bone
 regeneration and methods related thereof
 JOURNAL Patent: WO 2005016368-A 10 24-FEB-2005;
 University of Pittsburgh of the Commonwealth System of Hi gher
 Education (US); Carnegie Mellon University (US)
 FEATURES
 Location/Qualifiers
 source 1..1581
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"
 ORIGIN
 Alignment Scores:
 Pred. No.: 1.89e-135 Length: 1581
 Score: 2098.00 Matches: 396
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0
 US-10-801-648-2 (1-396) x CS038212 (1-1581)
 QY 1 MetValAlaGlyThrArgCysLeuLeuAlaLeuLeuLeuProGlnValLeuLeuGlyGly 20
 Db 324 ATGTGGCGCGGACCGCTGCTTCTAGCTTGTCTTCTCCCGAGTCTCTCTGGCGCGC 383
 QY 21 AlaAlaGlyLeuValProGlnLeuGlyArgArgLysPheAlaAlaSerSerGlyArg 40
 Db 384 GCGGCTGGCTGCTTCCGAGCTGGCGCGCAGGAGTTCCGGCGCGCTGCTGGCGCGC 443
 QY 41 ProSerSerGlnProSerAspGluValLeuSerGluPheGluLeuArgLeuLeuSerMet 60
 Db 444 CCTCATCCAGCCCTCTGACAGAGTCTGACGAGTTCGAGTTCGAGTTCGAGTTCGAGT 503
 QY 61 PheGlyLeuLysGlnArgProThrProSerArgAspAlaValProProProThrMetLeu 80
 Db 504 TTGGCGCTGGAACAGAGACCCACCCAGCAGGAGCGCGTGGTGGTGGTGGTGGTGGT 563
 QY 81 AspLeuTyrArgArgHisSerGlyGlnProGlySerProAlaProAspHisArgLeuGlu 100
 Db 564 GACCTGTATCGCAGGCACTCAGGTCCAGCGCGCTCAGCGCGCGCCAGACCCAGCGGTGGAG 623
 QY 101 ArgAlaAlaSerArgAlaAsnThrValArgSerPheHisGluGluSerLeuGluGlu 120
 Db 624 AGGGCAGCGCAGCGCAGCAACTGTCGCGCAGTTCACCATGAAGAATCTTTTGAAGAA 683
 QY 121 LeuProGluThrSerGlyLysThrThrArgArgPhePheAsnLeuSerSerilePro 140
 Db 684 CTACAGAAACGAGTGGGAAACACACCGGAGATCTCTCTTTAAATTTAAGTTCTATATCCC 743
 QY 141 ThrGluGluPheIleThrSerAlaGluLeuGlnValPheArgGluGlnMetGlnAspAla 160


```
|||||
744  ACGGAGGAGTTTATCACCTCAGCAGAGCTTCAGGTTTTCCGAGAACAGATCCAGATGCT 803
Qy 161  LeuGlyAenAenSerSerPheHisHisArgIleAenIleTyrGluIleIleLysProAla 180
Db 804  TTAGGAAACAATAGCAGTTTCCATCACCGAATTAATATTTATGAATCATAAACCTGCA 863
Qy 181  ThrAlaAenSerLysPheProValThrArgLeuLeuAenPheThrArgLeuValAenGlnAen 200
Db 864  ACAGCCAACTCGAAATTCCTCGTGACCCAGACTTTTGGACACAGGTTGGTGAATCAGAA 923
Qy 201  AlaSerArgTrpGluSerPheAspValThrProAlaValMetArgTrpThrAlaGlnGly 220
Db 924  GCAAGCAGTGGGAAAGTTTTGATGTCAACCCCGCTGTGATGCGTGGAGTGCACAGGA 983
Qy 221  HisAlaAenHisGlyPheValValGluValAlaHisLeuGluGluLysGlnGlyValSer 240
Db 984  CACGCCAACCATGGATTCGTGTGGAGTGGCCCACTTTGGAGGAGAAACAGGTGTCTCC 1043
Qy 241  LysArgHisValArgIleSerArgSerLeuHisGlnAenPheGluHisSerTrpSerGlnIle 260
Db 1044  AAGAGACATGTAGATTAAGCAGGTCTTTGACCAGATGAACACAGCTGGTGTACAGATA 1103
Qy 261  ArgProLeuLeuValThrPheGlyHisAspGlyLysGlyHisProLeuHisLysArgGlu 280
Db 1104  AGGCCATTGCTAGTAACCTTTGGCCATGATCGAAAGGCACTCTCTCCAAAGAGAA 1163
Qy 281  LysArgGlnAlaLysHisLysGlnArgLysArgLeuLysSerSerCysLysArgHisPro 300
Db 1164  AAAGCTCAAGCCAAACACAAACAGCGGAAACGCCTTAAGTCCAGCTGTAAAGACACCCCT 1223
Qy 301  LeuTyrValAenPheSerAspValGlyTrpAenAspTrpIleValAlaProProGlyTyr 320
Db 1224  TTGTACGTGGACTTCAGTACGTGGGTGGAAATGACTGATGTGGCTTCCCGGGGTAT 1283
Qy 321  HisAlaPheTyrCysHisGlyGluCysProPheProLeuAlaAspHisLeuAenSerThr 340
Db 1284  CACGCCITTTACTGCCAGGAGATGCCCTTTTCTCTGGCTGATCATCTGAACTCCACT 1343
Qy 341  AsnHisAlaIleValGlnThrLeuValAenSerValAenSerLysIleProLysAlaCys 360
Db 1344  AATCATGCCATTGTTGACAGCTTGGTCAACTCTGTAACTCTAAGATTCTTAAGGCATGC 1403
Qy 361  CysValProThrGluLeuSerAlaIleSerMetLeuTyrLeuAspGluAenGluLysVal 380
Db 1404  TGTGTCCCGACAGAACTCAGTGCTATCTCGATGCTGTACCTTTGACGAGAAATGAAGGTT 1463
Qy 381  ValLeuLysAenTyrGlnAspMetValValGluGlyCysGlyCysArg 396
Db 1464  GTATTAAAGAACTATCAGGACATGTTGTGGAGGGTTGTGGGTCTCGC 1511
```

RESULT 9

```
AR157708
LOCUS AR157708 1607 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 3 from patent US 6245889.
ACCESSION AR157708
VERSION AR157708.1 GI:16218701
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
```

REFERENCE 1 (bases 1 to 1607)

Wang, B.A., Wozney, J.M. and Rosen, V.A.

BMP-4 products

Patent: US 6245889-A 3 12-JUN-2001;

Location/Qualifiers

1. .1607

/organism="unknown"

/mol_type="unassigned DNA"

ORIGIN

```
Alignment Scores:
Pred. No.: 1.93e-135 Length: 1607
```

Score: 2098.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 6
DB: 6

Matches: 396

Conservative: 0

Mismatch: 0

Indels: 0

Gaps: 0

US-10-801-648-2 (1-396) x AR157708 (1-1607)

```
Qy 1  MetValAlaGlyThrArgCysLeuLeuAlaIleLeuLeuProGlnValLeuLeuGlyGly 20
Db 356  ATGTGTGCGCGGAGACCCGCTGTCTTAGCGTTGCTGTCTCCAGGTCTCTCTCGGGGGC 415
Qy 21  AlaAlaGlyLeuValProGluLeuGlyArgArgLysPheAlaAlaLysSerSerGlyArg 40
Db 416  CGGCTCGCTCGTTCTCGGAGCTGGCCCGCAGGAAGTTCGCGGGCGGTGCTCGGGGGC 475
Qy 41  ProSerSerGlnProSerAspGluValLeuSerGluPheGluLeuArgLeuLeuSerMet 60
Db 476  CCCTCATCCCGAGCCCTCTGACGAGTCTCTGAGGAGTTCGAGTTGCGGCTGCTCAGCATG 535
Qy 61  PheGlyLeuLysGlnArgProThrProSerArgAspAlaValValProProTyrMetLeu 80
Db 536  TTCGGCTGAAACAGAGACACCCCGCAGCAGGAGCGCGTGTGTCGCCCTCATCATGCTA 595
Qy 81  AspLeuTyrArgArgHisSerGlyGlnProGlySerProAlaProAspHisArgLeuGlu 100
Db 596  GACCTGTATCGCAGGCACTCAGGTACCGGGCTCACCCGCCCGCAGACCACCGGTTGGAG 655
Qy 101  ArgAlaAlaSerArgAlaAenThrValArgSerPheHisHisGluGluSerLeuGluGlu 120
Db 656  AGGCGACCGACCGGAGCAACACTGTGCGCAGCTTCCACCATGAAGATCTTTGGAGAA 715
Qy 121  LeuProGluThrSerGlyLysThrThrArgArgPhePheAenLeuSerSerIlePro 140
Db 716  CTACCAAAACGAGTGGGAAACAAACCCGAGATTCCTCTTTAATTTAAGTCTATCCCC 775
Qy 141  ThrGluGluPheIleThrSerAlaGluLeuGluValPheArgGluGlnMetGlnAspAla 160
Db 776  ACGGAGAGTTTATCACCTCAGCAGAGCTTCAGGTTTTCCGAGAAACAGATGCAAGATGCT 835
Qy 161  LeuGlyAenAenSerSerPheHisHisArgIleAenIleTyrGluIleIleLysProAla 180
Db 836  TTAGGAAACAATAGCAGTTTCCATCACCGAATTAATATTTATGAATCATAAACCTGCA 895
Qy 181  ThrAlaAenSerLysPheProValThrArgLeuLeuAspThrArgLeuValAenGlnAen 200
Db 896  ACAGCCAACTCGAAATTCGCCGTGACCCAGACTTTTGGACACCCAGGTTGGTGAATCAGAAT 955
Qy 201  AlaSerArgTrpGluSerPheAspValThrProAlaValMetArgTrpThrAlaGlnGly 220
Db 956  GCAAGCAGTGGGAAAGTTTTGATGTCAACCCCGCTGTGATGCGGTGGACTGCAAGGGA 1015
Qy 221  HisAlaAenHisGlyPheValValGluValAlaHisLeuGluLysGlnGlyValSer 240
Db 1016  CACGCCAACCATGGATTCGTGTGGAGTGGCCCACTTTGGAGGAGAAACAGGTTGCTCC 1075
Qy 241  LysArgHisValArgIleSerArgSerLeuHisGlnAspGluHisSerTrpSerGlnIle 260
Db 1076  AAGAGACATGTAGGATAAGCAGTCTTTGACCAAGATGAACACAGCTGCTGTACAGATA 1135
Qy 261  ArgProLeuLeuValThrPheGlyHisAspGlyGlyGlyHisProLeuHisLysArgGlu 280
Db 1136  AGGCCATTGCTAGTAACCTTTTGGCCATGATGGAAGGAGGATCTCTCTCCAAAGAGAA 1195
Qy 281  LysArgGlnAlaLysHisLysGlnArgLysArgLeuLysSerSerCysLysArgHisPro 300
Db 1196  AAACGTCAAGCCAAACACAAACAGCGGAAACGCCTTAAGTCCAGCTGTAAAGACACCT 1255
Qy 301  LeuTyrValAspPheSerAspValGlyTrpAenAspTrpIleValAlaProProGlyTyr 320
Db 1256  TTGTACGTGACTTCAGTACGTGGGTGGAAATGACTGGATTTGTGGCTTCCCGGGGTAT 1315
Qy 321  HisAlaPheTyrCysHisGlyGluCysProPheProLeuAlaAspHisLeuAenSerThr 340
```



```
Db 1316 CACGCGCTTTACTGCGCAGAGATGCCCTTTCTCTGGCTGATCATCTGAATCCACT 1375
Qy 341 AenHisAlaIleValGlnThrLeuValAenSerValAenSerIleProLysAlaCys 360
Db 1376 AATCATGCCATGTTTCAGACGTTGCTCAACTCTGTAACTCTAAAGATTCCCTAAGGCATGC 1435
Qy 361 CysValProThrGluLeuSerAlaIleSerMetLeuTyrLeuAenGluAenGluLysVal 380
Db 1436 TGTGTCCCGCAGCACTCAGTCTATCTCGATCTGTACCTGTACCTGACGAGATGAAAGGTT 1495
Qy 381 ValLeuLysAenTyrGlnAenMetValValGluGlyCysGlyCysArg 396
Db 1496 GTATTAAAGAACTATCAGACATGTTGTGGAGGTTGTGGGTGTGCG 1543

RESULT 10
LOCUS AR447458 3526 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 11 from patent US 6673549.
ACCESSION AR447458
VERSION AR447458.1 GI:42675782
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 3526)
AUTHORS Furness, L.M. and Buchbinder, J.L.
TITLE Genes expressed in C3A liver cell cultures treated with steroids
JOURNAL Patent: US 6673549-A 11 06-JAN-2004;
Incyte Corporation; Palo Alto, CA
FEATURES
source
1..3526
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Alignment Scores:
Pred. No.: 5e-135 Length: 3526
Score: 2098.00 Matches: 396
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-801-648-2 (1-396) x AR447458 (1-3526)
Qy 1 MetValAlaGlyThrArgCysLeuLeuAlaLeuLeuProGlnValLeuLeuGly 20
Db 1180 ATGGTGGCGGAGCCGCTGTCTTAGCGTTGCTCTTCCCGAGTCTCTCCGCGCGC 1239
Qy 21 AlaAlaGlyLeuValProGluLeuGlyArgArgLysPheAlaAlaSerSerGlyArg 40
Db 1240 GCGGCTGGCTCGTTCGCGAGCTGGCGCGCAGAAAGTTTCGCGCGCGCGTCTGGCGCGC 1299
Qy 41 ProSerSerGlnProSerAspGluValLeuSerGluPheGluLeuArgLeuLeuSerMet 60
Db 1300 CCTCATCCAGCCCTCTGACGAGGTTCTGACGAGGTTGAGTTCGAGTTCGAGTTCGAGT 1359
Qy 61 PheGlyLeuLysGlnArgProThrProSerArgAspAlaValProProTyrMetLeu 80
Db 1360 TTCCGCGCTGAACACAGACAGACCCACCCCGCAGCGAGCGCGTGGTGGTGGTGGTGA 1419
Qy 81 AspLeuTyrArgArgHisSerGlnProGlySerProAlaProAspHisArgLeuGlu 100
Db 1420 GACCTGTATCGCAGGCACTCAGGTTCAGCGCGGCTCACCGCGCCAGACACCGGTTGGAG 1479
Qy 101 ArgAlaAlaSerArgAlaAenThrValArgSerPheHisHisGluGluSerLeuGlu 120
Db 1480 AGGCGAGCCGAGCGAGCCCAACTGTGCGCAGCTTCCACATGAGAAATCTTTGGAGNA 1539
Qy 121 LeuProGluThrSerGlyLysThrThrArgArgPhePheAenLeuSerIlePro 140
Db 1540 CTACCAGAAACGAGTGGGAAACCAACCCGAGATCTCTTTAAATTTAAGTTCTATCCCC 1599
```

```
Qy 141 ThrGluGluPheIleThrSerAlaGluLeuGlnValPheArgGluGlnMetGlnAspAla 160
Db 1600 ACGGAGGAGTTTATCACCCTCAGCAGAGCTTCAGGTTTCCGAGAACAGATCAAGATGCT 1659
Qy 161 LeuGlyAenAenSerSerPheHisHisArgIleAenIleTyrGluIleIleLysProAla 180
Db 1660 TTAGAAACAATAGCAGTTTCCATCACCGAAATTAATATTTATGAATCATAAACCTGCA 1719
Qy 181 ThrAlaAenSerLysPheProValThrArgLeuLeuAenThrArgLeuValAenGlnAen 200
Db 1720 ACAGCAACTCGAAATTCCTCCGTCACCAAGCTTTTGGACACAGGTTTGTGAATCAGAA 1779
Qy 201 AlaSerArgTTPGluSerPheAspValThrProAlaValMetArgTyrThrAlaGlnGly 220
Db 1780 GCAAGCAGGTGGGAAAGTTTGTATGTACCCCGCTGTGATGCGGTGGACTGCACAGGA 1839
Qy 221 HisAlaAenHisGlyPheValValGluValAlaHisLeuGluGluLysGlnGlyValSer 240
Db 1840 CACGCCAACCATGGAATTCGTGTGAGAGTGCCCACTTTGGAGGAGAAACNAGGTGTCTCC 1899
Qy 241 LysArgHisValArgIleSerArgSerLeuHisGlnAenGluHisSerTyrSerGlnIle 260
Db 1900 AAGAGACATGTAGGATAAGCAGGTCCTTTCACCAAGATGAACACAGCTGTGCACAGTA 1959
Qy 261 ArgProLeuLeuValThrPheGlyHisAspGlyLysGlyHisProLeuHisLysArgGlu 280
Db 1960 AGGCCATGTCTAGTAACCTTTTGGCCATGATGGAAAGGCGCATCTCTCCACAAAAGAGAA 2019
Qy 281 LysArgGlnAlaLysHisLysGlnArgLysArgLeuLysSerSerCysLysArgHisPro 300
Db 2020 AAAGCTCAAGCCAAACACAAACAGCGGAAACGCTTAAAGTCCAGCTGTAAAGAGACACCT 2079
Qy 301 LeuTyrValAspPheSerAspValGlyTyrPheAenAspTyrIleValAlaProProGlyTyr 320
Db 2080 TTGTACGTGGACTTCAGTGACGTGGGTGGAAATGACTGGATTTGGCTCCCGGGGTAT 2139
Qy 321 HisAlaPheTyrCysHisGlyGluCysProPheProLeuAlaAspHisLeuAenSerThr 340
Db 2140 CACGCTTTTACTGCCAGGAGATGCCCTTTTCTCTGGCTGATCATCTGAATCCACT 2199
Qy 341 AenHisAlaIleValGlnThrLeuValAenSerValAenSerLysIleProLysAlaCys 360
Db 2200 AATCATGCCATTTGTTTCAGACGTTGGTCAACTCTGTAACTCTTAAGTTCCTAAGGCATGC 2259
Qy 361 CysValProThrGluLeuSerAlaIleSerMetLeuTyrLeuAspGluAenGluLysVal 380
Db 2260 TGTGTCCCGCAGCAACTCAGTCTATCTCGATGCTGTACCTTTCAGCAGAAATGAAAGGTT 2319
Qy 381 ValLeuLysAenTyrGlnAspMetValValGluGlyCysGlyCysArg 396
Db 2320 GTATTAAAGAACTATCAGACATGTTGTGGAGGTTGTGGGTGTGCG 2367

RESULT 11
LOCUS AR031482 1607 bp DNA linear PAT 29-SRP-1999
DEFINITION Sequence 1 from patent US 5866364.
ACCESSION AR031482
VERSION AR031482.1 GI:5945771
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1607)
AUTHORS Israel, D. and Wolfman, N.M.
TITLE Recombinant bone morphogenetic protein heterodimers
JOURNAL Patent: US 5866364-A 1 02-FEB-1999;
FEATURES
1..1607
Location/Qualifiers
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
```

Alignment Scores:

```
Pred. No.: 3,11e-135 Length: 1607
Score: 2095.00 Matches: 395
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.75% Mismatches: 0
Query Match: 99.86% Indels: 0
DB: 6 Gaps: 0

US-10-801-648-2 (1-396) x AR031482 (1-1607)

Qy 1 MetValAlaGlyThrArgCysLeuLeuAlaLeuLeuProGlnValLeuLeuGlyGly 20
Db 356 ATGGTGGCGGAGACCGCTGTCTTAGCGTTGCTCTCCAGGTCTCTCTGGCGGC 415
Qy 21 AlaAlaGlyLeuValProGluLeuGlyArgArgLysPheAlaAlaAspSerGlyArg 40
Db 416 GCGCTGCGCTCGTTCCGAGCTGGCGGAGTTCGGCGGCGTCTCGCGGCGC 475
Qy 41 ProSerSerGlnProSerAspGluValLeuSerGluPheGluLeuArgLeuSerMet 60
Db 476 CCTCATCCAGCCCTCTGACGAGTCTGAGCGAGTTCGAGTTGCGGTGCTCAGCATG 535
Qy 61 PheGlyLeuLysGlnArgProThrProSerArgAspAlaValValProProTyrMetLeu 80
Db 536 TTCGGCTGAAACAGAGACCCACCCAGCAGGAGCGCGTGTGCCCTCATGCTA 595
Qy 81 AspLeuTyrArgArgHisSerGlyGlnProGlySerProAlaProAspHisArgLeuGlu 100
Db 596 GACCTGTATCCAGGCACTCAGGTGAGCGGGCTCACCCGCCAGACCCACCGGTGGAG 655
Qy 101 ArgAlaAlaSerArgAlaAsnThrValArgSerPheHisHisGluGluSerLeuGluGlu 120
Db 656 AGGCGAGCCAGCCAGCCACACTGTGCGGAGCTTCACCATGAGATCTTTGGAGAA 715
Qy 121 LeuProGluThrSerGlyLysThrThrArgArgPhePheAsnLeuSerSerIlePro 140
Db 716 CTACCAGAAACGAGTGGGAAACAAACCGGAGATCTCTTTAATTTAAGTTCTATCCC 775
Qy 141 ThrGluGluPheIleThrSerAlaGluLeuGlnValPheArgGluGlnMetGlnAspAla 160
Db 776 ACGAGGAGGTTTATCACTCAGCAGAGCTTCAGGTTTCCGAGAACAGATGCAAGATGCT 835
Qy 161 LeuGlyAsnAsnSerSerPheHisArgIleAsnIleTyrGluIleLysProAla 180
Db 836 TTAGAAACATAGCAGTTTCATCACCAGATTTAATTTATGAAATCATAAACCTTGA 895
Qy 181 ThrAlaAsnSerLysPheProValThrArgLeuLeuAspThrArgLeuValAsnGlnAsn 200
Db 896 ACAGCAACTCGAAATTCCTCGTGACACAGACTTTTGGACACACAGGTTGGTGAATCAGA 955
Qy 201 AlaSerArgTyrGluSerPheAspValThrProAlaValMetArgTyrThrAlaGlnGly 220
Db 956 GCAAGCAGTGGGAAACTTTTGATGTCAACCCCGCTGTGATGCGGTGACTGTCACAGGA 1015
Qy 221 HisAlaAsnHisGlyPheValValAlaIleHisLeuGluLysGlnGlyValSer 240
Db 1016 CACGCCAACCATGATTCGTGTGAAGTGCCACCTTGAGAGAGAAACAAGGTGTCTCC 1075
Qy 241 LysArgHisValArgIleSerArgSerLeuHisGlnAspGluHisSerTyrSerGlnIle 260
Db 1076 AAGAGACATGTTAGGATAAGCAGGTCTTTTGACCAAGATGAACAGCTGGTTCACAGATA 1135
Qy 261 ArgProLeuLeuValThrPheGlyHisAspGlyLysGlyHisProLeuHisLysArgGlu 280
Db 1136 AGGCCATGTGTAGTAACCTTTTGGCCATGATGGAAGAGGCGATCTCTCCACAAAGAGAA 1195
Qy 281 LysArgGlnAlaLysHisLysGlnArgLysArgLeuLysSerSerCysLysArgHisPro 300
Db 1196 ANAGCTCAAGCCAAACAAACAGCGGAAACGCCCTTAAGTCAAGCTGTAAAGACACCCCT 1255
Qy 301 LeuTyrValAspPheSerAspValGlyTyrAsnAspTyrIleValAlaProProGlyTyr 320
Db 1256 TTGTACGTGGACTTCAGTGACGTGGGTGGAATGACTGATTTGTGGCTCCCCCGGGTAT 1315
```

```
Qy 321 HisAlaPheTyrCysHisGlyGluCysProPheProLeuAlaAspHisLeuAsnSerThr 340
Db 1316 CAGCCCTTTTACTGCCACGAGAAATGCCCTTTCTCTGGCTGATCATCTGAACCTCCACT 1375
Qy 341 AsnHisAlaIleValGlnThrLeuValAsnSerValAsnSerLysIleProLysAlaCys 360
Db 1376 AATCATGCCATTGTTTCAGAGCTTGGTCAACTCTGTTAACTCTAAGATTCTTAAGCATGC 1435
Qy 361 CysValProThrGluLeuSerAlaIleSerMetLeuTyrLeuAspGluAsnGluLysVal 380
Db 1436 TGTGTCCCGACAGAACTCAGTCTATCTCGATGCTGTACCTTGACGAGAAATGAAAGGTT 1495
Qy 381 ValLeuLysAsnTyrGlnAspMetValValGluGlyCysGlyCysArg 396
Db 1496 GTATTAAAGAACTATCAGGACATGGTTGTGGAGGTTGTGGGTGTCTGC 1543

RESULT 12
LOCUS AR130859 1607 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 1 from patent US 6190880.
ACCESSION AR130859
VERSION AR130859.1 GI:14119184
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1607)
AUTHORS Israel, D. and Wolfman, N.M.
TITLE Recombinant bone morphogenetic protein heterodimers, compositions
and methods of use
JOURNAL Patent: US 6190880-A 1 20-FEB-2001;
FEATURES Location/Qualifiers
source
1..1607
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Alignment Scores:
Pred. No.: 3,11e-135 Length: 1607
Score: 2095.00 Matches: 395
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.75% Mismatches: 0
Query Match: 99.86% Indels: 0
DB: 6 Gaps: 0

US-10-801-648-2 (1-396) x AR130859 (1-1607)

Qy 1 MetValAlaGlyThrArgCysLeuLeuAlaLeuLeuProGlnValLeuLeuGlyGly 20
Db 356 ATGGTGGCGGAGACCGCTGTCTTAGCGTTGCTCTCCAGGTCTCTCTGGCGGC 415
Qy 21 AlaAlaGlyLeuValProGluLeuGlyArgArgLysPheAlaAlaAspSerGlyArg 40
Db 416 GCGCTGCGCTCGTTCCGAGCTGGCGGAGTTCGGCGGCGTCTCGCGGCGC 475
Qy 41 ProSerSerGlnProSerAspGluValLeuSerGluPheGluLeuArgLeuSerMet 60
Db 476 CCTCATCCAGCCCTCTGACGAGTCTGAGCGAGTTCGAGTTGCGGTGCTCAGCATG 535
Qy 61 PheGlyLeuLysGlnArgProThrProSerArgAspAlaValValProProTyrMetLeu 80
Db 536 TTCGGCTGAAACAGAGACCCACCCAGCAGGAGCGCGTGTGCCCTCATGCTA 595
Qy 81 AspLeuTyrArgArgHisSerGlyGlnProGlySerProAlaProAspHisArgLeuGlu 100
Db 596 GACCTGTATCCAGGCACTCAGGTGAGCGGGCTCACCCGCCAGACCCACCGGTGGAG 655
Qy 101 ArgAlaAlaSerArgAlaAsnThrValArgSerPheHisHisGluGluSerLeuGluGlu 120
Db 656 AGGCGAGCCAGCCAGCCACACTGTGCGGAGCTTCACCATGAGATCTTTGGAGAA 715
Qy 121 LeuProGluThrSerGlyLysThrThrArgArgPhePheAsnLeuSerSerIlePro 140
```

```

Db      716 CTACAGAAACGAGTGGGAAACACACCGGAGATTCTCTTAATTTAAGTTCTATCCCC 775
Qy      141 ThrGluGluPheIleThrSerAlaGluLeuGlnValPheArgGluGlnMetGlnAspAla 160
Db      776 ACGGAGGAGTTTATCACTCCAGCAGAGCTTCAGGTTTCCGAGAACACATGCAAGATGCT 835
Qy      161 LeuGlyAsnAsnSerSerPheHisHisArgIleAsnIleTyrGluIleIleLysProAla 180
Db      836 TTAGGAAACATAGCAGTTTCCATCCCGAATTATATTTATGAATCATATAAACCTGCA 895
Qy      181 ThrAlaAsnSerLysPheProValThrArgLeuLeuAspThrArgLeuValAsnGlnAsn 200
Db      896 ACAGCCAACTCGAAATTCCTCCGTGACAGACTTTTGGACACAGGTTGGTGAATCAGAA 955
Qy      201 AlaSerArgTrpGluSerPheAspValThrProAlaValMetArgTrpThrAlaGlnGly 220
Db      956 GCAAGCAGTGGGAAACTTTTGTATGTCACTCCCGCTGTGATGCGGTGACTGCACAGGGA 1015
Qy      221 HisAlaAsnHisGlyPheValGluValAlaHisLeuGluGluLysGlnGlyValSer 240
Db      1016 CACGCCAACCATGGATTCTGTGTGAAGTGGCCACTTGGAGGAGAACAGAGTGTCTCC 1075
Qy      241 LysArgHisValArgIleSerArgSerLeuHisGlnAspGluHisSerTrpSerGlnIle 260
Db      1076 AAGACACATGTTAGGATAAGCAGGCTTTTGCACCAAGATGAACACAGCTGGTCCACAGA 1135
Qy      261 ArgProLeuLeuValThrPheGlyHisAspGlyLysGlyHisProLeuHisLysArgGlu 280
Db      1136 AGGCCATTGCTAGTAATCTTTGGCCATGATGGAAAGGGCATCTCTCCACAAAAGAGAA 1195
Qy      281 LysArgGlnAlaLysHisLysGlnArgLysArgGlyLysSerSerCysLysArgHisPro 300
Db      1196 AAACGTCAAGCCAAACACAAACGCGGAAACGCTTTAAGTCCAGCTGTGAAGACACCCCT 1255
Qy      301 LeuTyrValAspPheSerAspValGlyTrpAsnAspTrpIleValAlaProProGlyTyr 320
Db      1256 TTGTAGCTGGACTTCAGTGAGCTGGGGTGGATGACTGGATTGTGGCTCCCGCGGGTAT 1315
Qy      321 HisAlaPheTyrCysHisGlyGluCysProPheProLeuAlaAspHisLeuAsnSerThr 340
Db      1316 CACGCTCTTTACTGCCACGAGAAATGCCCTTTTCTCTGGCTGATCATCTGAACCTCACT 1375
Qy      341 AsnHisAlaIleValGlnThrLeuValAsnSerValAsnSerLysIleProLysAlaCys 360
Db      1376 AATCATGCCATGTTTCAGACGTGTGTCAACTCTGTAACTCTTAAGATCTTAAGCATGC 1435
Qy      361 CysValProThrGluLeuSerAlaIleSerMetLeuTyrLeuAspGluAsnGluLysVal 380
Db      1436 TGTGTCCCGACAGAACTCAGTCTATCTCGATGCTGTACTTGTACGAGAAATGAAAAGTT 1495
Qy      381 ValLeuLysAsnTyrGlnAspMetValValGluGlyCysGlyCysArg 396
Db      1496 GTATTAAAGAACTATCAGGACATGTTGTGGAGGGTGTGGGTGTGCG 1543

```

```

RESULT 13
AR353792
LOCUS   AR353792 1607 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 1 from patent US 6593109.
ACCESSION AR353792
VERSION   AR353792.1 GI:33759850
KEYWORDS
SOURCE   Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1607)
AUTHORS Israel D. and Wolfman, N.M.
TITILE Recombinant bone morphogenetic protein heterodimers, compositions
        and methods of use
JOURNAL Patent: US 6593109-A 1 15-JUL-2003;
        Genetics Institute, Inc.; Cambridge, MA;
        WOX; Location/Qualifiers
FEATURES

```

```

source 1. 1607
        /organism="unknown"
        /mol_type="genomic DNA"

ORIGIN

Alignment Scores:
Pred. No.: 3.11e-135 Length: 1607
Score: 2095.00 Matches: 395
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.75% Mismatches: 0
Query Match: 99.86% Indels: 0
DB: 6 Gaps: 0

US-10-801-648-2 (1-396) x AR353792 (1-1607)

Qy      1 MetValAlaGlyThrArgCysLeuLeuAlaLeuLeuProGlnValLeuLeuGly 20
Db      356 ATGTGTGCGCGGAGCCCGCTGCTTCTAGCGTGTGTCTCCCGAGGTCTCTCTGGGCGGC 415
Qy      21 AlaAlaGlyLeuValProGluLeuGlyArgArgLysPheAlaAlaAlaSerSerGlyArg 40
Db      416 CGGCTGGCTCTGTTCCGAGCTGGGCGCAGGAGTTCCGCGGCGGCTCTCTGGGCGGC 475
Qy      41 ProSerSerGlnProSerAspGluValLeuSerGluPheGluLeuArgLeuLeuSerMet 60
Db      476 CCTCATCCAGCCCTCTGACGAGTCTGAGCGAGTTCCGAGTTCGCGCTGCTCAGCATG 535
Qy      61 PheGlyLeuLysGlnArgProThrProSerArgAspAlaValValProProTyrMetLeu 80
Db      536 TTGCGCTGAAACAGAGACCCACCCCGAGCGGAGCGCGTGGTGGTCCCGCTTACATGCTA 595
Qy      81 AspLeuTyrArgArgHisSerGlyGlnProGlySerProAlaProAspHisArgLeuGlu 100
Db      596 GACCTGTATCCAGGCACTCAGGTGAGCGGGCTCACCGCGCCAGACACCGGTTGGAG 655
Qy      101 ArgAlaAlaSerArgAlaAsnThrValArgSerPheHisHisGluGluSerLeuGlu 120
Db      656 AGGCAGCAGCCAGCCAGCCACACTGTGCGCAGCTTCCACCATGAAGAAATCTTTGGAAGA 715
Qy      121 LeuProGluThrSerGlyLysThrThrArgArgPhePheAsnLeuSerSerIlePro 140
Db      716 CTACAGAAACGAGTGGGAAACACCCGAGATCTCTCTTTAATTTAAGTTCTATATCCCC 775
Qy      141 ThrGluGluPheIleThrSerAlaGluLeuGlnValPheArgGluGlnMetGlnAspAla 160
Db      776 ACGGAGGAGTTTATCACTCCAGCAGAGCTTCAGGTTTCCGAGAACACATGCAAGATGCT 835
Qy      161 LeuGlyAsnAsnSerSerPheHisHisArgIleAsnIleTyrGluIleIleLysProAla 180
Db      836 TTAGGAAACATAGCAGTTTCCATCCCGAATTATATTTAATTTAAGTTCATATAAACCCTG 895
Qy      181 ThrAlaAsnSerLysPheProValThrArgLeuLeuAspThrArgLeuValAsnGlnAsn 200
Db      896 ACAGCCAACTCGAAATTCCTCCGTGACAGACTTTTGGACACAGGTTGGTGAATCAGAA 955
Qy      201 AlaSerArgTrpGluSerPheAspValThrProAlaValMetArgTrpThrAlaGlnGly 220
Db      956 GCAAGCAGTGGGAAACTTTTGTATGTCACTCCCGCTGTGATGCGGTGACTGCACAGGGA 1015
Qy      221 HisAlaAsnHisGlyPheValGluValAlaHisLeuGluGluLysGlnGlyValSer 240
Db      1016 CACGCCAACCATGGATTCTGTGTGAAGTGGCCACTTGGAGGAGAACAGAGTGTCTCC 1075
Qy      241 LysArgHisValArgIleSerArgSerLeuHisGlnAspGluHisSerTrpSerGlnIle 260
Db      1076 AAGACACATGTTAGGATAAGCAGGCTTTTGCACCAAGATGAACACAGCTGGTCCACAGA 1135
Qy      261 ArgProLeuLeuValThrPheGlyHisAspGlyLysGlyHisProLeuHisLysArgGlu 280
Db      1136 AGGCCATTGCTAGTAATCTTTGGCCATGATGGAAAGGGCATCTCTCTCCACAAAAGAGAA 1195
Qy      281 LysArgGlnAlaLysHisLysGlnArgLysArgGlyLysSerSerCysLysArgHisPro 300

```

Db 1196 AACGTCAGCCAAACACAAACAGCGGAAACGCCCTTAAGTCCAGCTGTAAGAGACACCCCT 1255
Qy 301 LeuTyrValAspPheSerAspValGlyTyrPheAspThrPheValAlaProProGlyTyr 320
Db 1256 TTGTACGTGGACTTCAGTGACGTGGGTGGGAATGACTGGATTGTGGCTCCCGGGGTAT 1315
Qy 321 HisAlaPheTyrCysHisGlyGluCysProPheProLeuAlaAspHisLeuAsnSerThr 340
Db 1316 CACGCCCTTTACTGCCAGGAGATGCCCTTTCTCTGGCTGATCATCTGAATCCACT 1375
Qy 341 AsnHisAlaIleValGlnThrLeuValAsnSerValAsnSerIleProLeuAlaCys 360
Db 1376 AATCATGCCATTGTCAGACGTGGTCAACTCTGTAACTTAAGATCTCTAAGCATGC 1435
Qy 361 CysValProThrGluLeuSerAlaIleSerMetLeuTyrLeuAspGluAsnGluVal 380
Db 1436 TGTGTCCCGACAGAACTCAGTGCTATCTCGATGCTGTACCTTGACGAGATGAAGAGTT 1495
Qy 381 ValLeuLysAsnTyrGlnAspMetValValGluGlyCysGlyCysArg 396
Db 1496 GTATTAAAGAACTATCAGACATGTTGTGAGGGTTGTGGGTGTCGC 1543

RESULT 14
AR075478
LOCUS AR075478 1260 bp DNA linear PAT 30-AUG-2000
DEFINITION Sequence 4 from patent US 5958441.
ACCESSION AR075478
VERSION AR075478.1 GI:10002228
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
UNCLASSIFIED.
REFERENCE 1 (bases 1 to 1260)
AUTHORS Oppermann,H., Ozkaynak,E., Kuberasampath,T., Rueger,D.C. and Pang,R.H.I.
TITLE Devices comprising chondrogenic protein and methods of inducing endochondral bone formation therewith
JOURNAL Patent: US 5958441-A 4 28-SEP-1999;
FEATURES Location/Qualifiers
1..1260
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Alignment Scores:
Pred. No.: 3.73e-135 Length: 1260
Score: 2092.00 Matches: 395
Percent Similarity: 99.75% Conservative: 0
Best Local Similarity: 99.75% Mismatches: 1
Query Match: 99.71% Indels: 0
DB: 6 Gaps: 0

US-10-801-648-2 (1-396) x AR075478 (1-1260)

Qy 1 MetValAlaGlyThrArgCysLeuLeuAlaLeuLeuProGlnValLeuLeuGlyGly 20
Db 9 ATGGTGGCGGGACCCCGCTGCTCTAGCGTGTGCTTCCCGAGGCTCTCTGGCGGC 68
Qy 21 AlaAlaGlyLeuValProGluLeuGlyArgArgLysPheAlaAlaAspSerSerGlyArg 40
Db 69 GCGGCTGCGCTGTTCCGAGCTGGCCGCGAGGAAGTTCCGCGCGGCTCTCGGCGGC 128
Qy 41 ProSerSerGlnProSerAspGluValLeuSerGluPheGluLeuArgLeuSerMet 60
Db 129 CCTCATCCAGCCCTCTGACGAGGTCCTGACGAGGTTCCGAGTTCGCGCTCTCAGCATG 188
Qy 61 PheGlyLeuLysGlnArgProThrProSerArgAspAlaValProProTyrMetLeu 80
Db 189 TTCGGCCCTGAAACAGAGACCCACCCCGAGGGAGCGCGGTGGTCCCTTACATGCTA 248
Qy 81 AspLeuTyrArgArgHisSerGlyGlnProGlySerProAlaProAspHisArgLeuGlu 100
Db 249 GACCTGTATCGACGCACTCGGGTCAGCGGGCTCACCGCGCCCGAGACACCGGTTGGAG 308

Qy 101 ArgAlaAlaSerArgAlaAsnThrValArgSerPheHisGlyGluSerLeuGluGlu 120
Db 309 AGGCGACCGACCGAGCAACACTGTGCGCAGCTTCACCATGAAGAATCTTTGGAGAA 368
Qy 121 LeuProGluThrSerGlyLysThrThrArgArgPhePheAsnLeuSerSerIlePro 140
Db 369 CTACCAAGAAACGAGTGGGAAAACACCCGGAGATCTCTCTTAATTTAAGTTCTATCCCC 428
Qy 141 ThrGluGluPheIleThrSerAlaGluLeuGlnValPheArgGluGlnMetGlnAspAla 160
Db 429 ACGGAGAGTTTATCACTCAGCAGAGCTTCAGGTTTCCGAGAACACAGATGCAAGATGCT 488
Qy 161 LeuGlyAsnAsnSerSerPheHisHisArgIleAsnIleTyrGluIleIleLysProAla 180
Db 489 TTAGGAAACAAATAGCAGTTTCCATCCCGAATTAATATTTATGAATCATAAAAACCTGCA 548
Qy 181 ThrAlaAsnSerLysPheProValThrArgLeuLeuAspThrArgLeuValAsnGlnAsn 200
Db 549 ACAGCCAACCTCGAAAATTCCTCGGTGACCAGCTCTTTGGACACCAAGTTGGTGAATCAGAT 608
Qy 201 AlaSerArgTrpGluSerPheAspValThrProAlaValMetArgTrpThrAlaGlnGly 220
Db 609 GCAAGCAGGTGGGAAAAGTTTGTGATGTCCCGCTGTGATCGGTGCGTGCACACGGA 668
Qy 221 HisAlaAsnHisGlyPheValValGluValAlaHisLeuGluGlyGlnGlyValSer 240
Db 669 CACGCCAACCATGATTGCTGGTGGGAAAGTGGCCCACTTGGAGGAGAAACAAAGGTGTCTCC 728
Qy 241 LysArgHisValArgIleSerArgSerLeuHisGlnAspGluHisSerTrpSerGlnIle 260
Db 729 AAGAGACATGTTAGGATAAGCAGGTCTTTGCACCAAGATGAACACACAGCTGGTACAGATA 788
Qy 261 ArgProLeuLeuValThrPheGlyHisAspGlyLysGlyHisProLeuHisLysLysArgGlu 280
Db 789 AGGCCATTGCTAGTAACCTTTTGGCCATGATGGAAAAGGCGATCTCTCCACAAAGAGAA 848
Qy 281 LysArgGlnAlaLysHisLysGlnArgLysArgLysSerSerCysLysArgHisPro 300
Db 849 AAGCGTCAGCCAAACACAAACACGCGGAAACGCCCTTAAGTCCAGCTGTAAAGACACCCCT 908
Qy 301 LeuTyrValAspPheSerAspValGlyTyrAsnAspTrpIleValAlaProProGlyTyr 320
Db 909 TTGTACGTGGACTTCAGTGAGCTGGGTGGAAATGACTGGATTGGGTCTCCCGGGGTAT 968
Qy 321 HisAlaPheTyrCysHisGlyGluCysProPheProLeuAlaAspHisLeuAsnSerThr 340
Db 969 CACGCCCTTTACTGCCACGAGAAATGCCCTTTCTCTGGCTGATCATCTGAACTCCACT 1028
Qy 341 AsnHisAlaIleValGlnThrLeuValAsnSerValAsnSerLysIleProLysAlaCys 360
Db 1029 AATCATGCCATTGTTCAAGCTGGTCACTCTGTAACTCTAAGATTCCTAAAGCATGC 1088
Qy 361 CysValProThrGluLeuSerAlaIleSerMetLeuTyrLeuAspGluAsnGluLysVal 380
Db 1089 TGTGTCCGACAGAACTCAGTGCTATCTCGATGCTGTACCTTGACGAGAAATGAAGGTT 1148
Qy 381 ValLeuLysAsnTyrGlnAspMetValValGluGlyCysGlyCysArg 396
Db 1149 GTATTAAAGAACTATCAGGATATGTTGTGAGGGTTGTGGGTGTCGC 1196

RESULT 15
LOCUS 115550 1260 bp DNA linear PAT 02-APR-1996
DEFINITION Sequence 4 from patent US 5468845.
ACCESSION 115550
VERSION 115550.1 GI:1250458
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
UNCLASSIFIED.
REFERENCE 1 (bases 1 to 1260)
AUTHORS Oppermann,H., Ozkaynak,E., Kuberasampath,T. and Rueger,D.C.

TITLE Antibodies to osteogenic proteins
JOURNAL Patent: US 5468845-A 4 21-NOV-1995;
FEATURES Location/Qualifiers
source 1..1260

ORIGIN /organism="unknown"
/mol_type="unassigned DNA"

Alignment Scores:

Pred. No.: 3,73e-135 Length: 1260
Score: 2092.00 Matches: 395
Percent Similarity: 99.75% Conservative: 0
Best Local Similarity: 99.75% Mismatches: 1
Query Match: 99.71% Indels: 0
DB: Gaps: 0

US-10-801-648-2 (1-396) x II5550 (1-1260)

```

QY 1 MetValAlaGlyThrArgCysLeuLeuAlaLeuLeuProGlnValLeuLeuGlyGly 20
DB 9 ATGTGGCGGGACCGGTCTTCTAGCGTGTCTTCCCGAGGTCTCTCGGGCGGC 68
QY 21 AlaAlaGlyLeuValProGluLeuGlyArgArgLysPheAlaAlaSerSerGlyArg 40
DB 69 GCGGCTGGCTCGTTCGGAGCTGGCGCGCAGGAAGTTCCGGCGCGCTCGTGGGCGGC 128
QY 41 ProSerSerGlnProSerAspGluValLeuSerGluPheGluLeuArgLeuLeuSerMet 60
DB 129 CCTCATCCAGCCCTCTGACGAGGTCTGAGCGAGTTCGAGGTTCGGCTGCTCAGCATG 188
QY 61 PheGlyLeuLysGlnArgProThrProSerArgAspAlaValValProProTyrMetLeu 80
DB 189 TTCGCCCTGAAACAGAGACCCACCCCGAGCGGACGCGGTGGTCCCGCTTACATGCTA 248
QY 81 AspLeuTyrArgArgHisSerGlyGlnProGlySerProAlaProAspHisArgLeuGlu 100
DB 249 GACCTGTATCGCAGGCACTCGGGTTCAGCGGGCTCACCGCGCCAGACACCGGGTTGGAG 308
QY 101 ArgAlaAlaSerArgAlaAsnThrValArgSerPheHisHisGluGluSerLeuGluGlu 120
DB 309 AGGCAGCGCCAGCGACCAACTGTGGCGAGTTCACCATGAAGAATCTTTGGAGAA 368
QY 121 LeuProGluThrSerGlyLysThrThrArgArgPhePheAsnLeuSerSerIlePro 140
DB 369 CTACAGAAACAGTGGGAAACAACCCGAGATTCCTCTTTAAATTAAGTTCTATCCCC 428
QY 141 ThrGluGluPheIleThrSerAlaGluLeuGlnValPheArgGluGlnMetGlnAspAla 160
DB 429 ACGGAGGAGTTTATCACCTCAGCAGAGCTTCAGGTTTTCGAGAGACAGATGCAAGTGT 488
QY 161 LeuGlyAsnAsnSerSerPheHisArgIleAsnIleTyrGluIleIleLysProAla 180
DB 489 TTAGGAAACAATAGCAGTTTCCATCACCGAATTAATATGAATCATAAACCTGCA 548
QY 181 ThrAlaAsnSerLysPheProValThrArgLeuLeuAspThrArgLeuValAsnGlnAsn 200
DB 549 ACAGCCAACTCGAAATTCCTCCGTGACCATCTTTTGGACACCCAGGTGGTGAATCAGAA 608
QY 201 AlaSerArgTyrGluSerPheAspValThrProAlaValMetArgTyrThrAlaGlnGly 220
DB 609 GCAGCAGGTGGGAAAGTTTGTATGTACCCCGCTGTGATCGGTGGACTGCACAGGGA 668
QY 221 HisAlaAsnHisGlyPheValValGluValAlaHisLeuGluGluLysGlnGlyValSer 240
DB 669 CAGCCCAACCATGGATTCGTGGTGAAGTGGCCCACTTGGAGGAGAAACAAGGTGTCTCC 728
QY 241 LysArgHisValArgIleSerArgSerLeuHisGlnAspGluHisSerTrpSerGlnIle 260
DB 729 AAGAGACATGTTAGGATAAGCAGGTCTTTGGCAACCAAGATGAACACAGCTGGTGCAGATA 788
QY 261 ArgProLeuLeuValThrPheGlyHisAspGlyLysGlyHisProLeuHisLysArgGlu 280
DB 789 AGGCCATTCTAGTAACCTTTTGGCCCATGTATGGAAAGGGCACTCTCTCCACAAAGAGAA 848

```

```

QY 281 LysArgGlnAlaLysHisLysGlnArgLysArgLeuLysSerSerCysLysArgHisPro 300
DB 849 AAACGTCAAGCCAAACACAAACAGCGGAAACGCTTAAGTCCAGCTGTAAAGAGACACCT 908
QY 301 LeuTyrValAspPheSerAspValGlyTrpAsnAspTrpIleValAlaProProGlyTyr 320
DB 909 TTGTACGTGGACTTCAGTACGTGGGTGGAAATGACTGGATTTGTGGCTCCCGGGGTAT 968
QY 321 HisAlaPheTyrCysHisGlyGluCysProPheProLeuAlaAspHisLeuAsnSerThr 340
DB 969 CACGCCCTTTACTGCCACGGAGAAATGCCCTTTCTCTGGCTGATCATCTGAACCTCCACT 1028
QY 341 AsnHisAlaIleValGlnThrLeuValAsnSerValAsnSerLysIleProLysAlaCys 360
DB 1029 AATCATGCCATTGTTTCAGACGTTGTCACCTCTGTAACTCTAAGATTCCTAAGGCATGC 1088
QY 361 CysValProThrGluLeuSerAlaIleSerMetLeuTyrLeuAspGluAsnGluLysVal 380
DB 1089 TGTGTCCCGACAGAACTCAGTGTCTATCTCGATGCTGTACCTTGACGAGATGAAAAGGTT 1148
QY 381 ValLeuLysAsnTyrGlnAspMetValValGluGlyCysGlyCysArg 396
DB 1149 GTATTAAAGAACTATCAGGATATGTTGTGGAGGGTTGTGGGTGTGCG 1196

```

Search completed: January 11, 2006, 01:11:54

Job time : 4475 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model
Run on: January 10, 2006, 22:09:25 ; Search time 530 Seconds
(without alignments)
4979.657 Million call updates/sec

Title: US-10-801-648-2
Perfect score: 2098
Sequence: 1 MVAGTRCILLALLPQVLIG.....NEKVLKNYQDMVVGCGCR 396

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters: -DEV=xlh
-MODE=frame_p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO.spool/US10801648/runat_09012006_143119_14750/app_query.fasta_1.583
-DB=N Geneseq -QFMT=fastap -SUFFIX=trng -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -ENDS=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10801648 @CNC_1_1_542 @runat_09012006_143119_14750 -NCPU=6 -ICPU=3
-NO WMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THRAD=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N Geneseq 21.1*

1: Geneseqm1980s:*
2: Geneseqm1990s:*
3: Geneseqm2000s:*
4: Geneseqm2001as:*
5: Geneseqm2001bs:*
6: Geneseqm2002as:*
7: Geneseqm2002bs:*
8: Geneseqm2003as:*
9: Geneseqm2003bs:*
10: Geneseqm2003cs:*
11: Geneseqm2003ds:*
12: Geneseqm2004as:*
13: Geneseqm2004bs:*
14: Geneseqm2005as:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----------|-------------------------|
| 1 | 2098 | 100.0 | 1191 | ADL13511 | ADL13511 Osteoarthritis |
| 2 | 2098 | 100.0 | 1215 | AAZ08554 | AAZ08554 KS-hBMP-2 |
| 3 | 2098 | 100.0 | 1547 | AAQ32851 | AAQ32851 BMP2. 3/2 |
| 4 | 2098 | 100.0 | 1547 | AAV01679 | AAV01679 Bone morph |

| | | | | | | |
|----|------|-------|------|----|----------|-------------------------|
| 5 | 2098 | 100.0 | 1547 | 6 | ABK90308 | ABK90308 DNA encod |
| 6 | 2098 | 100.0 | 1547 | 8 | ABX76358 | ABX76358 Lung canc |
| 7 | 2098 | 100.0 | 1547 | 8 | ACF34481 | ACF34481 Gene enco |
| 8 | 2098 | 100.0 | 1547 | 10 | ACF05920 | ACF05920 Human bon |
| 9 | 2098 | 100.0 | 1547 | 10 | ADD14609 | ADD14609 Human src |
| 10 | 2098 | 100.0 | 1547 | 10 | ADE85186 | ADE85186 Farnesyl |
| 11 | 2098 | 100.0 | 1547 | 10 | AAD63420 | AAD63420 Human bon |
| 12 | 2098 | 100.0 | 1547 | 10 | ABT17041 | ABT17041 Human MP2 |
| 13 | 2098 | 100.0 | 1547 | 10 | ADL13510 | ADL13510 Osteoarthritis |
| 14 | 2098 | 100.0 | 1547 | 11 | ADN38841 | ADN38841 Cancer/an |
| 15 | 2098 | 100.0 | 1547 | 12 | ADH11558 | ADH11558 Human bon |
| 16 | 2098 | 100.0 | 1547 | 12 | ADK90635 | ADK90635 Human CBM |
| 17 | 2098 | 100.0 | 1547 | 12 | ADO49064 | ADO49064 Human CBM |
| 18 | 2098 | 100.0 | 1547 | 13 | ADQ80231 | ADQ80231 Bone morph |
| 19 | 2098 | 100.0 | 1547 | 13 | ADG67125 | ADG67125 Human bla |
| 20 | 2098 | 100.0 | 1547 | 13 | ADG73742 | ADG73742 Human bon |
| 21 | 2098 | 100.0 | 1547 | 14 | ADW15055 | ADW15055 Bone morph |
| 22 | 2098 | 100.0 | 1547 | 14 | ADY15523 | ADY15523 DNA encod |
| 23 | 2098 | 100.0 | 1547 | 14 | ADX39020 | ADX39020 Human bon |
| 24 | 2098 | 100.0 | 1547 | 14 | ADY81389 | ADY81389 Human bon |
| 25 | 2098 | 100.0 | 1547 | 14 | ABA01570 | ABA01570 Human bon |
| 26 | 2098 | 100.0 | 1581 | 14 | ADY28715 | ADY28715 Human bon |
| 27 | 2098 | 100.0 | 1607 | 2 | AAQ14036 | AAQ14036 Human BMP |
| 28 | 2098 | 100.0 | 1607 | 2 | AAQ31869 | AAQ31869 Human BMP |
| 29 | 2098 | 100.0 | 1607 | 2 | AAQ41291 | AAQ41291 Human BMP |
| 30 | 2098 | 100.0 | 1607 | 2 | AAT64523 | AAT64523 Human BMP |
| 31 | 2098 | 100.0 | 1607 | 2 | AAT78941 | AAT78941 Human bon |
| 32 | 2098 | 100.0 | 1607 | 4 | AAQ16012 | AAQ16012 Human bon |
| 33 | 2098 | 100.0 | 1607 | 4 | AAQ90497 | AAQ90497 Human BMP |
| 34 | 2098 | 100.0 | 1607 | 12 | ADO40078 | ADO40078 Human BMP |
| 35 | 2098 | 100.0 | 3526 | 12 | ADL12282 | ADL12282 Human ste |
| 36 | 2092 | 99.7 | 1258 | 12 | ADM80488 | ADM80488 Human ost |
| 37 | 2092 | 99.7 | 1258 | 13 | ADO03610 | ADO03610 cDNA enco |
| 38 | 2092 | 99.7 | 1260 | 2 | AAQ53143 | AAQ53143 Sequence |
| 39 | 2092 | 99.7 | 1260 | 2 | AAT02602 | AAT02602 Human CBM |
| 40 | 2092 | 99.7 | 1260 | 2 | AAV15206 | AAV15206 Human ost |
| 41 | 2092 | 99.7 | 1260 | 2 | AAQ00231 | AAQ00231 Human ost |
| 42 | 2092 | 99.7 | 1260 | 2 | AAZ27581 | AAZ27581 Human pre |
| 43 | 2092 | 99.7 | 1260 | 10 | ADJ62679 | ADJ62679 Human CMB |
| 44 | 2092 | 99.7 | 1260 | 12 | ADE52750 | ADE52750 Human ost |
| 45 | 2092 | 99.7 | 2154 | 6 | ABK40276 | ABK40276 cDNA enco |

ALIGNMENTS

RESULT 1
ADL13511
ID ADL13511 standard; DNA; 1191 BP.

AC ADL13511;

DT 06-MAY-2004 (first entry)

DE Osteoarthritis-associated polymorphic nucleotide #43.

XX ds; gene; osteopathic; antiinflammatory; antiarthritic; gene therapy;
XX joint space narrowing; osteophyte development; joint pain;
XX osteoarthritis; SNP; single nucleotide polymorphism.

OS Homo sapiens.

PN WO2003054166-A2.

PD 03-JUL-2003.

PF 19-DEC-2002; 2002WO-US041225.

PR 20-DEC-2001; 2001US-0342603P.

XX (INCY-) INCYTE GENOMICS INC.

PI Jones KA, Schafer A;

XX

XX Hollinger JO, Winn SR, Frank E, Wong SC;
 XX WPI; 1999-494212/41.
 XX Composition for treating osseous defects e.g. traumatic bone loss,
 PT congenital insufficiency and/or malformations.
 XX
 XX Example 8; Page 32; 81pp; English.
 XX
 CC The present invention describes composition (I) for treating osseous
 CC defects comprising a porous matrix and a cell that is committed to an
 CC osteogenic lineage. The composition is useful for healing a bone defects,
 CC especially those caused by osteoporosis, cyst like cavities, surgical
 CC resection, traumatic avulsion and congenital insufficiency. The
 CC compositions assist in the repair and regeneration of bone. Osteoblast
 CC precursor cells (OPC's) boost bone making capability of an ill or aged
 CC individual where OPC's are numerically deficient or functionally
 CC impaired. OPC's can be administered to express BMP to repair bone
 CC defects. The implant is useful for promoting vascular ingrowth and bone
 CC formation, especially in treating bone defects e.g. osteopenic spine. The
 CC composition promotes vascular ingrowth and bone formation without
 CC becoming a barrier to the progression of bone formation. OPC's can be
 CC gently introduced into the cavity without disrupting the cells in the
 CC suspension and they also encourage additional bone formation in the
 CC surrounding bone. The present sequence represents a plasmid vector
 CC containing human bone morphogenic protein 2 (hBMP-2), given in an example
 CC from the present invention
 XX
 SQ Sequence 1215 BP; 300 A; 326 C; 324 G; 265 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 4,51e-174 Length: 1215
 Score: 2098.00 Matches: 396
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 2 Gaps: 0

US-10-801-648-2 (1-396) x AAQ208554 (1-1215)

QY 1 MetValAlaGlyThrArgCysLeuLeuAlaLeuLeuProGlnValLeuLeuGly 20
 DB 17 ATGGTGGCGGACCGGTCTTCTAGCTTGCTCTCCACAGTCTCTCTGGGCGGC 76
 QY 21 AlaAlaGlyLeuValProGlnLeuGlyArgArgPheAlaAlaSerSerGlyArg 40
 DB 77 GGGCTGGCTCGTTCCGAGCTGGGCGCGCAGGAAGTTCCGCGCGCGCTCGTGGGCGGC 136
 QY 41 ProSerSerGlnProSerAspGluValLeuSerGluPheGluLeuArgLeuSerMet 60
 DB 137 CCCTCATCCAGCCCTCTGACAGGTCTGACGAGTTCGAGTTCGGCTGCTCAGCATG 196
 QY 61 PheGlyLeuLysGlnArgProThrProSerArgAspAlaValValProThrMetLeu 80
 DB 197 TTCGGCTTGAACAGAGACCCACCCAGCAGGACGGTGTGCCCCCTACATGCTA 256
 QY 81 AspLeuTyrArgArgHisSerGlyGlnProGlySerProAlaProAspHisArgLeuGlu 100
 DB 257 GACCTGTATCGCAGGCACTCAGTCCAGCGGGCTCACCGCGCCAGACCCAGCGTGGAG 316
 QY 101 ArgAlaAlaSerArgAlaSerValArgSerPheHisGluGluSerLeuGluGlu 120
 DB 317 AGGGCAGCCAGCGAGCCAACTGTGGCAGCTTCCACCATGAAGAATCTTTGGAAGAA 376
 QY 121 LeuProGluThrSerGlyLysThrArgArgPhePheAsnLeuSerSerIlePro 140
 DB 377 CTACCAAGAACGGTGGGAAACACCCCGAGATCTTCTTAATTAAATTCATATCCC 436
 QY 141 ThrGluGluPheIleThrSerAlaGluLeuGlnValPheArgGluGlnMetGlnAspAla 160
 DB 437 ACGGAGGAGTTTATCACCTCAGCAGAGCTTCAGGTTTTCCGAGAACAGATGCAAGTGT 496

QY 161 LeuGlyAsnAsnSerSerPheHisHisArgIleAsnIleTyrGluIleIleLeuProAla 180
 DB 497 TTAGGAACAATAGCAGTTTCCATCACCGAATTAATATTATGAATCATATAAACCTGCA 556
 QY 181 ThrAlaAsnSerLysPheProValThrArgLeuLeuAspThrArgLeuValAsnGlnAsn 200
 DB 557 ACACCAACTCGAAATTCCTCGGTGACCCAGACTTTTGGACACACAGTTGGTGAATCAGAA 616
 QY 201 AlaSerArgTTPGluSerPheAspValThrProAlaValMetArgTTPAlaGlnGly 220
 DB 617 GCAAGCAGGTGGGAAGTTTGTATGTACCCCCCTGTGATGCGGTGACACTGCACAGGA 676
 QY 221 HisAlaAsnHisGlyPheValValGluValAlaHisLeuGluGluLysGlnGlyValSer 240
 DB 677 CACGCCAACCATGATTCGTGGTGGAAAGTGCCCACTTGGAGGAGAAACAAGGTGTCTCC 736
 QY 241 LysArgHisValArgIleSerArgSerLeuHisGlnAspGluHisSerTrpSerGlnIle 260
 DB 737 AAGAGACATGTTAGGATAAGCAGGTCTTTGACCACCAAGATGAACACAGCTGCTCAGATA 796
 QY 261 ArgProLeuLeuValThrPheGlyHisAspGlyLysGlyHisProLeuHisLysArgGlu 280
 DB 797 AGGCATTTGCTAGTAACCTTTTGGCCATGATGGAAGAGGCATCTCTCCACAAAGAGAA 856
 QY 281 LysArgGlnAlaLysHisLysGlnArgLysArgLeuLysSerSerCysLysArgHisPro 300
 DB 857 AACGTCAGGCCAACACACACACACAGCGGAAACGCCTTAAGTCCAGCTGTAAAGAGACACCT 916
 QY 301 LeuTyrValAspPheSerAspValGlyTrpAsnAspTrpIleValAlaProProGlyTyr 320
 DB 917 TTGTACGTGGACTTTCAGTACGTGGGTGGAAATGACTGGATTTGTGGCTCCCGGGGTAT 976
 QY 321 HisAlaPheTyrCysHisGlyGluCysProPheProLeuAlaAspHisLeuAsnSerThr 340
 DB 977 CACGCTTTTACTGCCAGGAGAAATGCCCTTTTCTCTGGCTGATCATCTGAATCCACT 1036
 QY 341 AsnHisAlaIleValGlnThrLeuValAsnSerValAsnSerLysIleProLysAlaCys 360
 DB 1037 AATCATGCCATTTGTCAGACGTTGTCACCTCTGTAACCTCTAAGATTTCTTAAGCATGC 1096
 QY 361 CysValProThrGluLeuSerAlaIleSerMetLeuTyrLeuAspGluAsnGluLysVal 380
 DB 1097 TGTGTCCCGACAGAACTCAGTCTATCTCGATGCTGTACCTTGACAGAGATGAAGAAGTT 1156
 QY 381 ValLeuLysAsnTyrGlnAspMetValValGluGlyCysGlyCysArg 396
 DB 1157 GTATTAAAGAACTATCAGGACATGTTGTGGAGGTTGTGGGTGTGCG 1204
 RESULT 3
 AAQ32851
 ID AAQ32851 standard; cDNA; 1547 BP.
 XX
 AC AAQ32851;
 XX
 DT 25-MAR-2003 (revised)
 DT 05-MAY-1993 (first entry)
 XX
 DE BMP2.
 XX
 KW Bone; morphogenetic; protein; BMP; growth; vitamin D; systemic;
 KW treatment; dimer; ss.
 XX
 OS Rattus rattus.
 XX
 PN W09221365-A1.
 XX
 PD 10-DEC-1992.
 XX
 PF 26-MAY-1992; 92WO-US004356.
 XX
 PR 05-JUN-1991; 91US-00709621.
 PR 27-MAR-1992; 92US-00856110.
 XX

(PROC) PROCTER & GAMBLE CO.

XX Stone RL;

XX WPI; 1992-433371/52.

XX Synergistic compen. for generating mammalian bone growth - comprises
PT vitamin=D cpd. and bone morphogenetic protein.

XX Disclosure; Page 27-29; 44pp; English.

XX The sequences given in AAQ32850-56 encode bone morphogenetic proteins
CC (BMP). BMP's increase bone growth and when used in conjunction with
CC vitamin D the level of new bone growth is greater than when a BMP or
CC vitamin D are used alone. The BMP's are administered for systemic
CC treatment at a dose range of 1pg to 100 microg. BMP are active as dimers.
CC (Updated on 25-MAR-2003 to correct FN field.)

XX Sequence 1547 BP; 377 A; 423 C; 410 G; 337 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 6.2e-174 Length: 1547
 Score: 2098.00 Matches: 396
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 2 Gaps: 0

US-10-801-648-2 (1-396) x AAQ32851 (1-1547)

QY 1 MetValAlaGlyThrArgCysLeuLeuAlaLeuLeuProGlnValLeuGlyGly 20
 DB 324 ATGTGGCGGGAGCCCGCTGCTTCTAGCGTGTGCTTCCCGAGGCTCTCTGGGGCGC 383
 QY 21 AlaAlaGlyLeuValProGluLeuGlyArgArgLysPheAlaAlaLeuSerSerGlyArg 40
 DB 384 GCGGCTGCGCTCGTTCGGAGCTGGCGCGCAGGAAGTTCCGGCGGCGTCTCGGGCGC 443
 QY 41 ProSerSerGlnProSerAspGluValLeuSerGluPheGluLeuArgLeuLeuSerMet 60
 DB 444 CCCTCATCCAGCCCTCTGACGAGGTCCTGACGAGGTTCCGAGGTTGCGGCTCTCAGCATG 503
 QY 61 PheGlyLeuLysGlnArgProThrProSerArgAspAlaValProProTyMetLeu 80
 DB 504 TTCGGCTTGAACAGAGACCCACCCCGCAGGAGCGCGGTGGTCCCGCTCATGCTA 563
 QY 81 AspLeuTyArgArgHisSerGlyGlnProGlySerProAlaProAspHisArgLeuGlu 100
 DB 564 GACCTGTATCCAGGCACTCAGGTACGGGGCTCACCGGCCCCAGACCACCGGTTGGAG 623
 QY 101 ArgAlaAlaSerArgAlaAsnThrValArgSerPheHisHisGluGluSerLeuGluGlu 120
 DB 624 AGGGCAGCCAGCCGAGCAACTGTGCGCAGCTTCCACCATGAAGAAATCTTTGGAAAGA 683
 QY 121 LeuProGluThrSerSerGlyLysThrThrArgArgPhePheAenLeuSerSerIlePro 140
 DB 684 CTACAGAAACGAGTGGGAAACAAACCCGGAGATCTCTTTAATTTAAGTTCTATCCCC 743
 QY 141 ThrGluGluPheIleThrSerAlaGluLeuGlnValPheArgGluGlnMetGlnAspAla 160
 DB 744 ACGGAGGAGTTTATCACTCAGCAGAGCTTCAGGTTTCCGAGAACAGATGCAAGATGCT 803
 QY 161 LeuGlyAenAenSerSerPheHisHisArgIleAenIleTyGluIleLysProAla 180
 DB 804 TTAGGAACAATAGCAGTTCCATCAGCGAATTAATTTATGAATCATAAACCTGCA 863
 QY 181 ThrAlaAenSerLysPheProValThrArgLeuLeuAspThrArgLeuValAenGlnAsn 200
 DB 864 ACAGCAACTCGAAATTTCCCGTGACACAGATTTTGGACACCGAGTTGGTGAATCAGAA 923
 QY 201 AlaSerArgTrpGluSerPheAspValThrProAlaValMetArgTrpThrAlaGlnGly 220
 DB 924 GCAAGCAGTGGGAAAGTTTTTGATGTACACCCCGCTGTGATCGGTGAGCTGCACAGGA 983

QY 221 HisAlaAenHisGlyPheValValGluValAlaHisLeuGluGluLysGlnGlyValSer 240
 DB 984 CAGCCCAACCATGGATTTCGTGGTGGAGTGGCCCACTTGGAGGAGAAACAAGGTGTCTCC 1043
 QY 241 LysArgHisValArgIleSerArgSerLeuHisGlnAspGluHisSerTrpSerGlnIle 260
 DB 1044 AAGAGACATGTTAGGATAAGCAGTCTTTGACCAAGATGAACACAGCTGTCAAGATA 1103
 QY 261 ArgProLeuLeuValThrPheGlyHisAspGlyLysGlyHisProLeuHisLysArgGlu 280
 DB 1104 AGGCCATTGCTAGTAACCTTTTGCCCATGATGGAAGAGGGCATCTCTCCACAAAGAGAA 1163
 QY 281 LysArgGlnAlaLysHisLysGlnArgLysArgLysSerSerCysLysArgHisPro 300
 DB 1164 AAACGTCAACCAACAACAACACGCGAAACGCCCTTAAGTCCAGCTGTAAAGAGACACCT 1223
 QY 301 LeuTyValAspPheSerAspValGlyTrpAsnAspTrpIleValAlaProProGlyTy 320
 DB 1224 TTGTACGTGACTTCAGTGACGTGGGTGGAATGACTGGATTTGGGTCCCCCGGGGTAT 1283
 QY 321 HisAlaPheTyrcysHisGlyGluCysProPheProLeuAlaAepHisLeuAenSerThr 340
 DB 1284 CAGCCCTTTTACTGCCAGCAGGAATGCCCTTTCTCTGCTGATCATCTGNACTCCACT 1343
 QY 341 AsnHisAlaIleValGlnThrLeuValAenSerValAenSerLysIleProLysAlaCys 360
 DB 1344 AATCATGCCATTGTTCAAGCGTTGGTCAACTCTGTTAACTCTAAGATTCCTAAGGCATGC 1403
 QY 361 CysValProThrGluLeuSerAlaIleSerMetLeuTyLeuAspGluAenGluLysVal 380
 DB 1404 TGTGTCCCGACAGAACTCAGTGCTATCTCGATGCTGTACCTTGACGAGAAATGAAGGTT 1463
 QY 381 ValLeuLysAenTyrcysHisGlyGluMetValValGluGlyCysGlyCysArg 396
 DB 1464 GTATTAAAGAACTATCAGGACATGTTGTGGAGGGTTGTGGGTGTGGTGTGC 1511

RESULT 4
 AAV01679
 ID AAV01679 standard; cDNA; 1547 BP.
 XX AC AAV01679;
 XX DT 25-MAR-2003 (revised)
 DT 27-MAR-1998 (first entry)
 XX DE Bone morphogenetic protein BMP-2 encoding DNA.
 KW Bone morphogenetic protein; BMP; growth; vitamin D; fracture; arthritis;
 KW surgical lesion; periodontal disease; osteoporosis; rickets; db.
 XX OS Unidentified.
 XX OS OS
 XX PN US5693615-A.
 XX PD 02-DEC-1997.
 XX PF 23-JAN-1995; 95US-00377292.
 XX PR 05-JUN-1991; 91US-00709621.
 PR 27-MAR-1992; 92US-00856110.
 PR 09-DEC-1992; 92US-00988363.
 PR 07-SEP-1993; 93US-00117367.
 PR 13-MAY-1994; 94US-00243435.
 XX (PROC) PROCTER & GAMBLE CO.
 XX Stone RL;
 XX WPI; 1998-031788/03.
 XX Generation of new bone growth - by co-administering bone morphogenetic
 PT protein and vitamin D.

XX Claim 1; Col 19-22; 18pp; English.

XX A new method has been developed for generating new bone growth in a

CC mammal. The method comprises administering a bone morphogenetic protein

CC in combination with a vitamin D compound, where: (a) the bone

CC morphogenetic protein is BMP-2 and is administered in an amount of 500-

CC 1000 ng in combination with about 6 ng vitamin D compound; or (b) the

CC bone morphogenetic protein is BMP-4 and is administered in an amount of

CC about 62.5 ng in combination with about 6 ng vitamin D compound. The

CC present sequence encodes BMP-2. The method is used for treating bone

CC defects or disorders, e.g. fractures, surgical lesions, periodontal

CC disease, osteoporosis, arthritis and rickets. (Updated on 25-MAR-2003 to

CC correct PF field.)

XX SQ Sequence 1547 BP; 377 A; 423 C; 410 G; 337 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 6.2e-174 Length: 1547

Score: 2098.00 Matches: 396

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 2 Gaps: 0

US-10-801-648-2 (1-396) x AAV01679 (1-1547)

QY 1 MetValAlaGlyThrArgCysLeuLeuAlaLeuLeuLeuProGlnValLeuLeuGlyGly 20

DB 324 ATGGTGGCGGACCGCTGCTTCTAGCGTTGCTGCTTCCCGCAGGTCCTCTCGGGCGC 383

QY 21 AlaAlaGlyLeuValProGluLeuGlyArgGlyPheAlaAlaSerSerGlyValArg 40

DB 384 GCGGCTGGCTGCTTCCGAGCTGGCGCGCAGAAAGTTCCGCGCGCGCGTGGCGGCGCGC 443

QY 41 ProSerSerGlnProSerAspGluValLeuSerGluPheGluLeuArgLeuLeuSerMet 60

DB 444 CCTCATCCAGCCCTCTGACGAGGTCTGAGCGAGTTTCGAGTTCGGGCTGCTCAGCATG 503

QY 61 PheGlyLeuLeuGlnArgProThrProSerArgAspAlaValValProProTyrMetLeu 80

DB 504 TTCCGCGCTGAACACAGAGACCCACCCCGCAGCGAGCGCGCTGCTGCTTACATGCTA 563

QY 81 AspLeuTyrArgArgHisSerGlyGlnProGlySerProAlaProAspHisArgLeuGlu 100

DB 564 GACCTGTATCGAGGCACTCAGTCCGCGGCTACCCCGCGCCAGACCCCGTTGGAG 623

QY 101 ArgAlaAlaSerArgAlaAlaThrValArgSerPheHisGluGluSerLeuGluGlu 120

DB 624 AGGGCAGCCAGCCGAGCAACTGTGCGCAGCTTCCACCATGAGNATCTTTGGAGAA 683

QY 121 LeuProGluThrSerGlyLeuThrArgArgPhePheAsnLeuSerSerIlePro 140

DB 684 CTACCAAGAACAGTGGGAAAAACAACCCGAGATTCTTCTTAATTTAAGTTCTATCC 743

QY 141 ThrGluGluPheIleThrSerAlaGluLeuGlnValPheArgGluGlnMetGlnAspAla 160

DB 744 ACGGAGGAGTTTATCACCTCAGCAGAGCTTCAGGTTTCCGAGAACAGATGCAAGATCT 803

QY 161 LeuGlyAsnAsnSerSerPheHisHisArgIleAsnIleTyrGluIleIleLeuProAla 180

DB 804 TTAGGAACAACATAGCAGTTTCCATCACCGCAATTAATTTATGAATCATAAACCTGCA 863

QY 181 ThrAlaAsnSerIysPheProValThrArgLeuLeuAspThrArgLeuValAsnGlnAsn 200

DB 864 ACAGCCAACTCGAAATTCGCCGTGACAGACCTTTGGACACAGGTTGGTGAATCAGAT 923

QY 201 AlaSerArgTyrGluSerPheAspValThrProAlaValMetArgTyrThrIleGlnGly 220

DB 924 GCAAGCAGTGGGAAAGTTTGTATGTCACCCCGCTGTGATGCGGTGGATCAGCAGGA 983

QY 221 HisAlaAsnHisGlyPheValValGluValAlaHisLeuGluGluLysGlnGlyValSer 240

DB 984 CACGCCAACCATGGATTCTGGTGGAGTGGCCCACTTTGGAGGAGAAACAAGGTGTCTCC 1043

QY 241 LysArgHisValArgIleSerArgSerLeuHisGlnAspGluHisSerTrpSerGlnIle 260

DB 1044 AAGAGACATGTTAGGATAAGCAGGTCTTTGCCAACAGATGAACACAGCTGGTGCACAGATA 1103

QY 261 ArgProLeuLeuValThrPheGlyHisAspGlyLysGlyHisProLeuHisIleLysArgGlu 280

DB 1104 AGGCCATTGCTAGTAACCTTTTGGCCATCATGGAAGAGGCGCATCTCTCCACAAAAGAGAA 1163

QY 281 LysArgGlnAlaLysHisGlyGlnArgLysArgLeuLysSerSerCysIleLysArgHisPro 300

DB 1164 AAACGTCAGCCAAACACAAACAGCGGAAACGCTTAAGTCCAGCTGTAAGAGACACCCCT 1223

QY 301 LeuTyrValAspPheSerAspValGlyTyrAsnAspTyrIleValAlaProProGlyTyr 320

DB 1224 TTGTACGTGGACTTCAGTGACGTGGGTGGATGACTGGTGTGGCTCCCGCGGGTAT 1283

QY 321 HisAlaPheTyrCysHisGlyGluCysProPheProLeuAlaAspHisLeuAsnSerThr 340

DB 1284 CAGCCCTTTTACTGCCACGAGAAATGCCCTTTTCTCTGCTGATCATCTGAACCTCCACT 1343

QY 341 AsnHisAlaIleValGlnThrLeuValAsnSerValAsnSerLysIleProLysAlaCys 360

DB 1344 AATCATGCCATTGTTTCAGACGTTGGTCAACTCTGTTAACCTCTAAGATTCTTAAGGCATGC 1403

QY 361 CysValProThrGluLeuSerAlaIleSerMetLeuTyrLeuAspGluAsnGluLysVal 380

DB 1404 TGTGTCCCGCAGAACACTCAGTCTATCTCGATGCTGTACCTTGACGAGAAATGAAGGTT 1463

QY 381 ValLeuLysAsnTyrGlnAspMetValValGluGlyCysGlyCysArg 396

DB 1464 GTATTAAAGAACTATCAGGACATGTTGTGGAGGGTGTGGGTGTGCG 1511

RESULT 5

ABK90308

ID ABK90308 standard; DNA; 1547 BP.

XX AC ABK90308;

XX 21-OCT-2002 (first entry)

XX DE DNA encoding human bone morphogenetic protein 2 (BMP2).

XX KW Bone morphogenetic protein 2; BMP2; cancer; breast cancer; lung cancer;

XX KW Gene; ss; human.

XX OS Homo sapiens.

XX FH Key

XX CDS Location/Qualifiers

FT 324..1514

FT /*tag= a

FT /product= "BMP2 protein"

FT 429..1127

FT /*tag= b

FT /note= "TGF-beta propeptide"

FT replace(432,G)

FT /*tag= c

FT /standard name= "Single nucleotide polymorphism"

FT replace(584,G)

FT /*tag= d

FT /standard name= "Single nucleotide polymorphism"

FT replace(893,A)

FT /*tag= e

FT /standard name= "Single nucleotide polymorphism"

FT 1209..1511

FT /*tag= f

FT /note= "TGF-beta-like domain"

XX WO200254940-A2.

XX 18-JUL-2002.

XX

PF 11-JAN-2002; 2002WO-US000610.
 XX
 PR 12-JAN-2001; 2001US-0261252P.
 XX
 PA (UTNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.
 XX
 PI Langenfeld J;
 XX
 DR WPI; 2002-575416/61.
 XX
 PT Treating cancer, e.g. lung cancer, comprises administering a bone
 PT morphogenic protein-2 (BMP-2) activity inhibitor, or a vector encoding
 PT the inhibitor or an antisense oligonucleotide that binds to a BMP-2
 PT nucleic acid sequence.
 XX
 PS Disclosure; Page 37-40; 162pp; English.
 XX
 CC This invention relates to a novel method for treating cancer comprising
 CC administering to a patient a bone morphogenic protein-2 (BMP-2) activity
 CC inhibitor or an expression vector which has a nucleic acid sequence
 CC encoding the BMP-2 activity inhibitor or which encodes an antisense
 CC oligonucleotide that binds to a BMP-2 nucleic acid sequence. Inhibitors
 CC of BMP-2 activity encompassed in the invention are the proteins noggin,
 CC chordin gremlin, cerberus 1 homologue and DAN. The method of the
 CC invention which utilises a BMP-2 activity inhibitor or an expression
 CC vector, is useful in diagnosing or treating cancers such as breast cancer
 CC or lung cancer. A kit is useful in the administration of the BMP-2
 CC activity inhibitor in the treatment of cancers. The present sequence
 CC represents the DNA encoding the human bone morphogenetic protein (BMP2)
 CC protein used in the method of the invention
 XX
 SQ Sequence 1547 BP; 377 A; 423 C; 410 G; 337 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 6.2e-174 Length: 1547
 Score: 2098.00 Matches: 396
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0

US-10-801-648-2 (1-396) x ABK90308 (1-1547)

Qy 1 MetValAlaGlyThrArgCysLeuLeuAlaLeuLeuLeuProGlnValLeuLeuGlyGly 20
 Db ATGTGGCCGGAGCCCGCTGCTTCTAGCGTGTCTTCCCGAGGTCCTCTCGGGCGGC 383
 Qy 21 AlaAlaGlyLeuValProGluLeuGlyArgGlyPheAlaAlaAlaSerSerGlyArg 40
 Db CGGCTGGCTCGTTCGGAGCTGGCGCCGAGGAAGTTCGGCGGCGGCTCGTCCGGCGGC 443
 Qy 41 ProSerSerGlnProSerAspGluValLeuSerGluPheGluLeuArgLeuSerMet 60
 Db CCTCATCCAGCCCTCTGACGAGTCTGAGCGAGTTCGAGTTTCGGCTGCTCAGCATG 503
 Qy 61 PheGlyLeuLeuGlnArgProThrProSerArgAspAlaValValProProTyrMetLeu 80
 Db TTCGGCTGGAACAGAGACCCACCCCGAGGAGCGCGTGGTCCCGCCCTACATGCTA 563
 Qy 81 AspLeuTyrArgArgHisSerGlyGlnProGlySerProAlaProAspHisArgLeuGlu 100
 Db GACTGTATCCAGGCACTAGGTGAGCCGGGCTCACCCGCCCCAGACACCGGTTGAG 623
 Qy 101 ArgAlaAlaSerArgAlaAsnThrValArgSerPheHisHisGluGluSerLeuGluGlu 120
 Db AGGCGAGCCAGCCGAGCCCAACACTGTGCGAGCTTCCACCATGAAGAATCTTTGGAGAA 683
 Qy 121 LeuProGluThrSerGlyValThrThrArgArgPhePheAsnLeuSerSerIlePro 140
 Db CTACAGAAACGAGTGGGAAACCAACCCGGAGATTCCTTTTAATTTAAGTTTCATCCCC 743
 Qy 141 ThrGluGluPheIleThrSerAlaGluLeuGlnValPheArgGluGlnMetGlnAspAla 160

Db 744 ACGGAGGAGTTTATCACTCTCAGCAGAGCTTTCAGGTTTTCCGAGAACAGATCAAGATGCT 803
 Qy 161 LeuGlyAsnAsnSerSerPheHisHisArgIleAsnIleTyrGluIleIleLeuProAla 180
 Db TTAGGAAACAATAGCAGTTTCCATCCAGAAATTAATATTTATGAATCATAAACCTGCA 863
 Qy 181 ThrAlaAsnSerLySbPheProValThrArgLeuLeuAspThrArgLeuValAsnGlnAsn 200
 Db ACAGCCAACTCGAAATTCCTCCGTCGACAGACTTTTGACACACAGGTTGGTGAATCAGAT 923
 Qy 201 AlaSerArgTyrGluSerPheAspValThrProAlaValMetArgTyrThrAlaGlnGly 220
 Db GCAAGCAGGTGGGAAAGTTTGTGTCACTCCCGCTGTGTGCGGTGAGTGCACAGGGA 983
 Qy 221 HisAlaAsnHisGlyPheValValGluValAlaHisLeuGluGluGlyValSer 240
 Db CAGCCCAACCATGATTCGTGTGTGGAGTGGCCCTTTCGAGGAGAAACAAGGTGTCTCC 1043
 Qy 241 LysArgHisValArgIleSerArgSerLeuHisGlnAspGluHisSerTyrSerGlnIle 260
 Db AAGAGACATGTTAGGATAAGCAGGTCTTTGCACCAAGATGAACACAGCTGTGTACAGATA 1103
 Qy 261 ArgProLeuLeuValThrPheGlyHisAspGlyLySbGlyHisProLeuHisLySbArgGlu 280
 Db AGCCATTGCTAGTAACCTTTTGCCCATGATGGAAAGGGCATCTCTCCACAAAGAGAA 1163
 Qy 281 LysArgGlnAlaLySbHisLySbGlnArgLySbArgLeuLySbSerCysLySbArgHisPro 300
 Db AAACGTCAAGCCAAACAACAACACGCGAAACGCTTAAGTCCAGCTGTAAAGAGACACCT 1223
 Qy 301 LeuTyrValAspPheSerAspValGlyTyrAsnAspTrpIleValAlaProProGlyTyr 320
 Db TTGTACGTGGACTTCAGTGACGTGGGTGGAAAGTGGATTTGGTCTCCCGGGGTAT 1283
 Qy 321 HisAlaPheTyrCysHisGlyGluCysProPheProLeuAlaAspHisLeuAsnSerThr 340
 Db CAGCCCTTTTACTGCCACGAGGAATGCCCTTTTCTCTGCTGATCATCTGAACTCCACT 1343
 Qy 341 AsnHisAlaIleValGlnThrLeuValAsnSerValAsnSerLySbIleProLySbAlaCys 360
 Db AATCATGCCATTGTTTCAGACGTTGGTCAACTCTGTAACTCTAAGATTCTTAAGGCATGC 1403
 Qy 361 CysValProThrGluLeuSerAlaIleSerMetLeuTyrLeuAspGluAsnGluLyVal 380
 Db TGTGTCCCGACAGAACTCAGTGTCTATCTCGATGCTGTACCTTGACGAGAATGAAAGGTT 1463
 Qy 381 ValLeuLySbAsnTyrGlnAspMetValValGluGlyCysGlyCysArg 396
 Db GTATTAAAGAACTATCAGGACATGGTTGTGGAGGTTGTGGGTCTCCG 1511
 RESULT 6
 ABX76358
 ID ABX76358 standard; DNA; 1547 BP.
 XX
 AC ABX76358;
 XX
 DT 02-APR-2003 (first entry)
 XX
 DE Lung cancer-associated polynucleotide #222.
 XX
 KW Lung cancer-associated polynucleotide; gene; ds; cytosatic; emphysema;
 KW antiinflammatory; antiasthmatic; non-small cell lung cancer; atelectasis;
 KW small cell lung cancer; benign lesion; precancerous lesion; bronchitis;
 KW chronic obstructive pulmonary disease; hypersensitivity pneumonitis;
 KW interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.
 OS Unidentified.
 XX
 FN WO200286443-A2.
 XX
 PD 31-OCT-2002.
 XX
 PF 18-APR-2002; 2002WO-US012476.

XX 18-APR-2001; 2001US-0284770P.
 PR 10-MAY-2001; 2001US-0290492P.
 PR 09-NOV-2001; 2001US-0339245P.
 PR 13-NOV-2001; 2001US-0350668P.
 PR 29-NOV-2001; 2001US-0334370P.
 PR 12-APR-2002; 2002US-0372246P.
 XX (EOSB-) EOS BIOTECHNOLOGY INC.
 XX
 XX PI Aziz N, Murray R;
 XX
 XX WPI; 2003-093161/08.
 DR P-PSDB; ABU56629.
 XX
 PT Detecting a lung cancer-associated transcript in a cell from a patient
 PT for treating lung cancer, by contacting a biological sample from the
 PT patient with a polynucleotide that exhibits increased or decreased
 PT expression in lung cancer.
 XX
 PS Claim 22; Page 357; 453pp; English.
 XX
 CC The invention relates to a method for detecting a lung cancer-associated
 CC transcript in a cell from a patient, comprising contacting a biological
 CC sample from the patient with a polynucleotide that selectively hybridizes
 CC to a sequence that is at least 80 % identical to a gene that exhibits
 CC increased or decreased expression in lung cancer samples. Lung cancer-
 CC associated polynucleotides and polypeptides are used for identifying a
 CC compound that modulates a lung cancer-associated polypeptide, for
 CC inhibiting proliferation of a lung cancer-associated cell to treat lung
 CC cancer in a patient and for treating a mammal having lung cancer by
 CC administering a modulatory compound identified. The methods are useful
 CC for treating lung cancer, such as small cell lung cancer, non-small cell
 CC lung cancer or other benign or precancerous lesions, e.g. atelectasis,
 CC emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis,
 CC hypersecretory pneumonia, interstitial pulmonary fibrosis, asthma and
 CC bronchiectasis. The genes, polynucleotides and polypeptides are useful
 CC for diagnostic purposes and as targets for screening for therapeutic
 CC compounds that modulate lung cancer, such as antibodies. Sequences
 CC ABX76124-ABX76474 represent lung cancer-associated polynucleotides of the
 CC invention
 XX
 SQ Sequence 1547 BP; 377 A; 423 C; 410 G; 337 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 6.2e-174 Length: 1547
 Score: 2098.00 Matches: 396
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 8 Gaps: 0

US-10-801-648-2 (1-396) x ABX76358 (1-1547)

QY 1 MetValAlaGlyThrArgCysLeuLeuAlaLeuLeuLeuProGlnValLeuLeuGlyGly 20
 DB 324 ATGTGTGGCGGACCGCTGCTTCTTACGTGTGCTTCCAGGTCTCTCTGGCGGCG 383
 QY 21 AlaAlaGlyLeuValProGluLeuGlyArgArgLysPheAlaAlaSerSerGlyArg 40
 DB 384 GCGGCTGGCTCTGTTCCGAGCTGGCGCGCAGGAAGTTCCGCGGCGGCTCTCTGGCGGCGC 443
 QY 41 ProSerSerGlnProSerAspGluValLeuSerGluPheGluLeuArgLeuLeuSerMet 60
 DB 444 CCTCATCCACCCCTCTGACAGAGTCTGAGCGAGTTCGAGTTCGCGCTCTCAGCATG 503
 QY 61 PheGlyLeuLysGlnArgProThrProSerArgAspAlaValValProProTyrMetLeu 80
 DB 504 TTCGGCTGGAACAGACAGACCCACCCAGAGGAGCGGTGGTGGTCCCTTACATGCTA 563
 QY 81 AspLeuTyrArgArgHisSerGlyGlnProGlySerProAlaProAspHisArgLeuGlu 100
 DB 564 GACCTGTATCGCAGGACCTCAGTCTCAGCGGGCTCACCGCGGCCAGACACCGCGTTGGAG 623

QY 101 ArgAlaAlaSerArgAlaAsnThrValArgSerPheHisGluGluSerLeuGluGlu 120
 DB 624 AGGCGAGCCAGCCGAGCCACACTGTGGCAGCTTCCACCATGAAGAAATCTTTGGAGAA 683
 QY 121 LeuProGluThrSerGlyLysThrThrArgArgPhePhePheAenLeuSerSerIlePro 140
 DB 684 CTACCAAAACGAGTGGGAAAACAAACCGGAGATCTCTTTAAATTTAAAGTTCTATCCCC 743
 QY 141 ThrGluGluPheIleThrSerAlaGluLeuGlnValPheArgGluGlnMetGluAspAla 160
 DB 744 ACGGAGGAGTTTATCACCCTCAGCAGAGCTTCCAGGTTTCCGAGAACAGATCGAGATGCT 803
 QY 161 LeuGlyAsnAsnSerSerPheHisArgIleAenIleTyrGluIleIleLysProAla 180
 DB 804 TTAGAAACATAGCAGTTCATCACCAGATTAATTAATTAATTAATTAATTAATTAATTA 863
 QY 181 ThrAlaAsnSerLysPheProValThrArgLeuLeuAspThrArgLeuValAsnGlnAen 200
 DB 864 ACAGCAACTCGAAATTCCTCCGTCACAGACTTTTGGACACACAGGTTGGTGAATCAGAA 923
 QY 201 AlaSerArgTTPGluSerPheAspValThrProAlaValMetArgTTPThrAlaGlnGly 220
 DB 924 GCAAGCAGGTGGGAAAGTTTGTATGTACCCCTGATGCGGTGGACTGCACAGGGA 983
 QY 221 HisAlaAsnHisGlyPheValValGluValAlaHisLeuGluGluLysGlnGlyValSer 240
 DB 984 CACGCCAACCCATGATTCGTGTGGAGTGGCCCACTTGGAGGAGAAACAGGTGTCTCC 1043
 QY 241 LysArgHisValArgIleSerArgSerLeuHisGlnAspGluHisSerTrpSerGlnIle 260
 DB 1044 AAGAGACATGTTAGGATAAGCAGGTCTTTGCAACCAAGATGAACACAGCTGGTTCAGATA 1103
 QY 261 ArgProLeuLeuValThrPheGlyHisAspGlyLysGlyHisProLeuHisLysArgGlu 280
 DB 1104 AGGCCATGTGTAGTAACCTTTTGGCCCATGATGAAAGAGGCGATCTCTCCACAAAGAGAA 1163
 QY 281 LysArgGlnAlaLysHisLysGlnArgLysArgLeuLysSerSerCysLysArgHisPro 300
 DB 1164 AAGCTCAGCCAAACACACACAGCGGAAAGCCCTTAAGTCCAGCTGTAAAGAGACACCT 1223
 QY 301 LeuTyrValAspPheSerAspValGlyTTPAsnAspTrpIleValAlaProProGlyTyr 320
 DB 1224 TTGTACGTGGACTTTCAGTGACGTGGGTGGAAATGACTGGATTGTGGCTCCCGGGGTAT 1283
 QY 321 HisAlaPheTyrCysHisGlyGluCysProPheProLeuAlaAspHisLeuAsnSerThr 340
 DB 1284 CACGCTTTTACTGCCAGGAGAAATGCCCTTTCTCTGGCTGATCATCTGAACCTCCACT 1343
 QY 341 AsnHisAlaIleValGlnThrLeuValAsnSerValAsnSerLysIleProLysAlaCys 360
 DB 1344 AATCATGCCATTTGTTACAGCTTGGTCAACTCTGTAACTCTAAGATTCTTAAGCATGTC 1403
 QY 361 CysValProThrGluLeuSerAlaIleSerMetLeuTyrLeuAspGluAsnGluLysVal 380
 DB 1404 TGTGTCCCGCAGAACTCAGTGTCTATCTCGATGCTGTACCTTGCAGAGATGAAGGTT 1463
 QY 381 ValLeuLysAsnTyrGlnAspMetValValGluGlyCysGlyCysArg 396
 DB 1464 GTATTAAAGAACTATCAGGACATGTTGTGGAGGGTTGTGGGTGTGTCG 1511
 RESULT 7
 ACF34481
 ID ACF34481 standard; DNA; 1547 BP.
 XX
 AC ACF34481;
 XX
 DT 15-OCT-2003 (first entry)
 XX
 DE Gene encoding angiogenesis protein BMO99.
 XX
 KW Cytostatic; antirheumatic; antiarthritic; antidiabetic; ophthalmological;
 KW antipsoriatic; antiarteriosclerotic; cardiant; vasotropic; angiogenesis;

KW gene therapy; vasculature; cancer; rheumatoid arthritis; psoriasis;
 KW diabetic retinopathy; cardiovascular disease; atherosclerosis;
 KW ischemic limb disease; coronary artery disease; gene; db.
 XX Homo sapiens.
 XX WO2003027285-A1.
 XX
 XX 03-APR-2003.
 PD
 XX 19-SEP-2002; 2002WO-AU001282.
 XX
 XX 27-SEP-2001; 2001AU-00007973.
 XX 27-SEP-2001; 2001AU-00007974.
 PR 11-OCT-2001; 2001AU-00008210.
 PR 29-OCT-2001; 2001AU-00008532.
 PR 13-NOV-2001; 2001AU-00008838.
 PR 28-AUG-2002; 2002AU-00951032.
 XX (BION-) BIONOMICS LTD.
 XX
 XX Gamble JR, Hahn CN, Vadas MA;
 XX P-PSDB; ABR64206.
 DR WPI; 2003-354655/33.
 XX
 XX New angiogenic genes and polypeptides, useful for diagnosing,
 PT prognosticating or treating an angiogenesis-related disorder, e.g.
 PT cancer, rheumatoid arthritis, diabetic retinopathy, psoriasis or
 PT cardiovascular diseases.
 XX
 XX Claim 2; SEQ ID NO 36; 90pp; English.
 XX
 CC The invention relates to the isolation of novel genes (ACF34446-ACF34559)
 CC encoding proteins (ABR64180-ABR64281) involved in the process of
 CC angiogenesis. The nucleic acid molecules are useful in identifying and/or
 CC obtaining full-length human genes involved in an angiogenic process. The
 CC nucleic acid molecule, polypeptides or complexes encoded, cells or
 CC genetically modified non-human animals derived from these are useful for
 CC the screening of candidate pharmaceutical compounds used in treating
 CC angiogenesis-related disorders. They are also useful for diagnosing,
 CC prognosticating or treating an angiogenesis-related disorder, which
 CC involves uncontrolled or enhanced angiogenesis or is a disorder in which
 CC a decreased vasculature is of benefit (e.g. cancer, rheumatoid arthritis,
 CC diabetic retinopathy, psoriasis or cardiovascular diseases such as
 CC atherosclerosis), or involves inappropriately arrested or decreased
 CC angiogenesis or is a disorder in which an expanding vasculature is of
 CC benefit (e.g. ischemic limb disease or coronary artery disease). The
 CC modulator of expression or activity of the polypeptide encoded by the
 CC nucleic acid sequence is useful for manufacturing a medicament for the
 CC treatment of an angiogenesis-related disorder. This sequence corresponds
 CC to the gene encoding one of the novel angiogenic protein
 XX
 XX Sequence 1547 BP; 377 A; 423 C; 410 G; 337 T; 0 U; 0 Other;
 SQ
 Alignment Scores:
 Pred. No.: 6.2e-174 Length: 1547
 Score: 2098.00 Matches: 396
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 8 Gaps: 0
 US-10-801-648-2 (1-396) x ACF34481 (1-1547)
 Qy 1 MetValAlaGlyThrArgCysLeuLeuAlaLeuLeuProGlnValLeuLeuGlyGly 20
 Db 324 ATGTGTGGCGGACCCGCTGTCTTCTAGCGTTGTCTTCCCGAGGTCTCTCGGGCGC 383
 Qy 21 AlaAlaGlyLeuValProGluLeuGlyArgArgLysPheAlaAlaLeuSerSerGlyArg 40
 Db 384 CGCGCTGGCTCTTTCGAGCTGGCGCGCAGGAAGTTGGCGGCGGCGTCTCGGGCGC 443

Qy 41 ProSerSerGlnProSerAspGluValLeuSerGluPheGluLeuArgLeuLeuSerMet 60
 Db 444 CCTCATCCAGCCCTCTGACGAGTCTCTGAGGAGTTCGAGTTGCGGCTGCTCAGCATG 503
 Qy 61 PheGlyLeuLysGlnArgProThrProSerArgAspAlaValValProProTyrMetLeu 80
 Db 504 TTCGGCTGAAACAGACAGACCCACCCAGCAGGAGCGCGTGGTGGCCCTACATGCTA 563
 Qy 81 AspLeuTyrArgArgHisSerGlyGlnProGlySerProAlaProAspHisArgLeuGlu 100
 Db 564 GACCTGTATCGCAGGCACTCAGGTTCAGCGGGTTCACCCGCCAGACCAACCGGTTGGAG 623
 Qy 101 ArgAlaAlaSerArgAlaAsnThrValArgSerPheHisGluGluSerLeuGluGlu 120
 Db 624 AGGCAGCCAGCCAGCAGCAACACTGTGCGGAGCTTCACCATGAAGATCTCTTGGAGAA 683
 Qy 121 LeuProGluThrSerGlyLysThrThrArgArgPhePheAsnLeuSerSerIlePro 140
 Db 684 CTACCAGAAACGAGTGGGAAACCAACCCGAGATCTCTCTTAATTTAAGTTCTATCCCC 743
 Qy 141 ThrGluGluPheIleThrSerAlaGluLeuValPheArgGluGlnMetGlnAspAla 160
 Db 744 ACGGAGGAGTTTATCACTCAGCAGAGCTTCAGGTTTTCGAGAACAGATGCAAGATGCT 803
 Qy 161 LeuGlyAsnAsnSerSerPheHisHisArgIleAsnIleTyrGluIleIleLysProAla 180
 Db 804 TTAGGAAACAAATAGCAGTTCCTCATCCAGATTAATTAATTAATTAATTAATTAATTA 863
 Qy 181 ThrAlaAsnSerLysPheProValThrArgLeuLeuAspThrArgLeuValAsnGlnAsn 200
 Db 864 ACAGCCAACTCGAAATTCCTCCGTCAGCAGACTTTTGACACACAGTTGGTGGTGAATCAGAAT 923
 Qy 201 AlaSerArgTrpGluSerPheAspValThrProAlaValMetArgTrpThrAlaGlnGly 220
 Db 924 GCAAGCAGTGGGAAAGTTTGTATGTCACTCCCGCTGTGATGCGGTGAGATGCAAGGGA 983
 Qy 221 HisAlaAsnHisGlyPheValValGluValAlaHisLeuGluGluLysGlnValSer 240
 Db 984 CAGCCCAACCATGATTCGTGGTGGAAAGTGGCCACTTGGAGGAGAAACAGGTGTCTCC 1043
 Qy 241 LysArgHisValArgIleSerArgSerLeuHisGlnAspGluHisSerTrpSerGlnIle 260
 Db 1044 AAGAGACATGTAGGATAAGCAGTCTTTGCCAACAGATGAACACAGCTGGTCCACAGATA 1103
 Qy 261 ArgProLeuValThrPheGlyHisAspGlyLysGlyHisProLeuHisLysArgGlu 280
 Db 1104 AGGCCATTGTCTAGTAATCTTTTGGCCATGATGGAAGGCGCATCTCTCCACAAAGAGAA 1163
 Qy 281 LysArgGlnAlaLysHisLysGlnValArgLysArgLeuLysSerSerCysLysArgHisPro 300
 Db 1164 AAAGCTACAGCCAAACAAACAGCGGAAACGCCCTTAAGTCCAGCTGTAGAGACACCT 1223
 Qy 301 LeuTyrValAspPheSerAspValGlyTrpAsnAspTrpIleValAlaProProGlyTyr 320
 Db 1224 TTGTACGTGGACTTCAGTGAGCTGGGTGGAAATGACTGGATTTGGTCTCCCGGGGTAT 1283
 Qy 321 HisAlaPheTyrCysHisGlyGluCysProPheProLeuAlaAspHisLeuAsnSerThr 340
 Db 1284 CACGCTTTTACTGCCACGAGGAATGCCCTTTCTCTGCTGATCATCTGAACTCCACT 1343
 Qy 341 AsnHisAlaIleValGlnThrLeuValAsnSerValAsnSerLysIleProLysAlaCys 360
 Db 1344 AATCATGCCATTGTTTACAGCTTGGTCACTCTGTTAACCTCTAAGATTTCTAAGGCATGC 1403
 Qy 361 CysValProThrGluLeuSerAlaIleSerMetLeuTyrLeuAspGluAsnGluLysVal 380
 Db 1404 TGTGTCCGACAGAACTCAGTGCTATCTCGATGCTGTACCTTTGACGAGAAATGAAGAGTT 1463
 Qy 381 ValLeuLysAsnTyrGlnAspMetValValGluGlyCysGlyCysArg 396
 Db 1464 GTATTAAAGAACTATCAGGACATGCTGTTGTGGAGGGTTGTGGGTGTGCG 1511
 RESULT 8

ACF05920
 ID ACF05920 standard; cDNA; 1547 BP.
 XX AC ACF05920;
 XX DT 04-DEC-2003 (first entry)
 XX DE Human bone morphogenic protein 2A polynucleotide.
 XX KW Bone morphogenic protein 2A; BMP-2A; human; glaucoma; diagnosis; therapy;
 XX KW ophthalmological; gene; ss.
 XX OS Homo sapiens.
 XX FH Key Location/Qualifiers
 XX CDS 324..1514
 XX FT /*tag= a
 XX FT /product= "BMP-2A"
 XX PN WO2003055443-A2.
 XX PD 10-JUL-2003.
 XX PF 31-OCT-2002; 2002WO-US035251.
 XX PR 31-OCT-2001; 2001US-0334852P.
 XX PA (ALCO-) ALCON INC.
 XX PA (UYNT-) UNIV NORTH TEXAS HEALTH SCI CENT.
 XX PI Clark AF, Wordinger RJ;
 XX WPI: 2003-559253/52.
 XX P-PSDB; ABR62824.
 XX DR Diagnosing glaucoma in a sample comprises detecting altered expression of
 XX PT bone morphogenic proteins in sample from a cell or bodily fluid.
 XX PS Claim 1; Fig 1a-c; 55pp; English.
 XX CC The present sequence is a nucleotide sequence for human bone morphogenic
 XX CC protein 2A (BMP-2A). RT-PCR showed BMP-2 to be expressed in the human
 XX CC trabecular meshwork and optic nerve head. A claimed method for diagnosing
 XX CC glaucoma involves detecting altered expression of a BMP family member
 XX CC such as BMP-2A by PCR in a sample obtained e.g. from blood or buccal
 XX CC cells. Primers used in the PCR may comprise contiguous nucleotides of the
 XX CC present sequence. A claimed method for treating glaucoma comprises
 XX CC administering an agonist of BMP-2, BMP-4, BMP-5, BMP-7 or Smad 1/5, or an
 XX CC antagonist of chordin, gremlin or follistatin. A claimed method of
 XX CC identifying a therapeutic agent for treatment of glaucoma comprises
 XX CC identifying a substance that inhibits or stimulates BMP-induced Smad
 XX CC signalling pathways or BMP-regulated gene expression, using recombinant
 XX CC cells expressing BMP-2A, BMP-4, BMP-5 or BMP-7
 XX SQ Sequence 1547 BP; 377 A; 423 C; 410 G; 337 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 6,2e-174 Length: 1547
 Score: 2098.00 Matches: 396
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 10 Gaps: 0

US-10-801-648-2 (1-396) x ACF05920 (1-1547)

QY 1 MetValAlaGlyThrArgCysLeuLeuAlaLeuLeuProGlnValLeuLeuGlyGly 20
 Db 324 ATGGTGGCCGGACCGCGCTGCTTCTAGCGTTGCTTCCCGAGTCTCTCTGGCGGC 383
 QY 21 AlaAlaGlyLeuValProGlnLeuGlyArgArgLysPheAlaAlaAlaSerSerGlyArg 40
 Db 384 GCGGCTGGCTCGTTCGGGAGCTGGGCGCGAGAGTTCCGCGCGCGCTCGTGGCGGC 443

QY 41 ProSerSerGlnProSerAspGluValLeuSerGluPheGluLeuArgLeuLeuSerMet 60
 Db 444 CCTCATCCAGCCCTCTGACGAGTCTGAGCGAGTTCCGAGTTGGGCTGCTCAGCATG 503
 QY 61 PheGlyLeuLysGlnArgProThrProSerArgAspAlaValProProTyrMetLeu 80
 Db 504 TTGGGCTGAAACAGACAGACCCACCCAGCAGGAGCGCGTGGTGGTGGTGGTGGTGGT 563
 QY 81 AspLeuTyrArgArgHisSerGlyGlnProGlySerProAlaProAspHisArgLeuGlu 100
 Db 564 GACCTGTATCGAGGCACTCAGGTACGCGGGCTCACCCGCGCCAGACACCGGTGGAG 623
 QY 101 ArgAlaAlaSerArgAlaAenThrValArgSerPheHisHisGluGluSerLeuGluGlu 120
 Db 624 AGGCGAGCCAGCCAGCCCAACACTGTGCGCAGCTTCCACCATGAAGATCTTTGGAAGAA 683
 QY 121 LeuProGluThrSerGlyLysThrThrArgArgPhePheAenLeuSerSerIlePro 140
 Db 684 CTACCGAAACGAGTGGGAAACCAACCGGAGATTTCTTTTAAATTTAAGTTCTATCCCC 743
 QY 141 ThrGluGluPheIleThrSerAlaGluLeuGlnValPheArgGluGlnMetGlnAspAla 160
 Db 744 ACGGAGGAGTTTATCACCCTCAGCAGAGCTTCCAGGTTTTCCGAGACACATGCAAGATGCT 803
 QY 161 LeuGlyAenAenSerSerPheHisArgIleAenIleTyrGluIleIleLysProAla 180
 Db 804 TTAGGAACATAGCAGTTTCCATCCCGAATTAATTAATTAATTAATTAATTAATTAATTA 863
 QY 181 ThrAlaAenSerLysPheProValThrArgLeuLeuAspThrArgLeuValAenGlnAen 200
 Db 864 ACAGCCAACTCGAAATTCCTCCGTGACACAGACTTTTGGACACAGGTTGGTGAATCAGAAT 923
 QY 201 AlaSerArgTyrGluSerPheAspValThrProAlaValMetArgTyrThrAlaGlnGly 220
 Db 924 GCAAGCAGGTGGGAAAGTTTGTATGTACCCCGCTGTGTGATGCGGTGACGTGCACAGGA 983
 QY 221 HisAlaAenHisGlyPheValValAlaHisLeuGluGluLysGlnGlyValSer 240
 Db 984 CACGCCAACCATGGATTCGTGTGGAGTGGCCCACTTGGAGAGAAACAGGTGTCTCTCC 1043
 QY 241 LysArgHisValArgIleSerArgSerLeuHisGlnAspGluHisSerTyrSerGlnIle 260
 Db 1044 AAGACATGTTAGGATAAGCAGGTCTTTGCAACCAAGATGAACACAGCTGTGTGCACAGATA 1103
 QY 261 ArgProLeuLeuValThrPheGlyHisAspGlyLysGlyHisProLeuHisLysArgGlu 280
 Db 1104 AGGCCATTGCTAGTAACCTTTTGGCCCATGATGGAAGAGGCGATCTCTCCACAAAAGAGAA 1163
 QY 281 LysArgGlnAlaLysHisLysGlnArgLysArgLeuLysSerSerCysLysArgHisPro 300
 Db 1164 AAACGTCAAGCCAAACACAAACAGCGGAAACGCTTAAGTCCAGCTGTGAAGACACCCCT 1223
 QY 301 LeuTyrValAspPheSerAspValGlyTyrPheAenAspTyrIleValAlaProProGlyTyr 320
 Db 1224 TTGTACGTGGACTTCAGTGACGTGGGTGGAATGACTGGATTTGGCTCTCCCGCGGTAT 1283
 QY 321 HisAlaPheTyrCysHisGlyGluCysProPheProLeuAlaAspHisLeuAenSerThr 340
 Db 1284 CACGCTTTTACTGCGCACGGAAATGCCCTTTTCTCTGGCTGATCATCTGAACTCCACT 1343
 QY 341 AenHisAlaIleValGlnThrLeuValAenSerValAenSerLysIleProLysAlaCys 360
 Db 1344 AATCATGCATTTGTTACAGCGTTGGTCACTCTGTAACTCTTAAGTTCTTAAGCATGTC 1403
 QY 361 CysValProThrGluLeuSerAlaIleSerMetLeuTyrLeuAspGluAenGluLysVal 380
 Db 1404 TGTGTCCCGACAGAACTCAGTGTCTATCTCGATGTGTACCTTGTGACGAGAAATGAAAGGTT 1463
 QY 381 ValLeuLysAenTyrGlnAspMetValValGluGlyCysGlyCysArg 396
 Db 1464 GTATTAAAGAACTATCAGGACATGTTGTGGAGGTTGTGGGTGTGTCG 1511

| | | | | |
|---|---|---------------|-------|---|
| RESULT 9 | DB: | 10 | Gaps: | 0 |
| ADD14609 | US-10-801-648-2 (1-396) x ADD14609 (1-1547) | | | |
| XX ID ADD14609 standard; cDNA; 1547 BP. | | | | |
| XX AC | | | | |
| XX AT | | | | |
| XX DT 01-JAN-2004 (first entry) | | | | |
| XX DE Human src biomarker polynucleotide SEQ ID NO:3. | | | | |
| XX KW predictor set; protein tyrosine kinase activity modulator; | | | | |
| XX KW protein tyrosine kinase pathway; protein tyrosine kinase; cytostatic; | | | | |
| XX KW gene therapy; drug sensitivity; genetic profile; cancer; human; gene; ss. | | | | |
| XX OS Homo sapiens. | | | | |
| XX WO2003062395-A2. | | | | |
| XX 31-JUL-2003. | | | | |
| XX 17-JAN-2003; 2003WO-US001981. | | | | |
| XX 18-JAN-2002; 2002US-0350061P. | | | | |
| XX (BRIM) BRISTOL-MYERS SQUIBB CO. | | | | |
| XX Huang F, Fairchild CR, Lee FY, Shaw P; | | | | |
| XX P-PSDB; ADD14015. | | | | |
| XX WPI; 2003-636735/60. | | | | |
| XX PT New polynucleotides and polypeptides for predicting the activity of | | | | |
| XX PT compounds that interact with protein tyrosine kinases and/or protein | | | | |
| XX PT tyrosine kinase pathways. | | | | |
| XX Claim 2; SEQ ID NO 3; 139pp; English. | | | | |
| XX The present invention describes a predictor set comprising a plurality of | | | | |
| XX polynucleotides or polypeptides whose expression pattern is predictive of | | | | |
| XX the response of cells to treatment with a compound that modulates protein | | | | |
| XX tyrosine kinase activity or members of the protein tyrosine kinase | | | | |
| XX pathway. Also described: (1) predicting whether a compound is capable of | | | | |
| XX modulating the activity of cells, comprising obtaining a sample of cells, | | | | |
| XX determining whether the cells express a plurality of markers, and | | | | |
| XX correlating the expression of the markers to the compound's ability to | | | | |
| XX modulate the activity of the cells; (2) a plurality of cell lines for | | | | |
| XX identifying polynucleotides and polypeptides whose expression levels | | | | |
| XX correlate with compound sensitivity or resistance of cells associated | | | | |
| XX with a disease state; and (3) identifying polynucleotides and | | | | |
| XX polypeptides that predict compound sensitivity or resistance of cells | | | | |
| XX associated with a disease state, comprising subjecting the plurality of | | | | |
| XX cell lines to one or more compounds, analysing the expression pattern of | | | | |
| XX a microarray of polynucleotides or polypeptides, and selecting | | | | |
| XX polynucleotides or polypeptides that predict the sensitivity or | | | | |
| XX resistance of cells associated with a disease state by using the | | | | |
| XX expression pattern of the microarray. The polynucleotides and | | | | |
| XX polypeptides have cytostatic activities, and can be used in gene therapy. | | | | |
| XX The polynucleotides and polypeptides are useful in predicting the | | | | |
| XX activity of compounds that interact with protein tyrosine kinases and/or | | | | |
| XX protein tyrosine kinase pathways. These may be used in determining drug | | | | |
| XX sensitivity in patients to allow the development of individualized | | | | |
| XX genetic profiles which aid in treating diseases and disorders (e.g. | | | | |
| XX cancer) based on patient response at a molecular level. The present | | | | |
| XX sequence is used in the exemplification of the present invention. | | | | |
| XX SQ Sequence 1547 BP; 377 A; 423 C; 410 G; 337 T; 0 U; 0 Other; | | | | |
| Alignment Scores: | | | | |
| Pred. No.: | 6.2e-174 | Length: | 1547 | |
| Score: | 2098.00 | Matches: | 396 | |
| Percent Similarity: | 100.00% | Conservative: | 0 | |
| Best Local Similarity: | 100.00% | Mismatches: | 0 | |
| Query Match: | 100.00% | Indels: | 0 | |

| | | | |
|----|------|--|------|
| Db | 1344 | AATCATGCCATGTGTTACAGACGTGTGTCAACTCTCTTAACTCTAAGATTCCTTAAGCATGC | 1403 |
| Qy | 361 | CysValProThrGluLeuSerAlaIleSerMetLeuTyrLeuAspGluAsnGluLysVal | 380 |
| Db | 1404 | TGTGTCCCGACAGAACTCAGTGTCTATCTCGATGCTGTACCTTGACGAGAATGAARAAGTT | 1463 |
| Qy | 381 | ValLeuLysAsnTyrGlnAspMetValValGluGlyCysGlyCysArg | 396 |
| Db | 1464 | GTATTAAAGAACTATCAGACATGTTGTGAGGAGTTGTGGGTGTGCG | 1511 |

RESULT 10

AD85186

IP ADE85186 standard: DNA: 1547 BP.

XX

AC ADE85186;

XX

DT 29-JAN-2004 (first entry)

XX

DE Farnesyl tran

XX

KW 88; cytostat.

KW quinolinone; leukemia; cancer

55

OS Homo sapiens.

1
 2
 3
 4
 5
 6
 7
 8
 9
 10
 11
 12
 13
 14
 15
 16
 17
 18
 19
 20
 21
 22
 23
 24
 25
 26
 27
 28
 29
 30
 31
 32
 33
 34
 35
 36
 37
 38
 39
 40
 41
 42
 43
 44
 45
 46
 47
 48
 49
 50
 51
 52
 53
 54
 55
 56
 57
 58
 59
 60
 61
 62
 63
 64
 65
 66
 67
 68
 69
 70
 71
 72
 73
 74
 75
 76
 77
 78
 79
 80
 81
 82
 83
 84
 85
 86
 87
 88
 89
 90
 91
 92
 93
 94
 95
 96
 97
 98
 99
 100
 101
 102
 103
 104
 105
 106
 107
 108
 109
 110
 111
 112
 113
 114
 115
 116
 117
 118
 119
 120
 121
 122
 123
 124
 125
 126
 127
 128
 129
 130
 131
 132
 133
 134
 135
 136
 137
 138
 139
 140
 141
 142
 143
 144
 145
 146
 147
 148
 149
 150
 151
 152
 153
 154
 155
 156
 157
 158
 159
 160
 161
 162
 163
 164
 165
 166
 167
 168
 169
 170
 171
 172
 173
 174
 175
 176
 177
 178
 179
 180
 181
 182
 183
 184
 185
 186
 187
 188
 189
 190
 191
 192
 193
 194
 195
 196
 197
 198
 199
 200
 201
 202
 203
 204
 205
 206
 207
 208
 209
 210
 211
 212
 213
 214
 215
 216
 217
 218
 219
 220
 221
 222
 223
 224
 225
 226
 227
 228
 229
 230
 231
 232
 233
 234
 235
 236
 237
 238
 239
 240
 241
 242
 243
 244
 245
 246
 247
 248
 249
 250
 251
 252
 253
 254
 255
 256
 257
 258
 259
 260
 261
 262
 263
 264
 265
 266
 267
 268
 269
 270
 271
 272
 273
 274
 275
 276
 277
 278
 279
 280
 281
 282
 283
 284
 285
 286
 287
 288
 289
 290
 291
 292
 293
 294
 295
 296
 297
 298
 299
 300
 301
 302
 303
 304
 305
 306
 307
 308
 309
 310
 311
 312
 313
 314
 315
 316
 317
 318
 319
 320
 321
 322
 323
 324
 325
 326
 327
 328
 329
 330
 331
 332
 333
 334
 335
 336
 337
 338
 339
 340
 341
 342
 343
 344
 345
 346
 347
 348
 349
 350
 351
 352
 353
 354
 355
 356
 357
 358
 359
 360
 361
 362
 363
 364
 365
 366
 367
 368
 369
 370
 371
 372
 373
 374
 375
 376
 377
 378
 379
 380
 381
 382
 383
 384
 385
 386
 387
 388
 389
 390
 391
 392
 393
 394
 395
 396
 397
 398
 399
 400
 401
 402
 403
 404
 405
 406
 407
 408
 409
 410
 411
 412
 413
 414
 415
 416
 417
 418
 419
 420
 421
 422
 423
 424
 425
 426
 427
 428
 429
 430
 431
 432
 433
 434
 435
 436
 437
 438
 439
 440
 441
 442
 443
 444
 445
 446
 447
 448
 449
 450
 451
 452
 453
 454
 455
 456
 457
 458
 459
 460
 461
 462
 463
 464
 465
 466
 467
 468
 469
 470
 471
 472
 473
 474
 475
 476
 477
 478
 479
 480
 481
 482
 483
 484
 485
 486
 487
 488
 489
 490
 491
 492
 493
 494
 495
 496
 497
 498
 499
 500
 501
 502
 503
 504
 505
 506
 507
 508
 509
 510
 511
 512
 513
 514
 515
 516
 517
 518
 519
 520
 521
 522
 523
 524
 525

PN WO2003038129-A2.

2000
 2001
 2002
 2003
 2004
 2005
 2006
 2007
 2008
 2009
 2010
 2011
 2012
 2013
 2014
 2015
 2016
 2017
 2018
 2019
 2020
 2021
 2022
 2023
 2024
 2025
 2026
 2027
 2028
 2029
 2030
 2031
 2032
 2033
 2034
 2035
 2036
 2037
 2038
 2039
 2040
 2041
 2042
 2043
 2044
 2045
 2046
 2047
 2048
 2049
 2050
 2051
 2052
 2053
 2054
 2055
 2056
 2057
 2058
 2059
 2060
 2061
 2062
 2063
 2064
 2065
 2066
 2067
 2068
 2069
 2070
 2071
 2072
 2073
 2074
 2075
 2076
 2077
 2078
 2079
 2080
 2081
 2082
 2083
 2084
 2085
 2086
 2087
 2088
 2089
 2090
 2091
 2092
 2093
 2094
 2095
 2096
 2097
 2098
 2099
 2100
 2101
 2102
 2103
 2104
 2105
 2106
 2107
 2108
 2109
 2110
 2111
 2112
 2113
 2114
 2115
 2116
 2117
 2118
 2119
 2120
 2121
 2122
 2123
 2124
 2125
 2126
 2127
 2128
 2129
 2130
 2131
 2132
 2133
 2134
 2135
 2136
 2137
 2138
 2139
 2140
 2141
 2142
 2143
 2144
 2145
 2146
 2147
 2148
 2149
 2150
 2151
 2152
 2153
 2154
 2155
 2156
 2157
 2158
 2159
 2160
 2161
 2162
 2163
 2164
 2165
 2166
 2167
 2168
 2169
 2170
 2171
 2172
 2173
 2174
 2175
 2176
 2177
 2178
 2179
 2180
 2181
 2182
 2183
 2184
 2185
 2186
 2187
 2188
 2189
 2190
 2191
 2192
 2193
 2194
 2195
 2196
 2197
 2198
 2199
 2200
 2201
 2202
 2203
 2204
 2205
 2206
 2207
 2208
 2209
 2210
 2211
 2212
 2213
 2214
 2215
 2216
 2217
 2218
 2219
 2220
 2221
 2222
 2223
 2224
 2225
 2226
 2227
 2228
 2229
 2230
 2231
 2232
 2233
 2234
 2235
 2236
 2237
 2238
 2239
 2240
 2241
 2242
 2243
 2244
 2245
 2246
 2247
 2248
 2249
 2250
 2251
 2252
 2253
 2254
 2255
 2256
 2257
 2258
 2259
 2260
 2261
 2262
 2263
 2264
 2265
 2266
 2267
 2268
 2269
 2270
 2271
 2272
 2273
 2274
 2275
 2276
 2277
 2278
 2279
 2280
 2281
 2282
 2283
 2284
 2285
 2286
 2287
 2288
 2289
 2290
 2291
 2292
 2293
 2294
 2295
 2296
 2297
 2298
 2299
 2300
 2301
 2302
 2303
 2304
 2305
 2306
 2307
 2308
 2309
 2310
 2311
 2312
 2313
 2314
 2315
 2316
 2317
 2318
 2319
 2320
 2321
 2322
 2323
 2324
 2325
 2326
 2327
 2328
 2329
 2330
 2331
 2332
 2333
 2334
 2335
 2336
 2337
 2338
 2339
 2340
 2341
 2342
 2343
 2344
 2345
 2346
 2347
 2348
 2349
 2350
 2351
 2352
 2353
 2354
 2355
 2356
 2357
 2358
 2359
 2360
 2361
 2362
 2363
 2364
 2365
 2366
 2367
 2368
 2369
 2370
 2371
 2372
 2373
 2374
 2375
 2376
 2377
 2378
 2379
 2380
 2381
 2382
 2383
 2384
 2385
 2386
 2387
 2388
 2389
 2390
 2391
 2392
 2393
 2394
 2395
 2396
 2397
 2398
 2399
 2400
 2401
 2402
 2403
 2404
 2405
 2406
 2407
 2408
 2409
 2410
 2411
 2412
 2413
 2414
 2415
 2416
 2417
 2418
 2419
 2420
 2421
 2422
 2423
 2424
 2425
 2426
 2427
 2428
 2429
 2430
 2431
 2432
 2433
 2434
 2435
 2436
 2437
 2438
 2439
 2440
 2441
 2442
 2443
 2444
 2445
 2446
 2447
 2448
 2449
 2450
 2451
 2452
 2453
 2454

FD 08-MAY-20
yy

XX
DE
DE
DE

FF
YY
30-UCT-2002; 2002MC-US034783.

30-OCT-2001: 2001US-0338997P

PK 30-OCT-2001; 2001US-0338397E.
PR 30-OCT-2001; 2001US-0340081P.

EK 30-OCT-2001; 2001US-034008LF;
 PR 30-OCT-2001: 2001US-0340938P

PR 30-OCT-2001: 2001US-0341012P.
PR 30-OCT-2001: 2001US-0341012P.
PR 30-OCT-2001: 2001US-0341012P.

1
 2
 3
 4
 5
 6
 7
 8
 9
 10
 11
 12
 13
 14
 15
 16
 17
 18
 19
 20
 21
 22
 23
 24
 25
 26
 27
 28
 29
 30
 31
 32
 33
 34
 35
 36
 37
 38
 39
 40
 41
 42
 43
 44
 45
 46
 47
 48
 49
 50
 51
 52
 53
 54
 55
 56
 57
 58
 59
 60
 61
 62
 63
 64
 65
 66
 67
 68
 69
 70
 71
 72
 73
 74
 75
 76
 77
 78
 79
 80
 81
 82
 83
 84
 85
 86
 87
 88
 89
 90
 91
 92
 93
 94
 95
 96
 97
 98
 99
 100
 101
 102
 103
 104
 105
 106
 107
 108
 109
 110
 111
 112
 113
 114
 115
 116
 117
 118
 119
 120
 121
 122
 123
 124
 125
 126
 127
 128
 129
 130
 131
 132
 133
 134
 135
 136
 137
 138
 139
 140
 141
 142
 143
 144
 145
 146
 147
 148
 149
 150
 151
 152
 153
 154
 155
 156
 157
 158
 159
 160
 161
 162
 163
 164
 165
 166
 167
 168
 169
 170
 171
 172
 173
 174
 175
 176
 177
 178
 179
 180
 181
 182
 183
 184
 185
 186
 187
 188
 189
 190
 191
 192
 193
 194
 195
 196
 197
 198
 199
 200
 201
 202
 203
 204
 205
 206
 207
 208
 209
 210
 211
 212
 213
 214
 215
 216
 217
 218
 219
 220
 221
 222
 223
 224
 225
 226
 227
 228
 229
 230
 231
 232
 233
 234
 235
 236
 237
 238
 239
 240
 241
 242
 243
 244
 245
 246
 247
 248
 249
 250
 251
 252
 253
 254
 255
 256
 257
 258
 259
 260
 261
 262
 263
 264
 265
 266
 267
 268
 269
 270
 271
 272
 273
 274
 275
 276
 277
 278
 279
 280
 281
 282
 283
 284
 285
 286
 287
 288
 289
 290
 291
 292
 293
 294
 295
 296
 297
 298
 299
 300
 301
 302
 303
 304
 305
 306
 307
 308
 309
 310
 311
 312
 313
 314
 315
 316
 317
 318
 319
 320
 321
 322
 323
 324
 325
 326
 327
 328
 329
 330
 331
 332
 333
 334
 335
 336
 337
 338
 339
 340
 341
 342
 343
 344
 345
 346
 347
 348
 349
 350
 351
 352
 353
 354
 355
 356
 357
 358
 359
 360
 361
 362
 363
 364
 365
 366
 367
 368
 369
 370
 371
 372
 373
 374
 375
 376
 377
 378
 379
 380
 381
 382
 383
 384
 385
 386
 387
 388
 389
 390
 391
 392
 393
 394
 395
 396
 397
 398
 399
 400
 401
 402
 403
 404
 405
 406
 407
 408
 409
 410
 411
 412
 413
 414
 415
 416
 417
 418
 419
 420
 421
 422
 423
 424
 425
 426
 427
 428
 429
 430
 431
 432
 433
 434
 435
 436
 437
 438
 439
 440
 441
 442
 443
 444
 445
 446
 447
 448
 449
 450
 451
 452
 453
 454
 455
 456
 457
 458
 459
 460
 461
 462
 463
 464
 465
 466
 467
 468
 469
 470
 471
 472
 473
 474
 475
 476
 477
 478
 479
 480
 481
 482
 483
 484
 485
 486
 487
 488
 489
 490
 491
 492
 493
 494
 495
 496
 497
 498
 499
 500
 501
 502
 503
 504
 505
 506
 507
 508
 509
 510
 511
 512
 513
 514
 515
 516
 517
 518
 519
 520
 521
 522
 523
 524
 525

PA (ORTH) ORTHO CLINICAL DIAGNOSTICS INC.

THE UNIVERSITY OF CHICAGO PRESS

PI Raponi M;

XX
-
7

DR WPI; 2003-513497/48.

XX

PT Determining whether a patient will respond to treatment with a farnesyl

PT transferase inhibitor, by analyzing the expression of gene that is

PT differentially modulated in the presence of the inhibitor.

XX

PS Disclosure; SEQ ID NO 405; 346pp; English.

11

The invention relates to a method of deter-

respond to treatment with a larnesyl trans

CC analyzing the expression of gene that is

presence of an FTL. The method is useful
patient will respond to treatment with a

CC patient will respond to treatment with a FII such as (B)-6-[amino(4-chlorophenyl)]-(1-methyl-1H-imidazo[5-y])methyl]-4-(3-chlorophenyl)]-1-

CC chlorphenyl (1-methyl-1H-1H-imidazol-3-yl)methyl-4-(3-chlorophenyl)-1-
CC methyl-2-(1H-imidazol-3-yl)methyl-4-(3-chlorophenyl)-1-
CC methyl-2-(1H-imidazol-3-yl)methyl-4-(3-chlorophenyl)-1-

| | | | |
|----|------|--|------|
| Db | 324 | ATGGTGCCCGGACCCGCTGTCTTTAGCGTTGCTGCTTCCCCAGGTCTCTCTGGGCGGC | 383 |
| Qy | 21 | AlaAlaGlyLeuValProGluLeuLeuGlyArgArgLysPheAlaAlaLaserSerGlyArg | 40 |
| Db | 384 | CGGCTGGCTCTGTTCCGGAGCTGGGCGCAGGAAGTTTCGCGCGCGCTGCTCGGCGCGC | 443 |
| Qy | 41 | ProSerSerGlnProSerAspGluValLeuSerGluPheGluLeuArgLeuLeuSerMet | 60 |
| Db | 444 | CCCTCATCCAGCCCTCTGACGAGGTCTCGAGCGAGTTTCGAGTTGCGGCTGCTCAGCATG | 503 |
| Qy | 61 | PheGlyLeuLysGlnArgProThrProSerArgAspAlaValValProProTyrMetLeu | 80 |
| Db | 504 | TTGCGCTGTAAACAGAGACCCACCCCGAGGAGCGCGTGTGTGCCCCCTACATGCTA | 563 |
| Qy | 81 | AspLeuTyrArgArgHisSerGlyGlnProGlySerProAlaProAspHisArgLeuGlu | 100 |
| Db | 564 | GACCTGATCGAGGCACTCAGTTCAGCCGGGCTCACCCGCCCCAGACCAACCGTTGGAG | 623 |
| Qy | 101 | ArgAlaLaserArgAlaAenThrValArgSerPheHisHisGluGluSerLeuGluGlu | 120 |
| Db | 624 | AGGCGACCCAGCGAGCAACACTGTGTGCGAGCTTCCACCATGAAGAATCTTTGGAGAA | 683 |
| Qy | 121 | LeuProGluThrSerGlyLysThrThrArgArgPhePheAsnLeuSerSerLePro | 140 |
| Db | 684 | CTACGAAACGAGTGGGAACAAACCCGAGATTTCTTTTAATTTAAGTTCTTATCCCC | 743 |
| Qy | 141 | ThrGluGluPheLeuThrSerAlaGluLeuGlnValPheArgGluGlnMetGlnAspAla | 160 |
| Db | 744 | ACGAGGAGTTTATCACTCAGCAGAGCTTCAGGTTTCCGAGAACAGATGCAAGATGCT | 803 |
| Qy | 161 | LeuGlyAenAenSerSerPheHisHisArgLysAenLleTyrGluLleLleLysProAla | 180 |
| Db | 804 | TTAGAAACAATAGCAGTTTCCATCACCGAATTAATTTATGAAATCATAAACCTGCA | 863 |
| Qy | 181 | ThrAlaAenSerLysPheProValThrArgLeuLeuAspThrArgLeuValAenGlnAsn | 200 |
| Db | 864 | ACGCCAACTCGAAATTTCCCGTGACACAGACTTTTGGACACCAAGTTGGTGAATCAGAAT | 923 |
| Qy | 201 | AlaSerArgTrpGluSerPheAspValThrProAlaValMetArgTrpThrAlaGlnGly | 220 |
| Db | 924 | GCAAGCAGGTGGGAAGTTTGTATGTACCCCCGCTGTGTATGCGTGGCATCTGCACAGGA | 983 |
| Qy | 221 | HisAlaAenHisGlyPheValValGluValAlaHisLeuGluLysGlnGlyValSer | 240 |
| Db | 984 | CACGCCAACCATGATTCGTGGTGGAAAGTGCCCACTTGGAGGAGAAACAAGGTGTCTCC | 1043 |
| Qy | 241 | LysArgHisValArgLleSerArgSerLeuHisGlnAspGluHisSerTrpSerGlnIle | 260 |
| Db | 1044 | AAGAGACATGTTAGGATTAACAGGTCTTTGCAACAGATGAACACACCTGGTTCACAGATA | 1103 |
| Qy | 261 | ArgProLeuLeuValThrPheGlyHisAspGlyLysGlyHisProLeuHisLysArgGlu | 280 |
| Db | 1104 | AGGCCATTGCTAGTAACTTTTGGCCATGATGGAAGAAGGGCATCTCTCTCCACAAAGAGAA | 1163 |
| Qy | 281 | LysArgGlnAlaLysHisLysGlnArgLysArgLeuLysSerSerCysLysArgHisPro | 300 |
| Db | 1164 | AAACGTCAAGCCAAACAAACACGCGAAACGCCCTTAAGTCCAGCTGTAAGAGACACCCCT | 1223 |
| Qy | 301 | LeuTyrValAspPheSerAspValGlyTrpAsnAspTrpIleValAlaProProGlyTyr | 320 |
| Db | 1224 | TTGTACGTGGCACTTCAGTGCAGTGGGTGGAATGACTGGAATGTGGCTCCCCCGGGTAT | 1283 |
| Qy | 321 | HisAlaPheTyrCysHisGlyGluCysProPheProLeuAlaAspHisLeuAenSerThr | 340 |
| Db | 1284 | CACGCCTTTACTGCCACGGGAATGCCCTTTTCTCTGGCTGATCATCTGAACTCCACT | 1343 |
| Qy | 341 | AenHisAlaIleValGlnThrLeuValAenSerValAenSerLysIleProLysAlaCys | 360 |
| Db | 1344 | AATCATGCCATTGTTACAGCGTTGTTCACTCTGTTAACTCTAAGATTTCTTAAGCATGC | 1403 |
| Qy | 361 | CysValProThrGluLeuSerAlaIleSerMetLeuTyrLeuAspGluAenGluLysVal | 380 |

Db 1404 TGTGTCGCGACAGAACTCAGTGTCTATCTCGATGCTGTACCTTGACGAGATGAAAGGTT 1463

Qy 381 ValLeuLysAsnTyrGlnAspMetValValGluGlyCysGlyCysArg 396
|||||
Db 1464 GTATTAAAGAACTATCAGGACATGTTGTGGAGGTTGTGGGTGTCGC 1511

RESULT 11
AAD63420
ID AAD63420 standard; DNA; 1547 BP.
XX
AC AAD63420;
XX
DT 12-FEB-2004 (first entry)
XX
DE Human bone morphogenetic protein (BMP)-2 DNA.
XX
KW Human; BMP; bone morphogenetic protein; cancer; therapy; gene; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 324..1514
FT FT /*tag= a
FT FT /product= "Human BMP-2 protein"
FT FT /*tag= b
FT FT /label= Signal_peptide
FT FT 429..1127
FT FT /*tag= d
FT FT /note= "Transforming growth factor (TGF)-beta propeptide
FT FT region"
FT FT replace(432,G)
FT FT /*tag= e
FT FT replace(584,G)
FT FT /*tag= f
FT FT replace(893,T)
FT FT /*tag= g
FT FT 1170..1511
FT FT /*tag= c
FT FT /product= "Mature human BMP-2 protein"
FT FT 1209..1511
FT FT /*tag= h
FT FT /note= "Transforming growth factor (TGF)-beta-like
FT FT domain"
XX
PN US2003134790-A1.
XX
XX 17-JUL-2003.
XX
XX 02-MAY-2002; 2002US-00139814.
XX
PR 11-JAN-2002; 2002US-00044716.
XX
XX (UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.
XX
PI Langenfeld J;
XX
XX WPI; 2003-829645/77.
DR P-PSDB; ABW01849.
XX
PT Treating cancer, e.g. carcinoma of the breast, bladder, colon, kidney,
FT lung, ovary, thyroid, endometrium, omental, testis or liver, comprises
FT administering to the patient a bone morphogenetic protein-4 activity
FT inhibitor.
XX
PS Disclosure; Page 15-17; 64pp; English.
XX
CC The present invention relates to the use of BMP (bone morphogenetic
CC protein)-2 and BMP-4 used in treating cancer. The invention is useful for
CC treating cancer, e.g. carcinoma of the breast, bladder, colon, lung,
CC kidney, ovary, thyroid, endometrium, omental, testis and liver. The
CC present sequence is human bone morphogenetic protein (BMP)-2 DNA
XX

SQ Sequence 1547 BP; 377 A; 423 C; 410 G; 337 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 6.2e-174 Length: 1547
Score: 2098.00 Matches: 396
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-10-801-648-2 (1-396) x AAD63420 (1-1547)

Qy 1 MetValAlaGlyThrArgCysLeuLeuAlaLeuLeuProGlnValLeuLeuGlyGly 20
|||||
Db 324 ATGTGGCCGGAGCCCGCTGTCTTAGCGGTGCTCTCCACAGGTCCTCTCGGGCGGC 383
|||||

Qy 21 AlaAlaGlyLeuValProGluLeuGlyArgArgLysPheAlaAlaLysSerSerGlyArg 40
|||||

Db 384 GCGCTGGCTCGTTCGGAGCTGGCCCGCAGAGTTTCGGGGGGGCTGTCGGGCGGC 443
|||||

Qy 41 ProSerSerGlnProSerAspGluValLeuSerGluPheGluLeuArgLeuLeuSerMet 60
|||||

Db 444 CCTCATCCAGGCCCTCTGACGAGTCTCTGAGCGAGTTCCGAGTTTCGGCTGCTCAGCATG 503
|||||

Qy 61 PheGlyLeuLysGlnArgProThrProSerArgAspAlaValValProProTyrMetLeu 80
|||||

Db 504 TTCGGCTGAACAGAGACCCACCCCGCAGGAGCCCGTGGTGGCCCTCATGCTA 563
|||||

Qy 81 AspLeuTyrArgArgHisSerGlyGlnProGlySerProAlaProAspHisArgLeuGlu 100
|||||

Db 564 GACCTGTATCGAGGCACTCAGTCCAGCGGGCTCACCCGCCCGCAGACACCGGTTCGAG 623
|||||

Qy 101 ArgAlaAlaSerArgAlaAsnThrValArgSerPheHisHisGluGluSerLeuGluGlu 120
|||||

Db 624 AGGCGAGCCAGCGAGCAACACTGTGCGCAGCTTCCACCATGAAGAATCTTTGGAGAA 683
|||||

Qy 121 LeuProGluThrSerGlyLysThrThrArgArgPhePheAsnLeuSerSerIlePro 140
|||||

Db 684 CTACCAGAAACGAGTGGGAAACAACCCGAGAGATTCTTTAATTTAAGTTCTATCCCC 743
|||||

Qy 141 ThrGluGluPheIleThrSerAlaGluLeuGlnValPheArgGluGlnMetGlnAspAla 160
|||||

Db 744 ACGGAGGAGTTTATCACCCTCAGCAGAGCTTCAGGTTTTCGAGACACAGATGCAAGTCT 803
|||||

Qy 161 LeuGlyAsnAsnSerSerPheHisHisArgIleAsnIleTyrGluIleLysProAla 180
|||||

Db 804 TTAGGAAACAATAGCAGTTCCATCACCGAATTAATATTATGAAATCATAAAACTGCA 863
|||||

Qy 181 ThrAlaAsnSerLysPheProValThrArgLeuAspThrArgLeuValAsnGlnAsn 200
|||||

Db 864 ACAGCCAACTCGAAATTCGCCGTGACCAAGCTTTTGACACCAAGTTGGTGAATCAGAA 923
|||||

Qy 201 AlaSerArgTyrGluSerPheAspValThrProAlaValMetArgTyrThrAlaGlnGly 220
|||||

Db 924 GCAGCAGGTGGGAAAGTTTGTATGTCACCCCGCTGTGTGATGCGTGGATGTCACAGGA 983
|||||

Qy 221 HisAlaAsnHisGlyPheValValGluValAlaHisLeuGluGluLysGlnGlyValSer 240
|||||

Db 984 CACGCCAACCATGATTCGTGGTGGAGTGCCCATTTGAGGAGAGAAACAAGGTGTCTCC 1043
|||||

Qy 241 LysArgHisValArgIleSerArgSerLeuHisGlnAspGluHisSerTyrSerGlnIle 260
|||||

Db 1044 AAGAGACATGTTAGGATAAGCAGTCTTTGACCAAGATGAACACAGCTGTCACAGATA 1103
|||||

Qy 261 ArgProLeuLeuValThrPheGlyHisAspGlyLysGlyHisProLeuHisLysArgGlu 280
|||||

Db 1104 AGGCCATTGCTAGTAATCTTTGGCCATGATGGAAAGGGCATCTCTCTCCAAAGAGAA 1163
|||||

Qy 281 LysArgGlnAlaLysHisLysGlnArgLysArgLeuLysSerSerCysLysArgHisPro 300
|||||

Db 1164 AAAGGTCAAGCCAAACAACAACAGCGGAAACGCTTAAGTCCAGCTGTAAAGAGACACCT 1223
|||||

Qy 301 LeuTyrValAspPheSerAspValGlyTyrAsnAspTrpIleValAlaProProGlyTyr 320
|||||

Db 1224 TTGTACGTGGACTTCAGTGACGTGGGTGGATGATGCTGCCCTCCCGGGGTAT 1283
Qy 321 HisAlaPheTyrCysHisGlyGluCysProPheProLeuAlaAspHisLeuAsnSerThr 340
Db 1284 CACGCTTTTACTGCGCAGGAGAAAGCCCTTTCTCTGCGCTGATCATCTGAACCTCCACT 1343
Qy 341 AsnHisAlaIleValGlnThrLeuValAsnSerValAsnSerLysIleProLysAlaCys 360
Db 1344 AATCATGCCATTGTTTCAGACGGTTGCTCAACTCTGTTAACTCTAAGATTCTTAAGGCATGC 1403
Qy 361 CysValProThrGluLeuSerAlaIleSerMetLeuTyrLeuAspGluAsnGluLysVal 380
Db 1404 TGTGTCCCGACAGAACTCAGTCTCTATCTCGATGCTGTACTTTCAGCAGATGAAGAAGTT 1463
Qy 381 ValLeuLysAsnTyrGluAspMetValValGluGlyCysGlyCysArg 396
Db 1464 GTATTAAAGAACTATCAGACATGTTGTGGAGGTTGTGGGTGTCGC 1511
RESULT 12
ABT17041
ID ABT17041 standard; DNA; 1547 BP.
XX AC ABT17041;
XX DT 03-APR-2003 (first entry)
XX DE Human MP21 gene BWP2 SEQ ID No 15.
XX KW Cytostatic; p21 pathway modulating agent; cancer; angiogenic; apoptotic;
KW cell proliferation disorder; MP21; gene; ds.
XX OS Homo sapiens.
XX PN WO2003006990-A1.
XX PD 23-JAN-2003.
XX PF 10-JUL-2002; 2002WO-US021549.
XX PR 12-JUL-2001; 2001US-0305017P.
PR 10-OCT-2001; 2001US-0328491P.
PR 15-FEB-2002; 2002US-0357452P.
XX PA (EXEL-) EXELIXIS INC.
XX PI Friedman L, Plowman GD, Belvin M, Li D, Funke RP;
XX P-PSDB; ABJ19767.
XX PT Identifying candidate p21 pathway modulator, by contacting an assay
PT system having modifiers of p21 polypeptide or gene with a test agent to
PT provide a reference activity in system and detecting test agent-biased
PT activity.
XX PS Example; Page 86-87; 199pp; English.
XX CC The invention relates to a novel method for identifying a candidate p21
CC pathway modulating agent. The novel method comprises contacting an assay
CC system, comprising a purified MP21 polypeptide (modifier of p21) or
CC nucleic acid, with a test agent under conditions, so that but for the
CC presence of a test agent, the assay system provides a reference activity
CC and detection of test agent-biased activity of the assay system. The
CC novel method of the invention is useful for identifying a candidate p21
CC pathway modulating agent. The invention also includes a method for
CC modulating the p21 pathway of a cell, and a method for diagnosing a
CC disease e.g. cancer in a patient. The identified modulators are useful in
CC diagnosis, therapy and pharmaceutical development. The modulators are
CC useful in a variety of diagnostic and therapeutic applications including
CC angiogenic, apoptotic and cell proliferation disorders. This
CC polynucleotide sequence represents a gene encoding an MP21 protein of the
CC invention

XX SQ Sequence 1547 BP; 377 A; 423 C; 410 G; 337 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 6.2e-174 Length: 1547
Score: 2098.00 Matches: 396
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0
US-10-801-648-2 (1-396) x ABT17041 (1-1547)
Qy 1 MetValAlaGlyThrArgCysLeuLeuAlaLeuLeuProGlnValLeuLeuGlyGly 20
Db 324 ATGTTGGCGGGACCCCGCTGCTTCTAGCGTTGCTCTCCAGGTCTCTCTCGGGCGC 383
Qy 21 AlaAlaGlyLeuValProGluLeuGlyArgArgLysPheAlaAlaAsnSerSerGlyArg 40
Db 384 GCGGCTGGCTTCGTTCCGAGCTGGCGCGCAGGAAGTTTCGGCGCGCGCTCGTCCGGCGCGC 443
Qy 41 ProSerSerGlnProSerAspGluValLeuSerGluPheGluLeuArgLeuLeuSerMet 60
Db 444 CCTCATCCAGCCCTCTGACGAGTCTGAGCGAGTTCGAGTTCGGGCTGCTCAGCATG 503
Qy 61 PheGlyLeuLysGlnArgProThrProSerArgAspAlaValValProProTyrMetLeu 80
Db 504 TTCGCTTGAACAGAGACCCACCCAGCAGGAGCGCGTGTGCTCCCTTACATGCTA 563
Qy 81 AspLeuTyrArgArgHisSerGlyGlnProGlySerProAlaProAspHisArgLeuGlu 100
Db 564 GACCTGTATCGAGGCACTCAGGTGAGCGCGGCTCAGCGCGCCAGACACCGGTGGAG 623
Qy 101 ArgAlaAsnSerArgAlaAsnThrValArgSerPheHisGluGluSerLeuGlu 120
Db 624 AGGCGAGCCGCGGAGCAACACTGTGCGAGCTTCCACCATGAAGAATCTTTGAAGAA 683
Qy 121 LeuProGluThrSerGlyLysThrArgArgPhePheAsnLeuSerSerIlePro 140
Db 684 CTACCGAAGACGAGTGGGAAACCAACCCGAGATCTTCTTTAATTAATTCATCCCC 743
Qy 141 ThrGluGluPheIleThrSerAlaGluLeuGlnValPheArgGluGlnMetGlnAspAla 160
Db 744 ACGGAGAGTATTATCACCTCAGCAGAGCTTCAGGTTTCCGAGAACAGATGCAAGTGT 803
Qy 161 LeuGlyAsnAsnSerSerPheHisArgIleAsnIleTyrGluIleLysProAla 180
Db 804 TTAGGAAACAATAGCAGTTTCCATCACCAGATTATATATTTATGAATCATAAACCTGCA 863
Qy 181 ThrAlaAsnSerLysPheProValThrArgLeuLeuAspThrArgLeuValAsnGlnAsn 200
Db 864 ACAGCCAACTCGAAATTCCTCCGTGACACAGACTTTTGGACACAGGTTGGTGANTCAGAT 923
Qy 201 AlaSerArgTTPGluSerPheAspValThrProAlaValMetArgTTPThrAlaGlnGly 220
Db 924 GCAAGCAGTGGGAAAGTTTTGATGTACCCCGCTGTGATGCGGTGGACTGCACAGGGA 983
Qy 221 HisAlaAsnHisGlyPheValValAlaHisLeuGluGluLysGlnGlyValSer 240
Db 984 CACGCCAACCACTGGATTCTGTTGGTGGAGTGGCCCACTTGGAGGAGAAACAAGGTGTCTCC 1043
Qy 241 LysArgHisValArgIleSerArgSerLeuHisGlnAspGluHisSerTrpSerGlnIle 260
Db 1044 AAGACACATGTTAGATGATGAGGCTTTTGCACCAAGATGAACACAGCTGGTGCACAGATA 1103
Qy 261 ArgProLeuLeuValThrPheGlyHisAspGlyLysGlyHisProLeuHisLysArgGlu 280
Db 1104 AGGCCATTGCTAGTAATCTTTGGCCATGATGAAAGGGCATCTCTCCACAAAAGAGAA 1163
Qy 281 LysArgGlnAlaLysHisGlnArgLysGlnArgLysSerSerCysLysArgHisPro 300
Db 1164 AAACGTCAAGCCAAACACAAAACAGCGGAAACGCCCTTAAGTCCAGCTGTAAGAGACACCT 1223

```
QY 301 LeuTyrValAspPheSerAspValGlyTrpAsnAspTrpIleValAlaProProGlyTyr 320
Db 1224 TTGTACGTGGACTTCAGTGGAGCTGGGGTGGGAATGACTGGATTTGGCTCCCGGGGTAT 1283
QY 321 HisAlaPheTyrCysHisGlyGluCysProPheProLeuAlaAspHisLeuAsnSerThr 340
Db 1284 CACGCCCTTTACTGCCACGGAGATGCCCTTTCTCTGGCTGATCATCTGAACCTCCACT 1343
QY 341 AsnHisAlaIleValGlnThrLeuValAsnSerValAsnSerIleProLysAlaCys 360
Db 1344 AATCATGCCATTGTTTCAGACGTTGGTCAACTCTGTTAACTCTAAGATTCTTAAGGCATGC 1403
QY 361 CysValProThrGluLeuSerAlaIleSerMetLeuTyrLeuAspGluAsnGluLysVal 380
Db 1404 TGTGTCCCGACAGAACTACAGTCTATCTCGATGCTGTACCTTTGACGAGAAATGAAAGGTT 1463
QY 381 ValLeuLysAsnTyrGlnAspMetValValGluGlyCysGlyCysArg 396
Db 1464 GTATTAAAGAACTATCAGGACATGGTTGTGGAGGGTTGTGGGTCTCGC 1511
```

RESULT 13

ID ADL13510 standard; DNA; 1547 BP.

XX AC ADL13510;

XX DT 06-MAY-2004 (first entry)

XX DE Osteoarthritis-associated polymorphic nucleotide #42.

XX KW ds; gene; osteopathic; antiinflammatory; antiarthritic; gene therapy;
joint space narrowing; osteophyte development; joint pain;
osteoarthritis; SNP; single nucleotide polymorphism.

XX OS Homo sapiens.

XX PN WO2003054166-A2.

XX PD 03-JUL-2003.

XX PF 19-DEC-2002; 2002WO-US041225.

XX PR 20-DEC-2001; 2001US-0342603P.

XX PX (INCY-) INCYTE GENOMICS INC.

XX PY Jones KA, Schafer A;

XX QZ WPI; 2003-559141/52.

XX FT Determining susceptibility of an individual to joint space narrowing,
osteophyte development and/or joint pain comprises identifying whether
the individual has at least one polymorphism in a polynucleotide encoding
a protein.

XX FS Disclosure; SEQ ID NO 42; 297pp; English.

XX CC The invention relates to a method of determining susceptibility of an
individual to joint space narrowing and/or osteophyte development and/or
joint pain comprising identifying whether the individual has at least one
polymorphism in a polynucleotide encoding at least one of the protein
listed in the specification. The methods, composition and agent are
useful for modulating the susceptibility of an individual to joint space
narrowing and/or osteophyte development and/or joint pain that is
associated with a disease, preferably osteoarthritis. The cell line and
the non-human animal are useful for screening for an agent for diagnosing
an individual having susceptibility to joint space narrowing and/or
osteophyte development and/or joint pain. This sequence corresponds to
the polynucleotide encoding a protein listed in the specification. (Note:
The sequence data for this patent did not form part of the printed
specification but was obtained in electronic format directly from WIPO at
ftp.wipo.int/pub/published_pct_sequences).

SQ Sequence 1547 BP; 377 A; 423 C; 410 G; 337 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 6.2e-174 Length: 1547
Score: 2098.00 Matches: 396
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-10-801-648-2 (1-396) x ADL13510 (1-1547)

```
QY 1 MetValAlaGlyThrArgCysLeuLeuAlaLeuLeuProGlnValLeuLeuGly 20
Db 324 ATGGTGGCCGGGACCCCGCTGTCTTAGCGTTGCTCCCGAGGTCCTCTGGGGCGGC 383
QY 21 AlaAlaGlyLeuValProGluLeuGlyArgArgLysPheAlaAlaAlaSerSerGlyArg 40
Db 384 GCGGCTGGCTCGTTCGGAGCTGGGCCGCGAGGAGTTCCGGGGGGGTCTCGGGCGGC 443
QY 41 ProSerSerGlnProSerAspGluValLeuSerGluPheGluLeuArgLeuSerMet 60
Db 444 CCCTCATCCAGCCCTCTGACGAGTCTCTGAGCGAGTTCCAGTTGCGGCTGCTCAGCATG 503
QY 61 PheGlyLeuLysGlnArgProThrProSerArgAspAlaValValProProTyrMetLeu 80
Db 504 TTCGGCTCGAAACAGAGACCCACCCCGAGGAGACCGCTGGTGGCCCCCTCATGCTA 563
QY 81 AspleuTyrArgArgHisSerGlyGlnProGlySerProAlaProAspHisArgLeuGlu 100
Db 564 GACTGTATCGCAGGCACTCAGGTCAGCCGGGCTCACCCGCCCCAGACACCGGTTGGAG 623
QY 101 ArgAlaAlaSerArgAlaAsnThrValArgSerPheHisHisGluGluSerLeuGluGlu 120
Db 624 AGGCGAGCCAGCCGAGCAACACTGTGCGCAGCTTCCACCATGAAGAATCTTTGGAAAGAA 683
QY 121 LeuProGluThrSerGlyLysThrThrArgArgPhePheAsnLeuSerSerIlePro 140
Db 684 CTACCGAAGAACGAGTGGGAAACAAACCCGAGAGTTCTTTTAATTTAAGTTCTATCCCC 743
QY 141 ThrGluGluPheIleThrSerAlaGluLeuGlnValPheArgGluGlnMetGlnAspAla 160
Db 744 ACGGAGGAGTTTATCACTCAGCAGAGCTTCAGGTTTCCGAGACACAGATGCAAGTGCT 803
QY 161 LeuGlyAsnAsnSerSerPheHisHisArgIleAsnIleTyrGluIleIleLysProAla 180
Db 804 TTAGGAAACAAATAGCAGTTTCCATCACCGAATTAATATTTTGAATCATATAAACCTGCA 863
QY 181 ThrAlaAsnSerLysPheProValThrArgLeuLeuAspThrArgLeuValAsnGlnAsn 200
Db 864 ACAGCCAACTCGAAATTTCCCGTGACCGAGACTTTTGGACACACAGGTTGGTGAATCAGAT 923
QY 201 AlaSerArgTrpGluSerPheAspValThrProAlaValMetArgTrpThrAlaGlnGly 220
Db 924 GCAGCAGGTTGGGAAAGTTTGTATGTCACCCCGCTGTGATCGGTGAGTCGACACAGGA 983
QY 221 HisAlaAsnHisGlyPheValValGluValAlaHisLeuGluGluLysGlnGlyValSer 240
Db 984 CACGCCAACCATGGATTGCTGGTGGAGTGGCCACCTTGGAGGAGAGAAACAGGTGTCTCC 1043
QY 241 LysArgHisValArgIleSerArgSerLeuHisGlnAspGluHisSerTrpSerGlnIle 260
Db 1044 AAGAGACATGTTAGGTAAGCAGGTCCTTTGCCAAGATGAACACACAGCTGCTCACAGATA 1103
QY 261 ArgProLeuLeuValThrPheGlyHisAspGlyLysGlyHisProLeuHisLysArgGlu 280
Db 1104 AGGCCATTGCTAGTAACCTTTTGGCCATGATGGAAAGGCGCATCTCTCCACAAAGAGAA 1163
QY 281 LysArgGlnAlaLysHisLysGlnArgLysArgLeuLysSerSerCysLysArgHisPro 300
Db 1164 AAACGTCAGGCCAAACAAACAAACAGCGGAAACGCGCTTAAGTCCAGCTGTAAAGAGACCCCT 1223
QY 301 LeuTyrValAspPheSerAspValGlyTrpAsnAspTrpIleValAlaProProGlyTyr 320
```


Db 864 ACAGCCAACTCGAAATCCCGTGACACAGACTTTTGGACACAGGTTGGTGAATCAGAAAT 923
 Qy 201 AlaserArgTTrpGluSerPheAspValThrProAlaValMetArgTTrpThrAlaGlnGly 220
 Db 924 GCAAGCAGGTGGGAAAGTTTGGATGTCAACCCCGCTGTGATCGGTGACTGCAAGGGA 983
 Qy 221 HisAlaAenHisGlyPheValValGluValAlaHisLeuGluGluLysGlnGlyValSer 240
 Db 984 CACGCCAACCATGGATTCTGGTGGAGTGCCCACTTGGAGGGAACAAGGTGTCTCC 1043
 Qy 241 LysArgHisValArgIleSerArgSerLeuHisGlnAspGluHisSerTrpSerGlnIle 260
 Db 1044 AAGACACATGTAGGATAAGCAGGTCTTTTGACCAAGATGAACAGCTGTGTACAGATA 1103
 Qy 261 ArgProLeuLeuValThrPheGlyHisAspGlyLysGlyHisProLeuHisLysArgGlu 280
 Db 1104 AGGCCATTGTGTAACTTTTGGCCATGATGGAAAGGGCATCTCTCCACAAAGAGAA 1163
 Qy 281 LysArgGlnAlaLysHisLysGlnArgLysArgLeuLysSerSerCysLysArgHisPro 300
 Db 1164 AATGCTCAAGCCAAACACAAACAGCGGAACGCCCTTAAGTCCAGCTGTAAGAGACACCT 1223
 Qy 301 LeuTyrValAspPheSerAspValGlyTrpAsnAspTrpIleValAlaProProGlyTyr 320
 Db 1224 TTGTACGTGGACTTCAGTGACGTGGGGTGGAAATGACTGGATTGTGGCTCCCGGGGTAT 1283
 Qy 321 HisAlaPheTyrCysHisGlyGluCysProPheProLeuAlaAspHisLeuAsnSerThr 340
 Db 1284 CACGCCCTTTACTGTCACAGAGATGCCCTTTCTCTGGTGTATCATCTGAATCCACT 1343
 Qy 341 AsnHisAlaLleValGlnThrLeuValAsnSerValAsnSerLysIleProLysAlaCys 360
 Db 1344 AATCATGCCATGTTCAGACGTTGTCAACTCTGTAACTCTAAGATTCTTAAGGCATGC 1403
 Qy 361 CysValProThrGluLeuSerAlaIleSerMetLeuTyrLeuAspGluAsnGluLysVal 380
 Db 1404 TGTGTCCCGACAGAACTCAGTGCTATCTCGATGCTGTACCTTGACGAGATGAAGAAGTT 1463
 Qy 381 ValLeuLysAsnTyrGlnAspMetValValGluGlyCysGlyCysArg 396
 Db 1464 GTATTAAAGAACTATCAGGACATGTTGTGGAGGGTTGTGGGTGTGCG 1511

RESULT 15

ADH11558
 ID ADH11558 standard; cDNA; 1547 BP.
 AC ADH11558;
 XX
 XX
 DT 11-MAR-2004 (first entry)
 XX
 XX
 DE Human bone morphogenic protein (BMP) polynucleotide #7.
 XX
 KW Human; bone morphogenic protein; BMP; gene; ss; weight gain;
 KW appetite suppression; fat mass reduction; cell sensitivity;
 KW glucose uptake; diabetes; insulin resistance; hyperglycaemia;
 KW hypertension; coronary artery disease; renal failure; neuropathy;
 KW metabolic disorder; glucose metabolism disorder; endocrine disorder;
 KW obesity; weight loss; liver disorder; cartilage growth disorder;
 KW bone growth disorder; inflammation; aberrant cell growth; liver cancer.
 XX
 OS Homo sapiens.
 XX
 XX US2003224501-A1.
 XX
 XX PD 04-DEC-2003.
 XX
 XX PF 14-FEB-2003; 2003US-00366345.
 XX
 XX PR 17-MAR-2000; 2000US-0190067P.
 PR 16-MAR-2001; 2001US-00809269.
 PR 23-MAR-2001; 2001WO-US009229.
 PR 17-JAN-2002; 2002US-0348621P.
 PR 22-JAN-2002; 2002US-0349356P.

PR 28-JAN-2002; 2002US-0351520P.
 PR 06-FEB-2002; 2002US-0354265P.
 PR 15-FEB-2002; 2002US-0356749P.
 PR 16-JAN-2003; 2003US-00345236.
 XX
 PA (YOUNG/) YOUNG P E.
 PA (RUBE/) RUBEN S M.
 XX
 FI Young PE, Ruben SM;
 XX
 XX WPI; 2004-022075/02.
 DR P-PSDB; ADH11579.
 XX
 PT New bone morphogenic protein polypeptides and polynucleotides, useful for
 PT diagnosing, preventing, treating or ameliorating a medical condition, e.g.
 PT e.g. diabetes, dyslipidemia, hypertension, coronary artery disease or
 PT neuropathy.
 XX
 XX Example 1; SEQ ID NO 10; 224pp; English.
 PS
 XX
 CC The invention relates to human bone morphogenic protein (BMP)
 CC polypeptides and the polynucleotides encoding them. The invention also
 CC relates to a method for limiting weight gain, suppressing appetite or
 CC reducing fat mass, comprising administering to a mammalian subject a
 CC therapeutic amount of a BMP polypeptide, and a method for increasing the
 CC sensitivity of a cell to insulin or increasing glucose uptake by a cell,
 CC comprising contacting the cell with a BMP polypeptide. The BMP
 CC polypeptides and polynucleotides are useful for diagnosing a pathological
 CC condition or a susceptibility to a pathological condition in a subject or
 CC for preventing, treating or ameliorating a medical condition, e.g.
 CC diabetes, insulin resistance, hyperglycaemia, hypertension, coronary
 CC artery disease, renal failure, neuropathy, metabolic disorders, glucose
 CC metabolism disorder, endocrine disorders, obesity, weight loss, liver
 CC disorders, cartilage and bone growth disorders, inflammation or aberrant
 CC cell growth such as liver cancer. The BMP polypeptides and
 CC polynucleotides are also useful for regulating nutritional partitioning,
 CC limiting weight gain, suppressing appetite, reducing fat mass, increasing
 CC the sensitivity of a cell to insulin or increasing glucose uptake by a
 CC cell. This sequence represents a human BMP polynucleotide of the
 CC invention.
 XX
 SQ Sequence 1547 BP; 377 A; 423 C; 410 G; 337 T; 0 U; 0 Other;

Alignment Scores:

Pred. NO.: 6.2e-174 Length: 1547
 Score: 2098.00 Matches: 396
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 12 Gaps: 0

US-10-801-648-2 (1-396) x ADH11558 (1-1547)

Qy 1 MetValAlaGlyThrArgCysLeuLeuAlaLeuLeuProGlnValLeuLeuGlyGly 20
 Db 324 ATGTGTGCGGAGACCCCTGTCTTCTAGCGTTGCTGTCTTCCACAGGTCCTCTCTGGGCGGC 383
 Qy 21 AlaAlaGlyLeuValProGluLeuGlyArgArgLysPheAlaAlaSerSerGlyArg 40
 Db 384 GCGGCTGCGCTCGTTTCGGAGCTGGGCGCAGGAAGTTTCGCGGCGGCGTCTCGGCGCGC 443
 Qy 41 ProSerSerGlnProSerAspGluValLeuSerGluPheGluLeuArgLeuLeuSerMet 60
 Db 444 CCTCATCCAGGCCCTCTGACGAGGTCCTGAGCGAGTTTCAGTTGCGGCTGCTCAGCATG 503
 Qy 61 PheGlyLeuLysGlnArgProThrProSerArgAspAlaValProProTyrMetIleu 80
 Db 504 TTGGGCTTGAACAGAGACCAACCCCGACGAGGACCGCGTGTGTCCTCATCTACTA 563
 Qy 81 AspLeuTyrArgArgHisSerGlyGlnProGlySerProAlaProAspHisArgLeuGlu 100
 Db 564 GACCTGTATCGAGGCACTCAGGTTCAGGTCAGCGGGCTCACC CGCCCGCCAGACCCCGGTTGGAG 623

QY 101 ArgAlaAlaSerArgAlaAsnThrValArgSerPheHisHisGluGluSerLeuGluGlu 120
Db |||||
624 AGGCAGCCAGCCGAGCCACACTCTGCGCAGCTTCCACCATTGAAGATCTTTGGAGAA 683
QY 121 LeuProGluThrSerGlyLysThrThrArgArgPhePheAsnLeuSerSerIlePro 140
Db |||||
684 CTACCAGAAACGAGTGGGAAACAAACCCGGAGATTCTCTTTAAATTAAGTTCTATCCCC 743
QY 141 ThrGluGluPheIleThrSerAlaGluLeuGlnValPheArgGluGlnMetGlnAspAla 160
Db |||||
744 ACGGAGGAGTTTATCACCTCAGCAGAGCTTCCAGTTTTCCGAGAACACATGCAAGATGCT 803
QY 161 LeuGlyAsnAsnSerSerPheHisHisArgIleAsnIleTyrGluIleIleLysProAla 180
Db |||||
804 TTAGGAACAATAGCAGTTTCCATCACCGAATTATATTTATGAATCATAAACCTGCA 863
QY 181 ThrAlaAsnSerLysPheProValThrArgLeuLeuAspThrArgLeuValAsnGlnAsn 200
Db |||||
864 ACAGCCAACTCGAAATTCGCCGTGACACAGACTTTTGGACACCAGGTTGGTGAATCAGAAT 923
QY 201 AlaSerArgTropGluSerPheAspValThrProAlaValMetArgTyrThrAlaGlnGly 220
Db |||||
924 GCAAGCAGTGGGAAAGTTTGGATGTACCCCCGTGTGATGCGGTGGACTGCACAGGGA 983
QY 221 HisAlaAsnHisGlyPheValValGluValAlaHisLeuGluGluLysGlnGlyValSer 240
Db |||||
984 CACGCCAACCATGGATTCTGTGTGGAGTGGCCCACTTGGAGGAGAAACAGGTCTCTCC 1043
QY 241 LysArgHisValArgIleSerArgSerLeuHisGlnAspGluHisSerTrpSerGlnIle 260
Db |||||
1044 AAGAGACATGTTAGGATAAGCAGGTCTTTTGACCAAGATGAACACAGCTGGTCCACAGATA 1103
QY 261 ArgProLeuLeuValThrPheGlyHisAspGlyLysGlyHisProLeuHisLysArgGlu 280
Db |||||
1104 AGGCCATTGCTAGTAACCTTTTGGCCATGATGAAAGGGCATCTCTCCAAAAAGAGAA 1163
QY 281 LysArgGlnAlaLysHisLysGlnArgLysArgLeuLysSerSerCysLysArgHisPro 300
Db |||||
1164 AAACGTCAGCCAAACACAAACAGCGGAAACGCCCTTAAGTCCAGCTGTAAAGACACCCCT 1223
QY 301 LeuTyrValAspPheSerAspValGlyTrpAsnAspTrpIleValAlaProProGlyTyr 320
Db |||||
1224 TTGTACGTGGACTTCAGTGACGTGGGTGGATGACTGGATTGTGGCTCCCCGGGGTAT 1283
QY 321 HisAlaPheTyrCysHisGlyGluCysProPheProLeuAlaAspHisLeuAsnSerThr 340
Db |||||
1284 CACGCCTTTTACTGCCACGAGAAATGCCCTTTTCTCTGGCTGATCATCTGAACCTCCACT 1343
QY 341 AsnHisAlaIleValGlnThrLeuValAsnSerValAsnSerLysIleProLysAlaCys 360
Db |||||
1344 AATCATGCCATTGTTTCAGACGTGGTGGTCACTCTGTTTAATCTTAAGATTCCTAAGGCATGC 1403
QY 361 CysValProThrGluLeuSerAlaIleSerMetLeuTyrLeuAspGluAsnGluLysVal 380
Db |||||
1404 TGTGTCCCGACAGAACTCAGTGCTATCTCGATGCTGTACCTTGGACGAGAAATGAAAAGGTT 1463
QY 381 ValLeuLysAsnTyrGlnAspMetValValGluGlyCysGlyCysArg 396
Db |||||
1464 GTATTAAAGAACTATCAGGACATGGTTGTGGAGGGTTGTGGGTGTGCG 1511

Search completed: January 10, 2006, 23:57:35
Job time : 556 secs

This Page Blank (usp10)

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: January 10, 2006, 23:43:25 ; Search time 177 Seconds
(without alignments)
3976.918 Million cell updates/sec

Title: US-10-801-648-2
Perfect score: 2098
Sequence: 1 MVAGTRCILLALLPQVLLG.....NEKVLKXNYQDMVVGCGCR 396

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODE=frame+bpn.model -DEV=xlh
-Q=/cgn2_1/USPTO_epool/US10801648/runat_09012006_143120_14803/app_query.fasta_1.583
-DB=Issued Patents NA -QWMT=fastap -SUFFIX=rn1 -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFWT=pco -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10801648@cgn_1_143@runat_09012006_143120_14803 -NCPUS=6 -ICPU=3
-NO MMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA:

- 1: /cgn2_6/ptodata/1/ina/1 COMB.seq.*
- 2: /cgn2_6/ptodata/1/ina/5 COMB.seq.*
- 3: /cgn2_6/ptodata/1/ina/6A COMB.seq.*
- 4: /cgn2_6/ptodata/1/ina/6B COMB.seq.*
- 5: /cgn2_6/ptodata/1/ina/H COMB.seq.*
- 6: /cgn2_6/ptodata/1/ina/PCUTUS COMB.seq.*
- 7: /cgn2_6/ptodata/1/ina/PP COMB.seq.*
- 8: /cgn2_6/ptodata/1/ina/RE COMB.seq.*
- 9: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|------------------|
| 1 | 2098 | 100.0 | 1547 | 2 | US-08-377-292-2 |
| 2 | 2098 | 100.0 | 1607 | 3 | US-07-721-847A-3 |
| 3 | 2098 | 100.0 | 1607 | 3 | US-08-925-779-3 |
| 4 | 2098 | 100.0 | 1607 | 3 | 5166058-3 |
| 5 | 2098 | 100.0 | 1607 | 3 | US-09-976-594-11 |
| 6 | 2095 | 99.9 | 1607 | 3 | US-07-989-847-1 |
| 7 | 2095 | 99.9 | 1607 | 3 | US-08-469-411-1 |
| 8 | 2095 | 99.9 | 1607 | 3 | US-09-780-601A-1 |
| 9 | 2092 | 99.7 | 1260 | 2 | US-07-841-646-4 |

| | | | | | | |
|----|--------|------|-------|---|---------------------|-------------------|
| 10 | 2092 | 99.7 | 1260 | 2 | US-07-901-703-14 | Sequence 14, Appl |
| 11 | 2092 | 99.7 | 1260 | 2 | US-08-147-023-4 | Sequence 4, Appl |
| 12 | 2092 | 99.7 | 1260 | 2 | US-08-447-570-4 | Sequence 4, Appl |
| 13 | 2092 | 99.7 | 1260 | 2 | US-08-449-700-4 | Sequence 4, Appl |
| 14 | 2092 | 99.7 | 1260 | 2 | US-08-449-699A-4 | Sequence 4, Appl |
| 15 | 2092 | 99.7 | 1260 | 3 | US-09-148-925C-4 | Sequence 4, Appl |
| 16 | 2092 | 99.7 | 1260 | 3 | US-08-957-425-4 | Sequence 4, Appl |
| 17 | 2092 | 99.7 | 1260 | 3 | US-10-321-799-4 | Sequence 4, Appl |
| 18 | 2092 | 99.7 | 1260 | 6 | PCT-US93-05446-14 | Sequence 14, Appl |
| 19 | 2092 | 99.7 | 1607 | 2 | US-07-679-451-1 | Sequence 1, Appl |
| 20 | 2092 | 99.7 | 2185 | 3 | US-09-949-016-4668 | Sequence 4668, Ap |
| 21 | 2043.5 | 97.4 | 1314 | 3 | US-08-713-556F-39 | Sequence 39, Appl |
| 22 | 1796.5 | 85.6 | 1233 | 2 | US-08-362-670B-27 | Sequence 27, Appl |
| 23 | 1796.5 | 85.6 | 1233 | 3 | US-08-333-376C-27 | Sequence 27, Appl |
| 24 | 1796.5 | 85.6 | 1233 | 3 | US-08-808-324-27 | Sequence 27, Appl |
| 25 | 1796.5 | 85.6 | 1233 | 3 | US-09-945-182-27 | Sequence 27, Appl |
| 26 | 1796.5 | 85.6 | 1233 | 6 | PCT-US94-14030A-27 | Sequence 27, Appl |
| 27 | 1542 | 73.5 | 1992 | 2 | US-08-455-550-6 | Sequence 6, Appl |
| 28 | 1511 | 72.0 | 14759 | 3 | US-09-661-887-1 | Sequence 1, Appl |
| 29 | 1505 | 71.7 | 15203 | 3 | US-09-949-016-16410 | Sequence 16410, A |
| 30 | 1412.5 | 67.3 | 15144 | 3 | US-08-458-434A-6 | Sequence 6, Appl |
| 31 | 1269 | 60.5 | 1751 | 2 | US-08-377-292-4 | Sequence 4, Appl |
| 32 | 1269 | 60.5 | 1788 | 2 | US-07-841-646-6 | Sequence 6, Appl |
| 33 | 1269 | 60.5 | 1788 | 2 | US-07-901-703-18 | Sequence 18, Appl |
| 34 | 1269 | 60.5 | 1788 | 2 | US-08-147-023-6 | Sequence 6, Appl |
| 35 | 1269 | 60.5 | 1788 | 2 | US-08-447-570-6 | Sequence 6, Appl |
| 36 | 1269 | 60.5 | 1788 | 2 | US-08-449-700-6 | Sequence 6, Appl |
| 37 | 1269 | 60.5 | 1788 | 2 | US-08-449-699A-6 | Sequence 6, Appl |
| 38 | 1269 | 60.5 | 1788 | 3 | US-09-148-925C-6 | Sequence 6, Appl |
| 39 | 1269 | 60.5 | 1788 | 3 | US-08-957-425-6 | Sequence 6, Appl |
| 40 | 1269 | 60.5 | 1788 | 3 | US-10-321-799-6 | Sequence 6, Appl |
| 41 | 1269 | 60.5 | 1788 | 6 | PCT-US93-05446-18 | Sequence 18, Appl |
| 42 | 1269 | 60.5 | 1945 | 3 | US-09-949-016-1476 | Sequence 1476, Ap |
| 43 | 1269 | 60.5 | 1954 | 2 | US-08-050-132A-3 | Sequence 3, Appl |
| 44 | 1269 | 60.5 | 1954 | 2 | US-07-989-847-3 | Sequence 3, Appl |
| 45 | 1269 | 60.5 | 1954 | 3 | US-08-750-222A-3 | Sequence 3, Appl |

ALIGNMENTS

RESULT 1
US-08-377-292-2
; Sequence 2, Application US/08377292
; Patent No. 5693615
; GENERAL INFORMATION:
; APPLICANT: STONE, ROGER L.
; TITLE OF INVENTION: THERAPEUTIC FORMULAS FOR OSTEOINDUCTION
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Procter & Gamble Company
; STREET: 11810 East Miami River Road
; CITY: Cincinnati
; STATE: Ohio
; COUNTRY: U.S.A.
; ZIP: 45239-8707
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/377,292
; FILING DATE: 23-JAN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION NUMBER: US/08/243,435
; FILING DATE:
; APPLICATION NUMBER: US/08/117,367
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Corstanje, Brahm J.
; REGISTRATION NUMBER: 34,804
; TELECOMMUNICATION INFORMATION:


```

CELL LINE: U-2OS
IMMEDIATE SOURCE:
LIBRARY: U2OS cDNA in Lambda GT10
CLONE: Lambda U2OS-39
POSITION IN GENOME:
UNITS: bp
FEATURE:
NAME/KEY: CDS
LOCATION: 356..1546
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 1202..1543
FEATURE:
NAME/KEY: mRNA
LOCATION: 14..1607
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 356..424
US-07-721-847A-3
Alignment Scores:
Pred. No.: 3,648-200 Length: 1607
Score: 2098.00 Matches: 396
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-10-801-648-2 (1-396) x US-07-721-847A-3 (1-1607)
QY 1 MetValAlaGlyThrArgCysLeuLeuAlaLeuLeuProGlnValLeuLeuGlyGly 20
DB 356 ATGGTGGCGGACCGGTCTTCTAGGTGCTGCTTCCCGAGTCTCTCTGGCGGC 415
QY 21 AlaAlaGlyLeuValProGluLeuGlyArgArgLysPheAlaAlaSerSerGlyArg 40
DB 416 GCGGTGGCGTCTTCCGAGCTGGCGCGCGCAGAAAGTTCCGCGCGCGCTGCTGGCGCGC 475
QY 41 ProSerSerGlnProSerAspGluValLeuSerGluPheGluLeuArgLeuSerMet 60
DB 476 CCCTCATCCAGCCCTCTGACAGAGTCTGACGAGTTCGAGTTCGCGCTGCTCAGCAG 535
QY 61 PheGlyLeuLysGlnArgProThrProSerArgAspAlaValValProProThrMetLeu 80
DB 536 TTCGCGCTGAAACAGACGACCCACCCAGCAGCGCGTGGTGGTCCCTACATGCTA 595
QY 81 AspLeuTyArgArgHisSerGlyGlnProGlySerProAlaProAspHisArgLeuGlu 100
DB 596 GACCTGTATCGCAGCACTCAGGTCAAGCGCGCTCAGCGCGCGCCAGACCCAGCGTTGGAG 655
QY 101 ArgAlaAlaSerArgAlaAsnThrValArgSerPheHisGluGluSerLeuGluGlu 120
DB 656 AGGCGAGCGAGCGGACCAACTGTGCGCAGCTTCCACCATGAAGAATCTTTGGAAGAA 715
QY 121 LeuProGluThrSerGlyLysThrThrArgArgPhePheAsnLeuSerSerIlePro 140
DB 716 CTACCAAGAACAGGTGGGAAACACCCGAGATCTCTTAAATTAAGTTCATATCCC 775
QY 141 ThrGluGluPheIleThrSerAlaGluLeuGlnValPheArgGluGlnMetGlnAspAla 160
DB 776 ACGGAGGAGTTTATCACCTCAGCAGAGCTTCAGGTTTTCCGAGAACAGATGATGT 835
QY 161 LeuGlyAsnAsnSerSerPheHisArgGlnIleTyThrGluIleIleLysProAla 180
DB 836 TTAGGAACCAATAGCAGTTTCATCACCGAATTAATTAATTAATTAATTAATTAATTA 895
QY 181 ThrAlaAsnSerLysPheProValThrArgLeuLeuAspThrArgLeuValAsnGlnAsn 200
DB 896 ACAGCCACTCGAATATCCCGTGACCACTTTTGGACACAGGTTGGTGGATCAGAT 955
QY 201 AlaSerArgTrpGluSerPheAspValThrProAlaValMetArgTrpThrAlaGlnGly 220
DB 956 GCAAGCAGGTGGGAAGTTTTCATGTACCCCGCTGTGATGCGGTGGACTGCACAGGGA 1015

```

```

QY 221 HisAlaAsnHisGlyPheValValGluValAlaHisLeuGluGluLysGlnGlyValSer 240
DB 1016 CACGCCAACCATGATTCGTGTGGAGTGGCCCACTTGGAGGAGAAACAGGTGTCTCC 1075
QY 241 LysArgHisValArgIleSerArgSerLeuHisGlnAspGluHisSerTrpSerGlnIle 260
DB 1076 AAGACATGTTAGGATAAGCAGGTCTTTTGACCAAGATGAACACAGCTGGTGCACAGATA 1135
QY 261 ArgProLeuLeuValThrPheGlyHisAspGlyLysGlyHisProLeuHisLysArgGlu 280
DB 1136 AGGCCATTGCTAGTAACCTTTTGGCCCATGATGAAAGAGGCGATCTCTCCACAAAGAGAA 1195
QY 281 LysArgGlnAlaLysHisLysGlnArgLysArgLeuLysSerSerCysLysArgHisPro 300
DB 1196 AAACGTCCAGCCAAACACAAACAGCGGAAACGCTTAAAGTCCAGCTGTAAGACACCT 1255
QY 301 LeuTyValAspPheSerAspValGlyTrpAsnAspTrpIleValAlaProProGlyTy 320
DB 1256 TTGTACGTGGACTTTCAGTGACGTGGGTGGATGACTGGATTTGTGGCTTCCCGGGGTAT 1315
QY 321 HisAlaPheTyCysHisGlyGluCysProPheProLeuAlaAspHisLeuAsnSerThr 340
DB 1316 CACGCTTTTACTGCCACGAGAAATGCCCTTTTCTCTGGCTGATCATCTGAACCTCCACT 1375
QY 341 AsnHisAlaIleValGlnThrLeuValAsnSerValAsnSerLysIleProLysAlaCys 360
DB 1376 AATCATGCCATTGTTCAAGCGTGGTCAACTCTGTAACTCTAAGATTCTTAAGCATGC 1435
QY 361 CysValProThrGluLeuSerAlaIleSerMetLeuTyLeuAspGluAsnGluLysVal 380
DB 1436 TGTGTCCGACAGAACTCAGTGCTATCTCGATCTGTGCTGTACCTTGACAGAAATGAAAGGTT 1495
QY 381 ValLeuLysAsnTyGlnAspMetValValGluGlyCysGlyCysArg 396
DB 1496 GTATTAAGAACTATCAGGACATGTTGTGGAGGTTGTGGGTGTGCG 1543

RESULT 3
US-08-925-779-3
; Sequence 3, Application US/08925779
; Patent No. 6245889
; GENERAL INFORMATION:
; APPLICANT: Wang, Elizabeth A.
; APPLICANT: Rosen, Vicki A.
; APPLICANT: Wozney, John M.
; TITLE OF INVENTION: No. 6245889el BMP Products
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LEGAL AFFAIRS, GENETICS INSTITUTE, INC.
; STREET: 87 CAMBRIDGE PARK DRIVE
; CITY: CAMBRIDGE
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/925,779
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/721,847
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Kapinos, Ellen J.
; REGISTRATION NUMBER: 32,245
; REFERENCE/DOCKET NUMBER: 5160C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-876-1170
; TELEFAX: 617-876-5851

```

; INFORMATION FOR SEQ ID NO: 3:

```

; SEQUENCE CHARACTERISTICS:
;   LENGTH: 1607 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: double
;   TOPOLOGY: linear
;   MOLECULE TYPE: cDNA to mRNA
;   HYPOTHETICAL: NO
;   ANTI-SENSE: NO
;   ORIGINAL SOURCE:
;     ORGANISM: Homo Sapiens
;     CELL TYPE: Osteosarcoma Cell Line
;     CLONING: U-20S
;   IMMEDIATE SOURCE:
;     LIBRARY: U20S cDNA in Lambda GT10
;     CLONE: Lambda U20S-39
;   POSITION IN GENOME:
;     UNITS: bp
;   FEATURE:
;     NAME/KEY: CDS
;     LOCATION: 356..1546
;   FEATURE:
;     NAME/KEY: mat_peptide
;     LOCATION: 1202..1543
;   FEATURE:
;     NAME/KEY: mRNA
;     LOCATION: 14..1607
;   FEATURE:
;     NAME/KEY: sig_peptide
;     LOCATION: 356..424

```

US-08-925-779-3

Alignment Scores:

```

Pred. No.: 3.64e-200 Length: 1607
Score: 2098.00 Matches: 396
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

```

US-10-801-648-2 (1-396) x US-08-925-779-3 (1-1607)

```

Qy 1 MetValalaGlyThrArgCysLeuLeuAlaLeuLeuProGlnValLeuGlyGly 20
Db 356 ATGTGTGCGCGGAGCCCGCTGCTTCTAGCGTGTCTTCCCGAGGCTCTCTCGGCGGC 415
Qy 21 AlaAlaGlyLeuValProGluLeuGlyArgArgLysPheAlaAlaSerSerGlyArg 40
Db 416 GCGGCTGGCCTCGTTCGGAGCTGGCGCGCAGGAAGTTCCGCGCGGCGTCTCGGCGGC 475
Qy 41 ProSerSerGlnProSerAspGluValLeuSerGluPheGluLeuArgLeuSerMet 60
Db 476 CCCTCATCCAGCCCTCTGACGAGCTCTGACGAGTTCGAGGTTGCGGCTCTCAGCATG 535
Qy 61 PheGlyLeuLysGlnArgProThrProSerArgAspAlaValProProTyrMetLeu 80
Db 536 TTCGGCTGAAACAGAGACCCACCCCGCAGGAGCGCGGTGGTCCCGCCCTATCGCTA 595
Qy 81 AspLeuTyrArgArgHisSerGlyGlnProGlySerProAlaProAspHisArgLeuGlu 100
Db 596 GACCTGTATCGAGGCACTCAGTTCAGCGCGGCTCACCCGCGCCAGACCCCGGTGGAG 655
Qy 101 ArgAlaAlaSerArgAlaAsnThrValArgSerPheHisHisGluGluSerLeuGluGlu 120
Db 656 AGGCGAGCCAGCCGACCACTGTGCGCAGCTTCACCATGAAGAATCTTTGGAAGAA 715
Qy 121 LeuProGluThrSerGlyLysThrThrArgArgPhePheAsnLeuSerSerIlePro 140
Db 716 CTACAGAAACGAGTGGGAAACAAACCCGAGATTCCTTTTAATTAAGTTCATCCCC 775
Qy 141 ThrGluGluPheIleThrSerAlaGluLeuGlnValPheArgGluGlnMetGlnAspAla 160
Db 776 ACGGAGGAGTTTATCACCTCAGCAGAGCTTCAGGTTTCCGAGAACAGATGCAAGATGCT 835

```

```

Qy 161 LeuGlyAsnAsnSerSerPheHisHisArgIleAsnIleTyrGluIleIleLysProIle 180
Db 836 TTAGGAAACAATAGCAGTTTCCATCACCGAATTAATATTTATGAATCATATAAACCTGCA 895
Qy 181 ThrAlaAsnSerLysPheProValThrArgLeuLeuAspThrArgLeuValAsnGlnAsn 200
Db 896 ACAGCCAACCTCGAAATTCCTCGTACCAGACTTTTGGACACCAAGTTGGTGAATCAGAT 955
Qy 201 AlaSerArgTyrGluSerPheAspValThrProAlaValMetArgTyrThrAlaGlnGly 220
Db 956 GCAAGCAGGTGGGAAAGTTTGTATGTCACTCCCGCTGTGATCGCGTGGAGTGCACAGGA 1015
Qy 221 HisAlaAsnHisGlyPheValValGluValAlaHisLeuGluGluLysGlnGlyValSer 240
Db 1016 CACGCCAACCATGATTCGTGTGTAAGTGTGCGTGGAGGAGAAACAAGGTGTCTCC 1075
Qy 241 LysArgHisValArgIleSerArgSerLeuHisGlnAspGluHisSerTyrSerGlnIle 260
Db 1076 AAGAGACATGTTAGGATAAGCAGTCTTTGGCCATGATGGAAGAGGCGATCTCTCCACAAAGAGAA 1135
Qy 261 ArgProLeuLeuValThrPheGlyHisAspGlyLysGlyHisProLeuHisLysArgGlu 280
Db 1136 AGGCCATTGCTAGTAACCTTTTGGCCATGATGGAAGAGGCGATCTCTCCACAAAGAGAA 1195
Qy 281 LysArgGlnAlaLysHisLysGlnArgLysArgLeuLysSerSerCysLysArgHisPro 300
Db 1196 AACGTCAAGCCAAACACAAACAGCGGAAAGCGCTTAAGTCCAGCTGTAAGAGACACCT 1255
Qy 301 LeuTyrValAspPheSerAspValGlyTyrAsnAspTrpIleValAlaProProGlyTyr 320
Db 1256 TTGTACGTGGACTTCAGTGACGTGGGTGGAATGACTTGGATTTGGCTTCCCGGGGTAT 1315
Qy 321 HisAlaPheTyrCysHisGlyGluCysProPheProLeuAlaAspHisLeuAsnSerThr 340
Db 1316 CACGCTTTTACTGCCACGAGAAATGCCCTTTCTCTGCTGATCATCTGAACCTCCACT 1375
Qy 341 AsnHisAlaIleValGlnThrLeuValAsnSerValAsnSerLysIleProLysAlaCys 360
Db 1376 AATCATGCCATTGTTTCAGACGTTGTCACACTCTGTTAACTCTTAAGATTCTTAAGGCGATGC 1435
Qy 361 CysValProThrGluLeuSerAlaIleSerMetLeuTyrLeuAspGluAsnGluLysVal 380
Db 1436 TGTGTCCCGACAGAACTCAGTGCTATCTCGATGCTGACCTTGACGAGAAATGAAGAAGTT 1495
Qy 381 ValLeuLysAsnTyrGlnAspMetValValGluGlyCysGlyCysArg 396
Db 1496 GTATTAAAGAACTATCAGGACATGTTGTGGAGGTTGTGGGTGTCTGC 1543

```

RESULT 4

```

5166058-3
; Patent No. 5166058
; APPLICANT: WANG, ELIZABETH A.; WOZNEY, JOHN M.; RPSEN, VICKI A.
; TITLE OF INVENTION: DNA SEQUENCES ENCODING THE OSTEOINDUCTIVE
; PROTEINS
; NUMBER OF SEQUENCES: 19
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/378,537
; FILING DATE: 11-JUL-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 179,100
; FILING DATE: 08-APR-1988
; APPLICATION NUMBER: 28,285
; FILING DATE: 20-MAR-1987
; APPLICATION NUMBER: 943,332
; FILING DATE: 17-DEC-1986
; APPLICATION NUMBER: 880,776
; FILING DATE: 01-JUL-1986
; SEQ ID NO: 3:
; LENGTH: 1607
5166058-3

```

Alignment Scores:

```
Pred. No.: 3,648-200 Length: 1607
Score: 2098.00 Matches: 396
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-10-801-648-2 (1-396) x 5166058-3 (1-1607)

QY 1 MetValAlaGlyThrArgCysLeuLeuAlaLeuLeuProGlnValLeuLeuGly 20
DB 356 ARGGGCGCGGACCGCTCTTCTAGCGTTGCTTCCCGAGGTCTCTCGGCGGC 415

QY 21 AlaAlaGlyLeuValProGlnLeuGlyArgArgLysPheAlaAlaSerSerGlyArg 40
DB 416 GCGGCTGCTCGGAGTGGCGCCGAGAGATTCCGCGCGCGCTGCTCGGCGCGC 475

QY 41 ProSerSerGlnProSerAspGluValLeuSerGluPheGluLeuArgLeuLeuSerMet 60
DB 476 CCTCATCCAGCCCTCTGACGAGTCTCTGAGCGAGTTCCAGTTCGGCTGCTCAGCATG 535

QY 61 PheGlyLeuLysGlnArgProThrProSerArgAspAlaValProProTyrMetLeu 80
DB 536 TTCGGCTGAAACAGACAGACCCACCCAGCAGGACGCGGTGCTCCCTTACATGCTA 595

QY 81 AspLeuTyrArgArgHisSerGlyGlnProGlySerProAlaProAspHisArgLeuGlu 100
DB 596 GACCTGTATCGAGCGACTCAGTTCAGCGGGCTCACCGCCCGCAGACCCCGTTGAG 655

QY 101 ArgAlaAlaSerArgAlaAsnThrValArgSerPheHisHisGluGluSerLeuGlu 120
DB 656 AGGCGAGCCAGCGAGCCAACTGTGCGCAGCTTCCACCATGAAGAATCTTTGGAAGA 715

QY 121 LeuProGluThrSerGlyLysThrThrArgArgPhePheAsnLeuSerSerIlePro 140
DB 716 CTACAGAAACAGTGGGAAACACACCGGAGATTCTCTTTAAATTAAGTTCTATCCCC 775

QY 141 ThrGluGluPheIleThrSerAlaGluLeuGlnValPheArgGluGlnMetGlnAspAla 160
DB 776 ACGGAGGAGTTTATCACCTCAGCAGAGCTTCAAGTTTCCGAGAACAGATGCAATGCT 835

QY 161 LeuGlyAsnAsnSerSerPheHisHisArgIleAsnIleTyrGluIleLysProAla 180
DB 836 TTAGGAAACAAATAGCAGTTTCCATCACCGAATTAATATTTATGAATCATAAACCTGCA 895

QY 181 ThrAlaAsnSerLysPheProValThrArgLeuLeuAspThrArgLeuValAsnGlnAsn 200
DB 896 ACAGCCAACTCGAAATTCCTCCGTGACCCAGACTTTTGGACACAGGTTGTTGAATCAGAT 955

QY 201 AlaSerArgTyrGluSerPheAspValThrProAlaValMetArgTyrThrAlaGlnGly 220
DB 956 GCAAGCAGGTGGGAAGTTTTCATGTACACCCCGCTGTGATCGCGTGGAGTGCACAGGA 1015

QY 221 HisAlaAsnHisGlyPheValValGluValAlaHisLeuGluGluLysGlnGlyValSer 240
DB 1016 CACGCCAACCATGGATTCTGTGTGGAGTGGCCACTTGGAGAGAGAACAGGTGTCTCC 1075

QY 241 LysArgHisValArgIleSerArgSerLeuHisGlnAspGluHisSerTrpSerGlnIle 260
DB 1076 AAGACACATGTTAGGATAAGCAGGTCTTTGACCAAGATGAACACAGCTGTGTGCAGATA 1135

QY 261 ArgProLeuLeuValThrPheGlyHisAspGlyLysGlyHisProLeuHisLysArgGlu 280
DB 1136 AGGCCATGCTAGTAACATTTTGGCCATGATGAAAGGGGCATCTCTCCACAAAAGAGAA 1195

QY 281 LysArgGlnAlaLysHisLysGlnArgLysArgLeuLysSerSerCysLysArgHisPro 300
DB 1196 AAACGTCAAGCCAAACACAAACAGCGGAAACCGCTTTAAGTCCAGCTGTGAAGACACCT 1255

QY 301 LeuTyrValAspPheSerAspValGlyTrpAsnAspTrpIleValAlaProProGlyTyr 320
DB 1256 TTGTAGCTGACTTTCAGTGACGTGGGTGGAATGACTGGATTGTGGCTCCCCCGGGTAT 1315
```

```
QY 321 HisAlaPheTyrCysHisGlyGluCysProPheProLeuAlaAspHisLeuAsnSerThr 340
DB 1316 CACGCTTTTACTGCGACGAGAAATGCCCTTTTCTCTGGTGATCATCTGAATCCCACT 1375

QY 341 AsnHisAlaIleValGlnThrLeuValAsnSerValAsnSerLysIleProLysAlaCys 360
DB 1376 AATCATGCCATGTTTCAGACGTTGCTCAACTCTGTAACTCTTAAGATTCCTTAAGCATGC 1435

QY 361 CysValProThrGluLeuSerAlaIleSerMetLeuTyrLeuAspGluAsnGluLysVal 380
DB 1436 TGTGTCCGACAGAACTCAGTGTCTATCTGATGCTGTACCTTGACGAGAAATGAAAGGTT 1495

QY 381 ValLeuLysAsnTyrGlnAspMetValValGluGlyCysGlyCysArg 396
DB 1496 GTATTAAAGAACTATCAGACATGTTGTGGAGGGTTGTGGGTGTCGC 1543

RESULT 5
US-09-976-594-11
; Sequence 11, Application US/09976594
; Patent No. 6673549
; GENERAL INFORMATION:
; APPLICANT: Furness, Michael
; APPLICANT: Buchinder, Jenny
; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
; FILE REFERENCE: PA-0041 US
; CURRENT APPLICATION NUMBER: US/09/976,594
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240,409
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 1143
; SOFTWARE: PERL Program
; SEQ ID NO 11
; LENGTH: 3526
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6673549 1016903.1
US-09-976-594-11

Alignment Scores:
Pred. No.: 1,198-199 Length: 3526
Score: 2098.00 Matches: 396
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-10-801-648-2 (1-396) x US-09-976-594-11 (1-3526)

QY 1 MetValAlaGlyThrArgCysLeuLeuAlaLeuLeuProGlnValLeuLeuGly 20
DB 1180 ATGGTGGCGGAGACCGCTGCTTCTAGCGTTGCTTCCCGAGGTCTCTCGGCGGC 1239

QY 21 AlaAlaGlyLeuValProGlnLeuGlyArgArgLysPheAlaAlaSerSerGlyArg 40
DB 1240 GCGGCTGCTCTGTTCCGAGCTGGCGCCGAGAGATTTCGCGCGCGCTGCTCGGCGCGC 1299

QY 41 ProSerSerGlnProSerAspGluValLeuSerGluPheGluLeuArgLeuLeuSerMet 60
DB 1300 CCTCATCCAGCCCTCTGACGAGTCTCTGAGCGAGTTTCGAGTTCGGCTGCTCAGCATG 1359

QY 61 PheGlyLeuLysGlnArgProThrProSerArgAspAlaValProProTyrMetLeu 80
DB 1360 TTCGGCTGAAACAGAGACCCACCCAGCAGGACGCGGTGCTCCCTTACATGCTA 1419

QY 81 AspLeuTyrArgArgHisSerGlyGlnProGlySerProAlaProAspHisArgLeuGlu 100
DB 1420 GACCTGTATCGAGCGACTCAGTTCAGCGGGCTCACCGCCCGCAGACCCCGTTGAG 1479

QY 101 ArgAlaAlaSerArgAlaAsnThrValArgSerPheHisHisGluGluSerLeuGlu 120
DB 1480 AGGCGAGCCAGCGAGCCAACTGTGCGCAGCTTCCACCATGAAGAATCTTTGGAAGAA 1539
```

```
Qy 121 LeuProGluThrSerGlyLysThrArgArgPhePheAenLeuSerSerIlePro 140
Db 1540 CTACAGAAACGAGTGGGAAACAAACCGGAGATCTCTTTAAATTTAAAGTTCTATCCCC 1599
Qy 141 ThrGluGluPheIleThrSerAlaGluLeuGlnValPheArgGluGlnMetGlnAspAla 160
Db 1600 ACGAGGAGTTTATCACTCAGCAGAGCTTCAGGTTTCCGAGAACAGATGCAAGATGCT 1659
Qy 161 LeuGlyAenAenSerSerPheHisArgIleAenIleTyrGluIleIleLysProAla 180
Db 1660 TTAGGAAACATAGCAGTTCCATCACCAGATTAATATATATGAAATCATAAAACTGCA 1719
Qy 181 ThrAlaAenSerLysPheProValThrArgLeuLeuAspThrArgLeuValAenGlnAen 200
Db 1720 ACAGCAACTCGAAATTCCTCGTACACAGACTTTTGGACACAGGTTGGTGAATCAGAAT 1779
Qy 201 AlaSerArgTrpGluSerPheAspValThrProAlaValMetArgTrpThrAlaGlnGly 220
Db 1780 GCAAGCAGTGGGAAAGTTTGTATGTACCCCGCTGTGATCGGTGGACTGCACAGGA 1839
Qy 221 HisAlaAenHisGlyPheValValGluValAlaHisLeuGluGluLysGlnGlyValSer 240
Db 1840 CACGCCAACCATGATTCGTGGTGAAGTGCCCACTTGGAGGAGAAACAAGGTGTCTCC 1899
Qy 241 LysArgHisValArgIleSerArgSerLeuHisGlnAspGluHisSerTrpSerGlnIle 260
Db 1900 AAGAGACATGTAGGATAAGCAGTCTTTGACCAGATGAACACAGCTGGTGCACAGATA 1959
Qy 261 ArgProLeuLeuValThrPheGlyHisAspGlyLysGlyHisProLeuHisLysArgGlu 280
Db 1960 AGGCATTTGTAGTAACCTTTTGGCATGATGGAAGGGCATCTCTCCACAAAGAGAA 2019
Qy 281 LysArgGlnAlaLysHisLysGlnArgLysArgLeuLysSerSerCysLysArgHisPro 300
Db 2020 AAACGTCAAGCCAAACACAAACAGCGGAAACGCCTTAAGTCCAGCTGTGAAGACACCCCT 2079
Qy 301 LeuTyrValAspPheSerAspValGlyTrpAenAspTrpIleValAlaProGlyTyr 320
Db 2080 TTGTACGTGGACTTTCAAGTACGTGGGTGGGAATGACTGGATTTGGTCTCCCGGGGTAT 2139
Qy 321 HisAlaPheTyrCysHisGlyGluCysProPheProLeuAlaAspHisLeuAenSerThr 340
Db 2140 CACGCTTTTACTGCCACGAGATGCCCTTTTCTCTGGCTGATCATCTGAACTCCACT 2199
Qy 341 AenHisAlaIleValGlnThrLeuValAenSerValAenSerLysIleProLysAlaCys 360
Db 2200 AATCATGCCATTGTTCAGACGTTGGTCAACTCTGTAACTCTAAGATTCTTAAGGCATGC 2259
Qy 361 CysValProThrGluLeuSerAlaIleSerMetLeuTyrLeuAspGluAenGluLysVal 380
Db 2260 TGTGTCCGACAGAACTCAGTGCTATCTCGATGCTGTACCTTGACGAGAAATGAAGAAGTT 2319
Qy 381 ValLeuLysAenTyrGlnAspMetValValGluGlyCysGlyCysArg 396
Db 2320 GTATTAAAGAACTATCAGACATGGTTGTGAGGGTTGTGGGTCTCGC 2367
```

RESULT 6

US-07-989-847-1

; Sequence 1, Application US/07989847

; Patent No. 5863364

; GENERAL INFORMATION:

; APPLICANT: Israel, David

; APPLICANT: Wolfman, Neil M.

; TITLE OF INVENTION: Recombinant Bone Morphogenetic Protein

; TITLE OF INVENTION: Heterodimers, Compositions and Methods of Use.

; NUMBER OF SEQUENCES: 30

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Legal Affairs, Genetics Institute, Inc.

; STREET: 87 CambridgePark Drive

; CITY: Cambridge

; STATE: MA

; COUNTRY: USA

```
; ZIP: 02140-2387
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Tape
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07989,847
; FILING DATE:
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: Kapinos, Ellen J.
; REGISTRATION NUMBER: 32,245
; REFERENCE/DOCKET NUMBER: GI-5192B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-876-1170
; TELEFAX: 617-876-5851
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1607 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 356..1543
; US-07-989-847-1
```

Alignment Scores:

```
Pred. No.: 7,27e-200 Length: 1607
Score: 2095.00 Matches: 395
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.75% Mismatches: 0
Query Match: 99.86% Indels: 0
DB: 2 Gaps: 0
```

US-10-801-648-2 (1-396) x US-07-989-847-1 (1-1607)

```
Qy 1 MetValAlaGlyThrArgCysLeuLeuAlaLeuLeuLeuProGlnValLeuLeuGlyGly 20
Db 356 ATGCTGGCCGGACCCCGCTGTCTTCTAGCGTTGCTGCTTCCACAGGTCTCTCTGGCGGC 415
Qy 21 AlaIadGlyLeuValProGluLeuGlyArgArgLysPheAlaAlaAspSerSerGlyArg 40
Db 416 GCAGCTCGCTCGCTTCCGAGCTGGCGGAGTTCGCGGAGTTCGCGGCGCTCTCTGGCGGC 475
Qy 41 ProSerSerGlnProSerAspGluValLeuSerGluPheGluLeuArgLeuLeuSerMet 60
Db 476 CCTCATCCAGCCCTCTGACGAGTCTCTGACGAGTTCGAGTTCGCGGTCTCAGCATG 535
Qy 61 PheGlyLeuLysGlnArgProThrProSerArgAspAlaValValProProTyrMetLeu 80
Db 536 TTCGGCTCTGAAACAGAGACCCACCCCGCAGGAGCGCGTGTGTCGCCCTACATGCTA 595
Qy 81 AspLeuTyrArgArgHisSerGlyGlnProGlySerProAlaProAspHisArgLeuGlu 100
Db 596 GACCTGTATCGAGGCACCTCAGGTTCAGCCCGGCTCACCCTCCAGACCCAGCGGTGAG 655
Qy 101 ArgAlaAlaSerArgAlaAenThrValArgSerPheHisGluGluSerLeuGluGlu 120
Db 656 AGGCACGACCGAGCCACACATGTCGCGGAGCTTCCACCATGAGAAATCTTTGGAAGAA 715
Qy 121 LeuProGluThrSerGlyLysThrArgArgPhePheAenLeuSerSerIlePro 140
Db 716 CTACCAGAAACGAGTGGGAAAAACAACCGGAGATTCCTCTTAAATTTAAAGTTCTATCCCC 775
Qy 141 ThrGluGluPheIleThrSerAlaGluLeuGlnValPheArgGluGlnMetGlnAspAla 160
Db 776 ACGAGGAGGTTTATCACCCTCAGCAGAGCTTCAGGTTTCCGAGAACAGATCAGATGCT 835
Qy 161 LeuGlyAenAenSerSerPheHisArgIleAenIleTyrGluIleIleLysProAla 180
```

Db 836 TTAGGAAACAATAGCAGTTTCCATCACCGAAATTAATATTTATGAATCATATAAAACCTGCA 895
Qy 181 ThrAlaAsnSerLysPheProValThrArgLeuLeuAspThrArgLeuValAsnGlnAsn 200
Db 896 ACAGCAACTCGAATTCCTCCGTGACACAGACTTTTGGACACAGGTTGGTGAATCAGAAT 955
Qy 201 AlaSerArgTTPGluSerPheAspValThrProAlaValMetArgTTPThrAlaGlnGly 220
Db 956 GCAAGCAGTGGAAACTTTTGATGTACCCCGCTGTGATCGGTGACGTGCACAGGA 1015
Qy 221 HisAlaAsnHisGlyPheValValGluValAlaHisLeuGluGluLysGlnGlyValSer 240
Db 1016 CACGCCAACCATGATTCGTGTGAAGTGGCCACTTGGAGGAGAAACAAGGTGTCTCC 1075
Qy 241 LysArgHisValArgLysSerArgSerLeuHisGlnAspGluHisSerTrpSerGlnIle 260
Db 1076 AAGACACATGTAGATAGCAGGTCTTTGACCAAGATGAACAGCTGTGTGCACAGATA 1135
Qy 261 ArgProLeuLeuValThrPheGlyHisAspGlyLysGlyHisProLeuHisLysArgGlu 280
Db 1136 AGGCCATTTGCTAGTAACCTTTTGGCCATGATGGAAAGGCATCTCTCCACAAAGAGAA 1195
Qy 281 LysArgGlnAlaLysHisLysGlnArgLysArgLeuLysSerSerCysLysArgHisPro 300
Db 1196 AAACGTCAAGCCAAACACAAACAGCGGAAACGCTTAAAGTCCAGCTGTAAGAGACACCCCT 1255
Qy 301 LeuTyrValAspPheSerAspValGlyTrpAsnAspTTPLeValAlaProGlyTyr 320
Db 1256 TTGTACGTGGACTTCAGTGACGTGGGGTGGATGATGTGGCTTCCCGCGGGTAT 1315
Qy 321 HisAlaPheTyrCysHisGlyGluCysProPheProLeuAlaAspHisLeuAsnSerThr 340
Db 1316 CACGCTTTTACTGCGACGAGAAATGCCCTTTTCTCTGGCTGATCATCTGACTCCACT 1375
Qy 341 AsnHisAlaIleValGlnThrLeuValAsnSerValAsnSerLysIleProLysAlaCys 360
Db 1376 AATCATGCCATTTGTTTCCAGACGTTGGTCAACTCTGTAACTCTTAAGATTCTTAAGGCATGC 1435
Qy 361 CysValProThrGluLeuSerAlaIleSerMetLeuTyrLeuAspGluAsnGluLysVal 380
Db 1436 TGTGTCCCGACAGAACTCAGTGTCTATCTCGATGCTGTACCTTTGACGAGAAATGAAAGGTT 1495
Qy 381 ValLeuLysAsnTyrGlnAspMetValValGluGlyCysGlyCysArg 396
Db 1496 GTATTAAAGAACTATCAGACACATGTTGTGGAGGGTTGTGGGTGCGC 1543

RESULT 7

US-08-469-411-1
; Sequence 1, Application US/08469411
; Patent No. 6190880
; GENERAL INFORMATION:
; APPLICANT: Israel, David
; Wolfman, Neil M.
; TITLE OF INVENTION: Recombinant Bone Morphogenetic Protein
; Heterodimers, Compositions and Methods of Use.
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESS: Legal Affairs, Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140-2387
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Tape
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,411
; FILING DATE: 06-Jun-1995
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:

NAME: Kapinos, Ellen J.
REGISTRATION NUMBER: 32,245
REFERENCE/DOCKET NUMBER: GI-5192B-CON
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-498-8622
TELEFAX: 617-876-5851
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1607 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 356..1543
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-08-469-411-1
Alignment Scores:
Pred. No.: 7,27e-200 Length: 1607
Score: 2095.00 Matches: 395
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.75% Mismatches: 0
Query Match: 99.86% Indels: 0
DB: 3 Gaps: 0
US-10-801-648-2 (1-396) x US-08-469-411-1 (1-1607)
Qy 1 MetValAlaGlyThrArgCysLeuLeuAlaLeuLeuProGlnValLeuLeuGlyGly 20
Db 356 ATGTGGCGGGAGCCCGCTGCTTCTAGCGTTGCTTCCCGAGGTCTCTCTGGCGCGC 415
Qy 21 AlaAlaGlyLeuValProGluLeuGlyArgArgLysPheAlaAlaSerSerGlyArg 40
Db 416 CGCGTGCCTCGTTTCCGAGCTGCGCGCGCAGAGATTCCGCGCGCGCTCGTGGCGCGC 475
Qy 41 ProSerSerGlnProSerAspGluValLeuSerGluPheGluLeuArgLeuLeuSerMet 60
Db 476 CCTCATCCAGCCCTCTGACGAGTCTCTGACGAGTTGCGAGTTGCGGCTGCTCAGCATG 535
Qy 61 PheGlyLeuLysGlnArgProThrProSerArgAspAlaValValProProTyrMetLeu 80
Db 536 TTGCGCCTGAAACAGAGACACCCAGAGAGGAGCGCGTGTGCTGCCCTTACATGCTA 595
Qy 81 AspLeuTyrArgArgHisSerGlyGlnProGlySerProAlaProAspHisArgLeuGlu 100
Db 596 GACCTGTATCGCAGCACTCAGGTGAGCGCGGCTCACCGCCCGCAGACCCCGTTGGAG 655
Qy 101 ArgAlaAlaSerArgAlaAsnThrValArgSerPheHisHisGluGluSerLeuGluGlu 120
Db 656 AGGCGAGCCAGCCGAGCCCAACACTGTGCGCAGTTCCACCATGAAGATCTTTGGAGAA 715
Qy 121 LeuProGluThrSerGlyLysThrThrArgArgPhePheAsnLeuSerSerIlePro 140
Db 716 CTACCAGAAACGAGTGGGAAACACACCGGAGATTCTTTTAAATTTAAGTTCTATCCCC 775
Qy 141 ThrGluGluPheIleThrSerAlaGluLeuGlnValPheArgGluGlnMetGlnAspAla 160
Db 776 ACGGAGGAGTTTATCACCTCAGCAGAGCTTTCAGGTTTTCGAGAGACAGATGCAAGATGCT 835
Qy 161 LeuGlyAsnAsnSerSerPheHisHisArgIleAsnIleTyrGluIleLysProAla 180
Db 836 TTAGGAAACAATAGCAGTTTCCATCACCGAATTAATATTTATGAATCATATAAAACCTGCA 895
Qy 181 ThrAlaAsnSerLysPheProValThrArgLeuLeuAspThrArgLeuValAsnGlnAsn 200
Db 896 ACAGCAACTCGAATTCCTCCGTGACACAGACTTTTGGACACAGGTTGGTGAATCAGAAT 955
Qy 201 AlaSerArgTTPGluSerPheAspValThrProAlaValMetArgTTPThrAlaGlnGly 220
Db 956 GCAAGCAGTGGAAACTTTTGTATGTCTCACCCCGCTGTGATCGGTGAGGTGCACAGGA 1015

```
Qy 221 HisAlaAenHisGlyPheValValGluValAlaHisLeuGluGluLysGlnGlyValSer 240
Db 1016 CACGCCAACCATGATTCGTGGTGAAGTGGCCACCTTGGAGGAAACAAGGTGTCTCC 1075
Qy 241 LysArgHisValArgIleSerArgSerLeuHisGlnAspGluHisSerTrpSerGlnIle 260
Db 1076 AAGAGACATGTTAGGATAAGCAGGTCTTTGCCACCAAGATGAACACAGCTGTCTACAGATA 1135
Qy 261 ArgProLeuLeuValThrPheGlyHisAspGlyLysGlyHisProLeuHisLysArgGlu 280
Db 1136 AGGCCATTGCTAGTAACATTTTGGCCATGATGGAAGGAGGATCTCTCCACAAAGAGAA 1195
Qy 281 LysArgGlnAlaLysHisLysGlnArgLysArgLeuLysSerSerCysLysArgHisPro 300
Db 1196 ANAGCTCAAGCCAAACACAAACAGCGGAACGCCTTAAAGTCAGCTGTAAAGACACCCCT 1255
Qy 301 LeuTyrValAspPheSerAspValGlyTrpAsnAspTrpIleValAlaProProGlyTyr 320
Db 1256 TTGTACGTGGACTTCAGTGACGTGGGTGGATGACTGGATTGTGGCTCCCGGGGTAT 1315
Qy 321 HisAlaPheTyrCysHisGlyGluCysProPheProLeuAlaAspHisLysAsnSerThr 340
Db 1316 CACGCTTTTACTGTCACGGAATGCCCTTTTCTCTGGCTGATCATCTGAACCTCCACT 1375
Qy 341 AsnHisAlaIleValGlnThrLeuValAsnSerValAsnSerLysLysIleProLysAlaCys 360
Db 1376 AATCATGCCATGTTCAGACGTGTGTCAACTCTGTAACTCTAAGATTCTTAAGGCATGC 1435
Qy 361 CysValProThrGluLeuSerAlaIleSerMetLeuTyrLeuAspGluAsnGluLysVal 380
Db 1436 TGTGTCCCGCAGAACTCAGTGCTATCTCGATGCTGTACCTTGACGAGATGAAGAAGTT 1495
Qy 391 ValLeuLysAsnTyrGlnAspMetValValGluGlyCysGlyCysArg 396
Db 1496 GTATTAAAGAACTATCAGGACATGTTGTGGAGGGTTGTGGGTGTGCG 1543
```

RESULT 8

```
US-09-780-601A-1
; Sequence 1, Application US/09780601A
; Patent No. 6593109
; GENERAL INFORMATION:
; APPLICANT: Israel, David
; APPLICANT: Wolfman, Neil M.
; TITLE OF INVENTION: Recombinant Bone Morphogenetic Protein
; TITLE OF INVENTION: Heterodimers, Compositions and Methods of Use.
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Legal Affairs, Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140-2387
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Tape
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/780,601A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,411
; FILING DATE: 06-Jun-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Kapinos, Ellen J.
; REGISTRATION NUMBER: 32,245
; REFERENCE/DOCKET NUMBER: GI-5192B-CON
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-498-8622
; TELEFAX: 617-876-5851
; INFORMATION FOR SEQ ID NO: 1:
```

```
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1607 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 356..1543
; US-09-780-601A-1
```

Alignment Scores:

```
Pred. No.: 7,27e-200 Length: 1607
Score: 2095.00 Matches: 395
Percent Similarity: 100.00% Conservativeness: 1
Best Local Similarity: 99.75% Mismatches: 0
Query Match: 99.86% Indels: 0
DB: 3 Gaps: 0
```

US-10-801-648-2 (1-396) x US-09-780-601A-1 (1-1607)

```
Qy 1 MetValAlaGlyThrArgCysLeuLeuAlaLeuLeuProGlnValLeuLeuGlyGly 20
Db 356 ATGGTGGCGGACCCGCTGCTTCTAGCGTTGCTTCCAGGTCTCTCTGGCGGC 415
Qy 21 AlaAlaGlyLeuValProGluLeuGlyArgArgLysPheAlaAlaAsnSerSerGlyArg 40
Db 416 GCGGCTGGCTCGCTTCGCGAGCTGGCGCGCAGGAGTTGCGCGCGGCTGCTCGGCGGC 475
Qy 41 ProSerSerGlnProSerAspGluValLeuSerGluPheGluLeuArgLeuSerMet 60
Db 476 CCTCATCCAGCCCTCTGACGAGTCTGAGCGAGTTGAGTTGCGGCTGCTCAGCATG 535
Qy 61 PheGlyLeuLysGlnArgProThrProSerArgAspAlaValValProProTyrMetLeu 80
Db 536 TTCGGCTGAAACAGAGACACCCCGCAGGAGCGCGGTGTGCGGCTACATGCTA 595
Qy 81 AspleuTyrArgArgHisSerGlyGlnProGlySerProAlaProAspHisArgLeuGlu 100
Db 596 GACCTGTATCGCAGGCATCTCAGGTGCGCGGGCTCACCCCGCCCGCAGACCCGTTGAG 655
Qy 101 ArgAlaAlaSerArgAlaAsnThrValArgSerPheHisGluGluSerLeuGluGlu 120
Db 656 AGGCAGCCAGCCGAGCCACACATGTGCGCAGCTTCCACCATGAGAGATCTTTGGAGAA 715
Qy 121 LeuProGluThrSerGlyLysThrThrArgArgPhePheAsnLeuSerSerIlePro 140
Db 716 CTACAGAAACGAGTGGGAAAAACAACCGGAGATTCTCTTTAATTTAAGTTCTATCCCC 775
Qy 141 ThrGluGluPheIleThrSerAlaGluLeuGlnValPheArgGluGlnMetGlnAspAla 160
Db 776 ACGGAGGAGTTTATCACCTCAGCAGAGCTTTCAGGTTTTCCGAGAACAGATCAAGATGCT 835
Qy 161 LeuGlyAsnAsnSerSerPheHisArgIleAsnIleTyrGluIleLeuLysProAla 180
Db 836 TTAGAAACATAGCAGTTTCCATCAGCAATTATATTTATGAATCATTAACCTGCA 895
Qy 181 ThrAlaAsnSerLysPheProValThrArgLeuLeuAspThrArgLeuValAsnGlnAsn 200
Db 896 ACAGCCAACTCGAAATTTCCCGTGACCCAGACTTTTGGACACACAGGTTGGTGAATCAGAAT 955
Qy 201 AlaSerArgTrpGluSerPheAspValThrProAlaValMetArgTrpThrAlaGlnGly 220
Db 956 GCAAGCAGGTGGGAAACTTTTGTATGTACCCCCCTGTGATGCGGTGGACTGCACAGGGA 1015
Qy 221 HisAlaAsnHisGlyPheValValAlaHisLeuGluGluLysGlnGlyValSer 240
Db 1016 CACGCCAACCATGATTCGTGGTGAAGTGGCCACCTTGGAGGAGAAACAAGGTGTCTCC 1075
Qy 241 LysArgHisValArgIleSerArgSerLeuHisGlnAspGluHisSerTrpSerGlnIle 260
Db 1076 AAGAGACATGTTAGGATAAGCAGGTCTTTGACCAAGATGAACACAGCTGTGTCTACAGATA 1135
```


Qy 261 ArgProLeuLeuValThrPheGlyHisAspGlyHisGlyHisProLeuHisLeuArgGlu 280
Db 1136 AGGCCATTGCTAGTAACCTTTGGCCATGATGGAAGGGCATCTCTCCACAAAGAGAA 1195
Qy 281 LysArgGlnAlaLysHisGlyGlnArgLysArgLeuLysSerCysLeuArgHisPro 300
Db 1196 AAACGTCAGGCCAAACACAAACAGCGGAACGCCTTAAGTCCAGCTGTGAAGAGACACCCCT 1255
Qy 301 LeuTyValAspPheSerAspValGlyTrpAsnAspTrpIleValAlaProGlyTyr 320
Db 1256 TTGTACGTGGACTTCAGTGAGCTGGGGTGGAGTGAATGACTGATTTGGCTCCCGGGGGTAT 1315
Qy 321 HisAlaPheTyrcysHisGlyGluCysProPheProLeuAlaAspHisLeuAsnSerThr 340
Db 1316 CACGCTTTTACTGCCACGGAGATGCCCTTTCTCTGGCTGATCATCTGAATCCACT 1375
Qy 341 AsnHisAlaIleValGlnThrLeuValAsnSerValAsnSerLysIleProLysAlaCys 360
Db 1376 AATCATGCCATTGTTACAGACGTTGGTCAACTCTGTAACTCTAAGATTCTTAAGGCATGC 1435
Qy 361 CysValProThrGluLeuSerAlaIleSerMetLeuTyLeuAspGluAsnGluLysVal 380
Db 1436 TGTGTCCCGCAGAACTCAGTGCTATCTCGATGCTGTACCTGACGAGAAATGAAGGTT 1495
Qy 381 ValLeuLysAsnTyrcysGlnAspMetValValGluGlyCysGlyCysArg 396
Db 1496 GTATTAAAGAACTATCAGACACATGTTGTGGAGGGTGTGGGTGTGCG 1543

RESULT 9

US-07-841-646-4
; Sequence 4, Application US/07841646
; Patent No. 5266683

GENERAL INFORMATION:

APPLICANT: OPPERMAN, HERMANN
APPLICANT: OZKAYNAK, ENGIN
APPLICANT: KUBERASAMPATH, THANGAVEL
APPLICANT: RUEGER, DAVID C.
APPLICANT: PANG, ROY H. L.
TITLE OF INVENTION: OSTEOGENIC DEVICES
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESS: TESTA, HURWITZ & THIBEAULT
STREET: 53 STATE STREET
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: U.S.A.
ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/841,646
FILING DATE: 19920221

CLASSIFICATION: 530

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 810,560

FILING DATE: 20-DEC-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 827,052
FILING DATE: 28-JAN-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 660,162
FILING DATE: 22-FEB-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 621,988
FILING DATE: 04-DEC-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 621,849
FILING DATE: 04-DEC-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 616,374

FILING DATE: 21-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 600,024
FILING DATE: 18-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 599,543
FILING DATE: 18-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 579,865
FILING DATE: 07-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 569,920
FILING DATE: 20-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 483,913
FILING DATE: 22-FEB-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 422,613
FILING DATE: 17-OCT-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 315,342
FILING DATE: 23-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 232,630
FILING DATE: 15-AUG-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 179,460
FILING DATE: 08-APR-1988
ATTORNEY/AGENT INFORMATION:
NAME: FITCHER, EDMUND R.
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: CRP-001CP6
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/248-7000
TELEFAX: 617/248-7100
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1260 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: HOMO SAPIENS
FEATURE:
NAME/KEY: CDS
LOCATION: 9..1196
OTHER INFORMATION: /function= "OSTEOGENIC PROTEIN"
OTHER INFORMATION: /product= "CBMP2A"
OTHER INFORMATION: /note= "CBMP2A (CDNA)"
US-07-841-646-4

Alignment Scores:

Pred. No.: 1,01e-199 Length: 1260
Score: 2092.00 Matches: 395
Percent Similarity: 99.75% Conservative: 0
Best Local Similarity: 99.75% Mismatches: 1
Query Match: 99.71% Indels: 0
DB: 2 Gaps: 0

US-10-801-648-2 (1-396) x US-07-841-646-4 (1-1260)

Qy 1 MetValAlaGlyThrArgCysLeuLeuAlaLeuLeuProGlnValLeuLeuGly 20
Db 9 ATGGTGGCCGGACCCGCTGCTTCTAGCGTTGCTGCTTCCCGACGGTCTCTCTGGGCGGC 68
Qy 21 AlaAlaGlyLeuValProGluLeuGlyArgGlyPheAlaAlaSerSerGlyArg 40
Db 69 GCGGCTGGCCCTCGTTCCGAGCTGGCGCCGCGGCTGCTGCGGCGCCG 128
Qy 41 ProSerSerGlnProSerAspGluValLeuSerGluPheGluLeuArgLeuSerMet 60

```
Db 129 CCTCATCCAGCCCTCTGACGAGGTCTGACGAGTTCGAGTTGGGCTGCTCAGCATG 188
Qy 61 PheGlyLeuLysGlnArgProThrProSerArgAspAlaValProProTyrMetLeu 80
Db 189 TTCGGCCTGAAACAGAGACCCACCCAGCAGGAGCGCGTGGTGCCTACATGCTA 248
Qy 81 AspLeuTyrArgArgHisSerGlyGlnProGlySerProAlaProAspHisArgLeuGlu 100
Db 249 GACCTGTATCGACGACCTCGGGTCAGCCGGGCTCACCCGCCCCAGACCCAGCGGTGGAG 308
Qy 101 ArgAlaLaserArgAlaAsnThrValArgSerPheHisHisGluGluSerLeuGluGlu 120
Db 309 AGGCGAGCCAGCCAGCCAACTGTGGCGAGCTTCCACCATGAGATCTTTGGAGAA 368
Qy 121 LeuProGluThrSerGlyLysThrThrArgArgPhePheAenLeuSerSerIlePro 140
Db 369 CTACCAAGACGAGTGGGAAACAAACCCGAGATCTCTCTTAATTTAAAGTTCTATCCC 428
Qy 141 ThrGluGluPheIleThrSerAlaGluLeuGlnValPheArgGluGlnMetGlnAspAla 160
Db 429 ACGGAGGAGTTATCACTCTCAGCAGAGCTTCAGGTTCCTCCGAGAACAGATCAAGATGCT 488
Qy 161 LeuGlyAenAenSerSerPheHisArgIleAenIleFyrGluIleIleLysProAla 180
Db 489 TTAGGAACATAGCAGTTCCTCATCCAGATTAATTAATTAATTAATTAATTAATTAATTA 548
Qy 181 ThrAlaAenSerLysPheProValThrArgLeuLeuAepThrArgLeuValAenGlnAen 200
Db 549 ACAGCCAACTCGAAATCCCGGTGACCACTCTTTGGACACACAGGTGGTGAATCAGAA 608
Qy 201 AlaSerArgTyrGluSerPheAspValThrProAlaValMetArgTyrThrAlaGlnGly 220
Db 609 GCAAGCAGTGGGAAAGTTTGTGATGTACCCCGCTGTGATGCGGTGACTGCACAGGA 668
Qy 221 HisAlaAenHisGlyPheValValGluValAlaHisLeuGluGluLysGlnGlyValSer 240
Db 669 CACGCCAACCATGATTCGTGGTGAAGTGCCCACTTGGAGGAGAAACAAGGTGTCTCC 728
Qy 241 LysArgHisValArgIleSerArgSerLeuHisGlnAepGluHisSerTrpSerGlnIle 260
Db 729 AAGAGACATGTTAGGATAAGCAGGTCTTTGACCAAGATGAACACAGCTGGTGCACAGTA 788
Qy 261 ArgProLeuLeuValThrPheGlyHisAspGlyLysGlyHisProLeuHisLysArgGlu 280
Db 789 AGGCCATTGCTAGTAACCTTTTGGCCATGATGGAAGGCACTCTCTCCACAAAGAGAA 848
Qy 281 LysArgGlnAlaLysHisLysGlnArgLysArgLeuLysSerSerCysLysArgHisPro 300
Db 849 AAGCGTCAGCCAAACACAAACAGCGGAAACGCTTAAGTCCAGCTGTAAAGACACCCCT 908
Qy 301 LeuTyrValAspPheSerAspValGlyTrpAenAspTrpIleValAlaProProGlyTyr 320
Db 909 TTGTACGTGGACTTCAGTGACGTGGGTGGAATGACTGATTTGGTTCCTCCCGGGGTAT 968
Qy 321 HisAlaPheTyrCysHisGlyGluCysProPheProLeuAlaAspHisLysAenSerThr 340
Db 969 CACGCCCTTTTACTGCGCAGAGATGCCCCCTTTCTCTGGCTGATCATCTGAATCCCACT 1028
Qy 341 AenHisAlaIleValGlnThrLeuValAenSerValAenSerLysIleProLysAlaCys 360
Db 1029 AATCATGCCATGTTTCAGACGTTGGTCAACTCTGTAACTCTTAAGATCTCTTAAGCATGC 1088
Qy 361 CysValProThrGluLeuSerAlaIleSerMetLeuTyrLeuAepGluAenGluLysVal 380
Db 1089 TGTGTCCCGACAGAACTCAGTGCTATCTCGATGCTGTACCTTTGACGAGATGAAGAGTT 1148
Qy 381 ValLeuLysAenTyrGlnAspMetValValGluGlyCysGlyCysArg 396
Db 1149 GTATTAAGAAGAACTATCAGGATATGTTGTGAGGGTTGTGGGTGCTCGC 1196
RESULT 10
US-07-901-703-14
```

```
; Sequence 14, Application US/07901703
; Patent No. 5344654
; GENERAL INFORMATION:
; APPLICANT: RUEGER, DAVID C
; APPLICANT: KUBERASAMPATH, THANGAVEL
; APPLICANT: OPPERMANN, HERMANN
; APPLICANT: OZAKAYNAK, ENGIN
; TITLE OF INVENTION: PROSTHETIC DEVICES HAVING ENHANCED
; TITLE OF INVENTION: OSTEOGENIC PROPERTIES
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TESTA, HURWITZ & THIBEAULT
; STREET: EXCHANGE PLACE, 53 STATE STREET
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07901,703
; FILING DATE: 19920616
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: PITCHER ESQ, EDMUND R
; REGISTRATION NUMBER: 27,829
; REFERENCE/DOCKET NUMBER: STK-057
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/248-7000
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1260 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: HOMO SAPIENS
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 9..1196
; OTHER INFORMATION: /function= "OSTEOGENIC PROTEIN"
; OTHER INFORMATION: /product= "BMP2A"
; OTHER INFORMATION: /note= "BMP2A (CDNA)"
; US-07-901-703-14

Alignment Scores:
Pred. No.: 1,01e-199 Length: 1260
Score: 2092.00 Matches: 395
Percent Similarity: 99.75% Conservative: 0
Best Local Similarity: 99.75% Mismatches: 1
Query Match: 99.71% Indels: 0
DB: 2 Gaps: 0

US-10-801-648-2 (1-396) x US-07-901-703-14 (1-1260)

Qy 1 MetValAlaGlyThrArgCysLeuLeuAlaLeuLeuLeuProGlnValLeuLeuGlyGly 20
Db 9 ATGTGTGCGCGGAGCCCTGTCTTAGCTGTCTCTCCAGGTCCTCTCGGCGGC 68
Qy 21 AlaAlaGlyLeuValProGluLeuGlyArgArgLysPheAlaAlaSerSerGlyArg 40
Db 69 CGGCTGCGCTTCGTTCCGAGAGCTGGCGCGAGAGTTCCGGCGGCGGTCTCGGCGGC 128
Qy 41 ProSerSerGlnProSerAspGluValLeuSerGluPheGluLeuArgLeuLeuSerMet 60
Db 129 CCCTCATCCAGCCCTCTGACGAGGTCTGACGAGTTCGAGTTGGGCTGCTCAGCATG 188
```

QY 61 PheGlyLeuLysGlnArgProThrProSerArgAspAlaValValProProTyrMetLeu 80
DB 189 TTCGGCTGAAACAGACAGACCCACCCAGCAGGACGGTGGTGGCTTACATGCTA 248
QY 81 AspLeuTyrArgArgHisSerGlyGlnProGlySerProAlaProAspHisArgLeuGlu 100
DB 249 GACCTGTATCGCAGCACTCGGGTCAGCGGGCTCACCGCCAGACCAACCGGTGGAG 308
QY 101 ArgAlaAlaSerArgAlaAsnThrValArgSerPheHisHisGluGluSerLeuGlu 120
DB 309 AGGGCAGCCGCGAGCAACACTGTGCGACCTCCACCATGAAGAATCTTTGGAAGAA 368
QY 121 LeuProGluThrSerGlyLysThrArgArgPhePheAsnLeuSerSerIlePro 140
DB 369 CTACCAGAAACGAGTGGGAAACAACCCGAGATCTCTTTAATTTAAGTCTATCC 428
QY 141 ThrGluGluPheIleThrSerAlaGluLeuGlnValPheArgGluGlnMetGlnAspAla 160
DB 429 ACGGAGGAGTTTATCACCTCAGCAGAGCTTCAGGTTTCCGAGAAACAGATGCAAGTCT 488
QY 161 LeuGlyAsnAsnSerSerPheHisHisArgIleAsnIleTyrGluIleIleLysProAla 180
DB 489 TTAGGAACAATAGCAGTTTCATCACCGAATTAATTTATGAATCATAAACCTGCA 548
QY 181 ThrAlaAsnSerLysPheProValThrArgLeuLeuAspThrArgLeuValAsnGlnAsn 200
DB 549 ACAGCCAACTCGAANTTCCCGTGACCACTCTTTTGGACACAGGTTGGTGNATCAGAT 608
QY 201 AlaSerArgTTPGluSerPheAspValThrProAlaValMetArgTTPThrAlaGlnGly 220
DB 609 GCNAGCAGGTGGGAAAGTTTGTATGTACCCCGCTGTGTATGCGGTGACCTGCACAGGA 668
QY 221 HisAlaAsnHisGlyPheValValGluValAlaHisLeuGluGluLysGlnGlyValSer 240
DB 669 CACGCCAACCAATGGATTCGTGTGGAAGTGGCCCACTTGGAGGAGAAACAAGGTCTCTCC 728
QY 241 LysArgHisValArgIleSerArgSerLeuHisGlnAspGluHisSerTTPSerGlnIle 260
DB 729 AAGACACATTTAGATAGCAGGTCTTTTGCACAGATGAACACAGCTGTGCACAGATA 788
QY 261 ArgProLeuLeuValThrPheGlyHisAspGlyLysGlyHisProLeuHisLysArgGlu 280
DB 789 AGGCCATTGCTAGTAATCTTTGGCCATGATGTGAAAGGCGCATCTCTCCACAAAAGAGAA 848
QY 281 LysArgGlnAlaLysHisLysGlnArgLysArgLeuLysSerSerCysLysArgHisPro 300
DB 849 AAACGTCAAGCCCAACACAAAACAGCGGAAACGCTTAAAGTCCAGCTGTAAGAGACACCC 908
QY 301 LeuTyrValAspPheSerAspValGlyTTPAsnAspTTPIleValAlaProProGlyTyr 320
DB 909 TTGTACGTGGACTTCAGTGACCTGGGTGGTGAATGACTGGATTTGGCTCCCCCGGGTAT 968
QY 321 HisAlaPheTyrCysHisGlyGluCysProPheProLeuAlaAspHisLeuAsnSerThr 340
DB 969 CACGCTTTTACTGCCAGCGAATGCTCTTTCTCTGCTGATCATCTGAATCCACT 1028
QY 341 AsnHisAlaIleValGlnThrLeuValAsnSerValAsnSerLysIleProLysAlaCys 360
DB 1029 AATCATGCCATTGTTTCAGACGTTGGTCAACTCTGTAACTCTAAGATCTCTAAGGCATGC 1088
QY 361 CysValProThrGluLeuSerAlaIleSerMetLeuTyrLeuAspGluAsnGluLysVal 380
DB 1089 TGTGTCCCGACAGAACTCAGTCTATCTCGATGCTGTATCTTGACGAGATGAAGAAGTT 1148
QY 381 ValLeuLysAsnTyrGlnAspMetValValGluGlyCysGlyCysArg 396
DB 1149 GTATTAAAGAACTATCAGGATATGTTGTGGAGGTTGTGGGTGTGCG 1196

RESULT 11

US-08-147-023-4

; Sequence 4, Application US/08147023

; Patent No. 546845

; GENERAL INFORMATION:

APPLICANT: OPPERMAN, HERMANN
APPLICANT: OZKAYNAK, ENGIN
APPLICANT: KUBERASAMPATH, THANGAVEL
APPLICANT: RUEGER, DAVID C.
APPLICANT: FANG, ROY H.L.
TITLE OF INVENTION: OSTROGENIC DEVICES
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: TESTA, HURWITZ & THIBEAULT
STREET: 53 STATE STREET
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: U.S.A.
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/147,023
FILING DATE: 21-FEB-1992
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 810,560
FILING DATE: 20-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 827,052
FILING DATE: 28-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 660,162
FILING DATE: 22-FEB-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 621,988
FILING DATE: 04-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 621,849
FILING DATE: 04-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 616,374
FILING DATE: 21-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 600,024
FILING DATE: 18-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 579,865
FILING DATE: 07-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 569,920
FILING DATE: 20-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 483,913
FILING DATE: 22-FEB-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 422,613
FILING DATE: 17-OCT-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 315,342
FILING DATE: 23-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 232,630
FILING DATE: 15-AUG-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 179,460
FILING DATE: 08-APR-1988
ATTORNEY/AGENT INFORMATION:
NAME: FITCHER, EDMUND R.
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: CRP-001CP6
TELECOMMUNICATION INFORMATION:

```
/ TELEPHONE: 617/248-7000
/ TELEFAX: 617/248-7100
/ INFORMATION FOR SEQ ID NO: 4:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1260 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA
/ HYPOTHEICAL: NO
/ ANTI-SENSE: NO
/ ORIGINAL SOURCE:
/ ORGANISM: HOMO SAPIENS
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 9..1196
/ OTHER INFORMATION: /function= "OSTEOGENIC PROTEIN"
/ OTHER INFORMATION: /product= "CBMP2A"
/ OTHER INFORMATION: /note= "CBMP2A (CDNA)"
US-08-147-023-4

Alignment Scores:
Pred. No.: 1.01e-199 Length: 1260
Score: 2092.00 Matches: 395
Percent Similarity: 99.75% Conservative: 0
Best Local Similarity: 99.75% Mismatches: 1
Query Match: 99.71% Indels: 0
Db: 2 Gaps: 0

US-10-801-648-2 (1-396) x US-08-147-023-4 (1-1260)

QY 1 MetValAlaGlyThrArgCysLeuLeuAlaLeuLeuProGlnValLeuLeuGlyGly 20
Db 9 ATGTGGCGCGGAGCCCGCTGCTTCTAGCGTGTCTCTCCAGGTCCTCTCCGGCGGC 68

QY 21 AlaAlaGlyLeuValProGluLeuGlyArgArgLysPheAlaAlaLaserSerGlyArg 40
Db 69 GCGGCTGCGCTCTCCGAGCTGGCGCGCAGGAAGTTCCGCGCGCGCTGCTCGCGCGC 128

QY 41 ProSerSerGlnProSerAspGluValLeuSerGluPheGluLeuArgLeuSerMet 60
Db 129 CCCTCATCCAGCCCTCTGACGAGGTCCTGACGAGGTCCTGACGAGTTGCGGCTGCTCAGCATG 188

QY 61 PheGlyLeuLysGlnArgProThrProSerArgAspAlaValValProProTyMetLeu 80
Db 189 TTCGGCTGAACAGAGACCCGCCCCAGCAGGAGCGCGTGGTCCCGCTCATGCTA 248

QY 81 AspLeuTyArgArgHisSerGlyGlnProGlySerProAlaProAspHisArgLeuGlu 100
Db 249 GACCTGTATCGCAGGCACTCGGGTCAGCGGGCTCACCGGCCCCAGACCACCGGTTGGAG 308

QY 101 ArgAlaLaserArgAlaAsnThrValArgSerPheHisHisGluGluSerLeuGluGlu 120
Db 309 AGGCGAGCCAGCCGAGCCCAACTGTGCGCAGCTTCCACCATGAAGAATCTTTGGAAGAA 368

QY 121 LeuProGluThrSerGlyLysThrThrArgArgPhePheAsnLeuSerSerIlePro 140
Db 369 CTACCAAGAACGAGTGGGAAACCAACCGGAGATCTCTTTAATTTAAGTTCTATCCCC 428

QY 141 ThrGluGluPheIleThrSerAlaGluLeuGlnValPheArgGluGlnMetGlnAspAla 160
Db 429 ACGGAGGAGTTATCACTCAGCAGAGCTTCAGGTTTCCGAGAACAGATGCAAGTGTCT 488

QY 161 LeuGlyAsnAsnSerSerPheHisHisArgIleAsnIleTyGluIleLysProAla 180
Db 489 TTAGGAACAATAGCAGTTCCATCAGCAGATTAATATTTATGAATCATATAAACCTGCA 548

QY 181 ThrAlaAsnSerLysPheProValThrArgLeuLeuAspThrArgLeuValAsnGlnAsn 200
Db 549 ACAGCCAACTCGAATTTCCCGTGCACCACTTTTGGACACCAAGTTGGTGAATCAGAA 608

QY 201 AlaSerArgTrpGluSerPheAspValThrProAlaValMetArgTrpThrAlaGlnGly 220
```

```
Db 609 GCAAGCAGGTGGGAAAGTTTTTGATGTCAACCCCGCTGTGATCGGTGAGCTGCACAGGA 668
QY 221 HisAlaAsnHisGlyPheValValGluValAlaHisLeuGluGluLysGlnGlyValSer 240
Db 669 CAGCCCAACCATGGATTCTGGTGGAAAGTGGCCCACTTGGAGGAGAAACAAGGTGTCTCC 728
QY 241 LysArgHisValArgIleSerArgSerLeuHisGlnAspGluHisSerTrpSerGlnIle 260
Db 729 AAGAGACATGTTAGGATAAGCAGGTCTTTGACCAACAGATGAACACAGCTGTTACAGATA 788
QY 261 ArgProLeuLeuValThrPheGlyHisAspGlyLysGlyHisProLeuHisLysArgGlu 280
Db 789 AGGCCATTGCTAGTAACCTTTTGGCCATGATGTAAGAAAGGGCATCTCTCCACAAAGAGAA 848
QY 281 LysArgGlnAlaLysHisLysGlnArgLysArgLeuLysSerSerCysLysArgHisPro 300
Db 849 AAACGTCACAGCCAAACACAAACACGCGAAACGCTTAAAGTCCAGCTGTAAAGACACCCCT 908
QY 301 LeuTyValAspPheSerAspValGlyTrpAsnAspTrpIleValAlaProProGlyTyx 320
Db 909 TTGTACGTGGACTTCAGTGACGTGGGTGGAATGACTGGATTTGGCTCCCCGGGGTAT 968
QY 321 HisAlaPheTyxCysHisGlyGluCysProPheProLeuAlaAspHisLeuAsnSerThr 340
Db 969 CAGCCCTTTTACTGCCACGCGAGAAATGCCCTTTTCTCTGGCTGATCATCTGAACCTCCACT 1028
QY 341 AsnHisAlaIleValGlnThrLeuValAsnSerValAsnSerLysIleProLysAlaCys 360
Db 1029 AATCATGCCATTGTTTCAGACGTTGGTCAACTCTGTTAACTCTAAGATTCTTAAGGCATGC 1088
QY 361 CysValProThrGluLeuSerAlaIleSerMetLeuTyLeuAspGluAsnGluLysVal 380
Db 1089 TGTGTCCCGACAGACTCAGTGTATCTCGATGCTGTACCTTGACGAGATGAAGAAGTT 1148
QY 381 ValLeuLysAsnTyGlnAspMetValValGluGlyCysGlyCysArg 396
Db 1149 GTATTAAAGAACTATCAGGATATGTTGTGGAGGGTTGTGGGTGTCTGC 1196

RESULT 12
US-08-447-570-4
; Sequence 4, Application US/08447570
; Patent No. 5714589
; GENERAL INFORMATION:
; APPLICANT: OPPERMAN, HERMANN
; APPLICANT: OZKAYNAK, ENGIN
; APPLICANT: KUBERASAMPATH, THANGAVEL
; APPLICANT: RUEGER, DAVID C.
; APPLICANT: PANG, ROY H.L.
; TITLE OF INVENTION: OSTEOGENIC DEVICES
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: TESTA, HURWITZ & THIBEAULT
; STREET: 53 STATE STREET
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: U.S.A.
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/447,570
; FILING DATE: 21-FEB-1992
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 810,560
; FILING DATE: 20-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 827,052
; FILING DATE: 28-JAN-1992
; PRIOR APPLICATION DATA:
```

```

; APPLICATION NUMBER: US 660,162
; FILING DATE: 22-FEB-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 621,988
; FILING DATE: 04-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 621,849
; FILING DATE: 04-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 616,374
; FILING DATE: 21-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 600,024
; FILING DATE: 18-OCT-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 599,543
; FILING DATE: 18-OCT-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 579,865
; FILING DATE: 07-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 569,920
; FILING DATE: 20-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 483,913
; FILING DATE: 22-FEB-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 422,613
; FILING DATE: 17-OCT-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 315,342
; FILING DATE: 23-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 232,630
; FILING DATE: 15-AUG-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 179,460
; FILING DATE: 08-APR-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: FITCHER, EDMUND R.
; REGISTRATION NUMBER: 27,829
; REFERENCE/DOCKET NUMBER: CRP-001CP6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/248-7000
; TELEFAX: 617/248-7100
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1260 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: HOMO SAPIENS
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 9..1196
; OTHER INFORMATION: /function= "OSTEOGENIC PROTEIN"
; OTHER INFORMATION: /product= "CBMP2A"
; OTHER INFORMATION: /note= "CBMP2A (CDNA) "
US-08-447-570-4

Alignment Scores:
Pred. No.: 1,01e-199 Length: 1260
Score: 2092.00 Matches: 395
Percent Similarity: 99.75% Conservative: 0
Best Local Similarity: 99.75% Mismatches: 1
Query Match: 99.71% Indels: 0
DB: 2 Gaps: 0

US-10-801-648-2 (1-396) x US-08-447-570-4 (1-1260)

```

1 MetValAlaGlyThrArgCysLeuLeuAlaLeuLeuProGlnValLeuLeuGlyGly 20
9 ATGGTGGCCGGGACCCGCTGCTTCTAGCGTGTGCTTCCCGAGGTCTCTCTGGCGGCG 68
21 AlaAlaGlyLeuValProGluLeuGlyArgArgLysPheAlaAlaAlaSerSerGlyArg 40
69 GCGGCTGGCTCGTTCGGGAGCTGGCGGCGAGAGTTTCGGCGGCGGCTCGTCGGCGCGC 128
41 ProSerSerGlnProSerAspGluValLeuSerGluPheGluLeuValProProTyrMetLeu 60
129 CCCTCATCCCGAGCCCTCTGACGAGGTCCTGACGAGTTCGAGTTCGGGCTGCTCAGCATG 188
61 PheGlyLeuLysGlnArgProThrProSerArgAspAlaValValProProTyrMetLeu 80
189 TTCGGCTGAAACAGAGACCCACCCCGAGGAGCGCGTGGTGGCCCTTACATGCTA 248
81 AspLeuTyrArgArgHisSerGlyGlnProGlySerProAlaProAspHisArgLeuGlu 100
249 GACCTGTATCGCAGGCACTCGGGTCAGCGGGCTCACCCCGCCCGAGACCACCGGTGGAG 308
101 ArgAlaAlaSerArgAlaAsnThrValArgSerPheHisHisGluGluSerLeuGlu 120
309 AGGCAGCGCCAGCCAGCACACTGTGGCGAGCTTCCACATGAGAAATCTTTGGAGAA 368
121 LeuProGluThrSerGlyLysThrThrArgArgPhePheAsnLeuSerSerLeuPro 140
369 CTACCAGAACGAGTGGGAAACAACCCGGAGATCTCTTTTAATTTAAGTTCTATCCC 428
141 ThrGluGluPheIleThrSerAlaGluLeuValPheArgGluGlnMetGlnAspAla 160
429 ACGGAGGAGTTTATCACCTCAGCAGAGCTTCAGGTTTTCCGAGAAACAGATGCAATGCT 488
161 LeuGlyAsnAsnSerSerPheHisHisArgIleAsnIleTyrGluIleIleValProAla 180
489 TTAGGAAACAATAGCAGTTTCCATCACCAGAAATTAATTTATGAATCATTAACCTGCA 548
181 ThrAlaAsnSerLysPheProValThrArgLeuLeuAspThrArgLeuValAsnGlnAsn 200
549 ACAGCCAACTCGAAATTTCCCGTGACCACTCTTTGGACACACAGTTGGTGAATCAGAT 608
201 AlaSerArgTyrGluSerPheAspValThrProAlaValMetArgTyrThrAlaGlnGly 220
609 GCAAGCAGTGGGAAAGTTTTGATGTACACCCCGCTGTGATGCGGTGACATGCACAGGGA 668
221 HisAlaAsnHisGlyPheValValAlaHisLeuGluGluLysGluGlyValSer 240
669 CACGCCAACCATGGATTCTGTGGTGAAGTGGCCCACTTGGAGGAGAAACAAGGTGTCTCC 728
241 LysArgHisValArgIleSerArgSerLeuHisGlnAspGluHisSerTyrSerGlnIle 260
729 AAGAGACATGTTAGGATNAGCAGGTCTTTGCCACCAAGATGAACACAGCTGGTCACAGATA 788
261 ArgProLeuLeuValThrPheGlyHisAspGlyLysGlyHisProLeuHisLysArgGlu 280
789 AGGCCATTGCTAGTAACCTTTTGGCCATGATGMAAAGGGCATCTCTCTCCACAAAAGAGAA 848
281 LysArgGlnAlaLysHisLysGlnArgLysArgLeuLysSerSerCysLysArgHisPro 300
849 AAACGCTCAAGCCAAACACAAACAGCGGAAACCGCTTAAGTCAGCTGTAAGAGACACCCCT 908
301 LeuTyrValAspPheSerAspValGlyTyrAsnAspTyrIleValAlaProProGlyTyr 320
909 TTGTACGTGGACTTCAGTGACGTGGGTGGAAATGACTGGATTGTGGCTCCCGCGGGTAT 968
321 HisAlaPheTyrCysHisGlyGluCysProPheProLeuAlaAspHisLeuAsnSerThr 340
969 CACGCTTTTACTGCCACGAGAAATGCCCTTTTCTCTGGCTGATCATCTGAATCCACT 1028
341 AsnHisAlaIleValGlnThrLeuValAsnSerValAsnSerLysIleProLysAlaCys 360
1029 AATCATGCCATTGTTTCAGACGTTGGTCAACTCTGTAACTCTTAAGATTCTTAAGGCATGC 1088

Qy 361 CysValProThrGluLeuSerAlaIleSerMetLeuTyrLeuAspGluAsnGluLysVal 380
Db 1089 TGTGTCGCGACAGACTCAGTCTATCTCGATGCTGTACCTTACGAGATGAAGGTT 1148
Qy 381 ValLeuLysAsnTyrGlnAspMetValValGluGlyCysGlyCysArg 396
Db 1149 GTATTAAAGAACTATCAGGATATGTTGTGAGGGTTGTGGGTCTGC 1196

RESULT 13

US-08-449-700-4
Sequence 4, Application US/08449700
Patent No. 5863758
GENERAL INFORMATION:
APPLICANT: OPPERMAN, HERMANN
APPLICANT: OZKAYNAK, ENGIN
APPLICANT: KUBERASAMPATH, THANGAVEL
APPLICANT: RUEGER, DAVID C.
APPLICANT: PANG, ROY H.L.
TITLE OF INVENTION: OSTEOGENIC DEVICES
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS: 33
ADDRESSEE: TESTA, HURWITZ & THIBEAULT
STREET: 53 STATE STREET
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: U.S.A.
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/08/449,700
APPLICATION NUMBER: US/08/449,700
FILING DATE: 21-FEB-1992
CLASSIFICATION: 530
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 810,560
FILING DATE: 20-DEC-1991
APPLICATION NUMBER: US 827,052
FILING DATE: 28-JAN-1992
APPLICATION NUMBER: US 660,162
FILING DATE: 22-FEB-1991
APPLICATION NUMBER: US 621,988
FILING DATE: 04-DEC-1990
APPLICATION NUMBER: US 621,849
FILING DATE: 04-DEC-1990
APPLICATION NUMBER: US 616,374
FILING DATE: 21-NOV-1990
APPLICATION NUMBER: US 599,543
FILING DATE: 18-OCT-1990
APPLICATION NUMBER: US 579,865
FILING DATE: 07-SEP-1990
APPLICATION NUMBER: US 569,920
FILING DATE: 20-AUG-1990
APPLICATION NUMBER: US 483,913
FILING DATE: 22-FEB-1990
APPLICATION NUMBER: US 422,613
FILING DATE: 17-OCT-1989
PRIORITY APPLICATION DATA:

APPLICATION NUMBER: US 315,342
FILING DATE: 23-FEB-1989
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 232,630
FILING DATE: 15-AUG-1988
APPLICATION DATA:
APPLICATION NUMBER: US 179,460
FILING DATE: 08-APR-1988
ATTORNEY/AGENT INFORMATION:
NAME: PITCHER, EDMUND R.
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: CRP-001CP6
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/248-7000
TELEFAX: 617/248-7100
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1260 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: HOMO SAPIENS
FEATURE:
NAME/KEY: CDS
LOCATION: 9..1196 /function= "OSTEOGENIC PROTEIN"
OTHER INFORMATION: /product= "CBMP2A"
OTHER INFORMATION: /note= "CBMP2A (CDNA)"
US-08-449-700-4

Alignment Scores:

| | | | |
|------------------------|-----------|---------------|------|
| Pred. No.: | 1,01e-199 | Length: | 1260 |
| Score: | 2092.00 | Matches: | 395 |
| Percent Similarity: | 99.75% | Conservative: | 0 |
| Best Local Similarity: | 99.75% | Mismatches: | 1 |
| Query Match: | 99.71% | Indels: | 0 |
| DB: | 2 | Gaps: | 0 |

US-10-801-648-2 (1-396) x US-08-449-700-4 (1-1260)

| | | | |
|----|-----|--|-----|
| Qy | 1 | MetValAlaGlyThrArgCysLeuLeuAlaLeuLeuProGlnValLeuLeuGlyGly | 20 |
| Db | 9 | ATGCTGGCGGAGCCCGCTGCTTCTAGCGTTGCTTCCCGAGGTCTCTCTGGGGCGG | 68 |
| Qy | 21 | AlaAlaGlyLeuValProGluLeuGlyArgArgPheAlaAlaSerSerGlyArg | 40 |
| Db | 69 | GCGGCTGGCTCGTTCCGAGCTGGCCCGCAGGAAGTTCGCGCGCGGTCTGTGGGGCGG | 128 |
| Qy | 41 | ProSerSerGlnProSerAspGluValLeuSerGluPheGluLeuArgLeuSerMet | 60 |
| Db | 129 | CCCTCATCCCGAGCCCTCTGACGAGGTCCTGACGAGTTGCGGTGCTCAGCATG | 188 |
| Qy | 61 | PheGlyLeuLysGlnArgProThrProSerArgAspAlaValValProProTyrMetLeu | 80 |
| Db | 189 | TTGCGCTGAACAGAGACCCACCCCGCAGGAGCCCGTGGTGGCCCGCCCTACATCTA | 248 |
| Qy | 81 | AspLeuTyrArgArgHisSerGlyGlnProGlySerProAlaProAspHisArgLeuGlu | 100 |
| Db | 249 | GACCTGTATCGAGGCACTCGGGTCAGCCGGGTTCACCCCGCCCGCAGACCCCGGTTGAG | 308 |
| Qy | 101 | ArgAlaAlaSerArgAlaAsnThrValArgSerPheHisGluGluSerLeuGluGlu | 120 |
| Db | 309 | AGGCGAGCAGCCGAGCCAACTGTGCGCAGCTTCCACCATGAAGAATCTTTGGAAGAA | 368 |
| Qy | 121 | LeuProGluThrSerGlyLysThrThrArgArgPhePheAsnLeuSerSerIlePro | 140 |
| Db | 369 | CTACCGAAACGAGTGGGAAAAACAACCCGAGATTCTCTTTAATTTTAAAGTTCTATCCCC | 428 |
| Qy | 141 | ThrGluGluPheIleThrSerAlaGluLeuGlnValPheArgGluGlnMetGlnAspAla | 160 |

```
Db 429 ACGGAGGAGTTTATCACTCAGCAGAGCTTCAGGTTTCGAGAACAGATGCAAGATGCT 488
Qy 161 LeuGlyAsnAsnSerSerPheHisArgIleAsnIleTyrGluIleIleLysProAla 180
Db 489 TTAGGAAACATACAGAGTTTCATCAGCAATTAATATTTATGAATCATAAACCTGCA 548
Qy 181 ThrAlaAsnSerLysPheProValThrArgLeuLeuAspThrArgLeuValAsnGlnAsn 200
Db 549 ACAGCCAACTCGAATTCCTCCGTCACCAAGTCTTTTGGACACCAAGTTGGTGAATCAGAT 608
Qy 201 AlaSerArgTrpGluSerPheAspValThrProAlaValMetArgTrpThrAlaGlnGly 220
Db 609 GCAAGCAGGTGGGAAAGTTTGTATGTACCCCGCTGTGATGCGGTGCACTGCACAGGA 668
Qy 221 HisAlaAsnHisGlyPheValValGluValAlaHisLeuGluGluLysGlnGlyValSer 240
Db 669 CACGCCAACCACTGATGCTGTGTGGAAAGTGCCCACTTGGAGGAGAAACAAGGTGTCTCC 728
Qy 241 LysArgHisValArgIleSerArgSerLeuHisGlnAspGluHisSerTrpSerGlnIle 260
Db 729 AAGAGACATGTTAGATAGCAGGTCTTTTGCCACCAAGATGAACACAGCTGTGTACAGATA 788
Qy 261 ArgProLeuLeuValThrPheGlyHisAspGlyLysGlyHisProLeuHisLysArgGlu 280
Db 789 AGGCCATTGCTAGTAATCTTTTGGCCATGATGGAAGGCGCATCTCTCCACAAAGAGAA 848
Qy 281 LysArgGlnAlaLysHisLysGlnArgLysArgLeuLysSerSerCysLysArgHisPro 300
Db 849 AAAGCTCAAGCCAAACACAAACAGCGGAAACGCTTAAAGTCCAGCTGTAAGAGACACCTT 908
Qy 301 LeuTyrValAspPheSerAspValGlyTrpAsnAspTrpIleValAlaProProGlyTyr 320
Db 909 TTGTACGTGGAGCTTCAAGTACGTGGGTGGAGTGAATGACTGTGTGTGCTCCCGGGGTAT 968
Qy 321 HisAlaPheTyrCysHisGlyGluCysProPheProLeuAlaAspHisLeuAsnSerThr 340
Db 969 CACGCCCTTTACTGCCAGGAGATGCTCTTTCTCTGCTGATCATCTGAACTCCACT 1028
Qy 341 AsnHisAlaIleValGlnThrLeuValAsnSerValAsnSerLysIleProLysAlaCys 360
Db 1029 AATCATGCCATTGTTACAGACGTTGTCACACTCTGTAACTCTTAAGATTCTTAAGGCATGC 1088
Qy 361 CysValProThrGluLeuSerAlaIleSerMetLeuTyrLeuAspGluAsnGluVal 380
Db 1089 TGTGTCCGACAGAACTCAGTGCTATCTCGATGCTGTACCTTGACGAGATGAAGAAGTT 1148
Qy 381 ValLeuLysAsnTyrGlnAspMetValValGluGlyCysGlyCysArg 396
Db 1149 GTATTAAAGAACTATCAGGATATGTTGTGGAGGGTTGTGGGTGTGCG 1196
```

RESULT 14

```
US-08-449-699A-4.
; Sequence 4, Application US/08449699A
; Patent No. 5958441
; GENERAL INFORMATION:
; APPLICANT: OPPERMAN, HERMANN
; APPLICANT: OZKANAK, ENGIN
; APPLICANT: KUBERASAMPATH, THANGAVEL
; APPLICANT: RUEGER, DAVID C.
; APPLICANT: PANG, ROY H. L.
; TITLE OF INVENTION: ANTIBODIES TO OSTEOGENIC PROTEINS
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TESTA, HURWITZ & THIBEAULT
; STREET: 125 HIGH STREET
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: U.S.A.
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/449,699A
FILING DATE: 24-MAY-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/147,023
FILING DATE: 01-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: PITCHER, EDMUND R.
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: STK-001CP6CN
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/248-7000
TELEFAX: 617/248-7100
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1260 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: HOMO SAPIENS
FEATURE:
NAME/KEY: CDS
LOCATION: 9..1196
OTHER INFORMATION: /function= "OSTEOGENIC PROTEIN"
OTHER INFORMATION: /product= "CBMP2A"
OTHER INFORMATION: /note= "CBMP2A (cDNA)"
US-08-449-699A-4

Alignment Scores:
Pred. No.: 1,01e-199 Length: 1260
Score: 2092.00 Matches: 395
Percent Similarity: 99.75% Conservative: 0
Best Local Similarity: 99.75% Mismatches: 1
Query Match: 99.71% Indels: 0
Gaps: 2

US-10-801-648-2 (1-396) x US-08-449-699A-4 (1-1260)

Qy 1 MetValAlaGlyThrArgCysLeuLeuAlaLeuLeuLeuProGlnValLeuLeuGlyGly 20
Db 9 ATGTTGCGCGGAGCCCGCTGTCTTCTAGCGTTGCTTCCCGAGGTCTCTCTGGCGGC 68
Qy 21 AlaAlaGlyLeuValProGluLeuGlyArgArgLysPheAlaAlaLysSerSerGlyArg 40
Db 69 GCGGCTGGCTTCGTTCCGGAGCTGGCGCGCAGGAAGTTCCGCGCGGCTCTCTGGCGGC 128
Qy 41 ProSerSerGlnProSerAspGluValLeuSerGluPheGluLeuArgLeuSerMet 60
Db 129 CCTCATCCCGAGCCCTCTGACGAGTCTCTGAGCGAGTTGAGTTGCGGCTCTCTCAGCATG 188
Qy 61 PheGlyLeuLysGlnArgProThrProSerArgAspAlaValProProTyrMetLeu 80
Db 189 TTCGGCTGAAACAGACAGACCCACCCAGCAGGAGCGCGTGTGTCGCCCTTACATGCTA 248
Qy 81 AspLeuTyrArgArgHisSerGlyGlnProGlySerProAlaProAspHisArgLeuGlu 100
Db 249 GACCTGTATCGAGCACTCTGGGTGACCGGGCTCACCCGCCCCAGACACCGGTTGAG 308
Qy 101 ArgAlaAlaSerArgAlaAsnThrValArgSerPheHisGluGluSerLeuGluGlu 120
Db 309 AGGCAGCCAGCCAGCCACACACTGTGGCAGCTTCCACCATGAAGATCTTTTGGAGAA 368
Qy 121 LeuProGluThrSerGlyLysThrThrArgArgPhePheAsnLeuSerSerIlePro 140
Db 369 CTACAGAAACGAGTGGGAAAAACAACCGGAGATTCTTCTTAATTTAAGTTCTATCCCC 428
```

Qy 141 ThrGluGluPheIleThrSerAlaGluLeuGlnValPheArgGluGlnMetGlnAspAla 160
Db 429 ACGGAGAGTTATACCTTCAGCAGAGCTTCAGGTTTCCGAGAACAGATGCAAGATGCT 488
Qy 161 LeuGlyAsnAsnSerSerPheHisGlyArgIleAsnIleTyrGluIleLeuLysProAla 180
Db 489 TTAGGAACATAGCAGTTTCATCCACCGAATTAATTTATGAATCATATAAACCTGCA 548
Qy 181 ThrAlaAsnSerLysPheProValThrArgLeuLeuAspThrArgLeuValAsnGlnAsn 200
Db 549 ACAGCCAACCTGAAATCCCGTCGACCACTCTTTGGACACACAGGTTGGTGAATCAGAA 608
Qy 201 AlaSerArgTTPGluSerPheAspValThrProAlaValMetArgTTPThrAlaGlnGly 220
Db 609 GCAAGCAGGTGGGAAAGTTTGTGATCACCCCGCTGTGATGCGGTGCATGCAACGGGA 668
Qy 221 HisAlaAsnHisGlyPheValValGluValAlaHisLeuGluGluLysGlnGlyValSer 240
Db 669 CACGCCAACCATGGATTGCTGTGGAAGTGGCCCACTTGGAGGAGAACAGGTGTCTCC 728
Qy 241 LysArgHisValArgIleSerArgSerLeuHisGlnAspGluHisSerTrpSerGlnIle 260
Db 729 AAGACATGTTAGGATAAGCAGGTCTTTGCACCAAGATGAACACAGCTGTGCACAGTA 788
Qy 261 ArgProLeuLeuValThrPheGlyHisAspGlyLysGlyHisProLeuHisLysArgGlu 280
Db 789 AGGCCATTGCTAGTAACCTTTTGGCCATGATGGAAGAGGCACTCTCTCCAAAGAGAA 848
Qy 281 LysArgGlnAlaLysHisLysGlnArgLysArgLeuLysSerSerCysLysArgHisPro 300
Db 849 AAACGTCAAGCAACCAACAAACAGCGGAAAGCCCTTAAGTCACCTGTAGAGACACCT 908
Qy 301 LeuTyrValAspPheSerAspValGlyTrpAsnAspTrpIleValAlaProProGlyTyr 320
Db 909 TTGTACGTGGACTTCAGTACGCGGTGGGAATGACTGGATTGTGGCTCCCGGGGTAT 968
Qy 321 HisAlaPheTyrCysHisGlyGluCysProPheProLeuAlaAspHisLeuAsnSerThr 340
Db 969 CACGCCCTTTACTGCCAGGAGATGCCCTTTCTCTGGCTGATCATCTGAATCCACT 1028
Qy 341 AsnHisAlaIleValGlnThrLeuValAsnSerValAsnSerLysIleProLysAlaCys 360
Db 1029 AATCATGCCATTGTTAGACGTTGGTCACTCTGTAACTTAAGATTCTTAAGCATGC 1088
Qy 361 CysValProThrGluLeuSerAlaIleSerMetLeuTyrLeuAspGluAsnGluLysVal 380
Db 1089 TGTGTCCCGACAGAACTCAGTCTATCTCGATGCTGTACCTTGACGAGAAATGAAGGTT 1148
Qy 381 ValLeuLysAsnTyrGlnAspMetValValGluGlyCysGlyCysArg 396
Db 1149 GTATTAAAGAACTATCAGGATATGTTGTGGAGGGTGTGGGTGTGCG 1196

RESULT 15

US-09-148-925C-4

; Sequence 4, Application US/09148925C

; Patent No. 6551995

; GENERAL INFORMATION:

; APPLICANT: OPPERMANN, HERMANN

; OZKAYNAK, ENGIN

; KUBERASAMPATH, THANGAVEL

; RUEGER, DAVID C.

; PANG, ROY H.L.

; TITLE OF INVENTION: OSTEOGENIC DEVICES

; NUMBER OF SEQUENCES: 33

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: TESTA, HURWITZ & THIBEAULT

; STREET: 125 HIGH STREET

; CITY: BOSTON

; STATE: MASSACHUSETTS

; COUNTRY: U.S.A.

; ZIP: 02110

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/148,925C
FILING DATE: 04-Sep-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/148,925
FILING DATE: 8-SEP-1998
APPLICATION NUMBER: US 08/449,699
FILING DATE: 24-MAY-1995
APPLICATION NUMBER: US 08/147,023
FILING DATE: 1-NOV-1993
APPLICATION NUMBER: US 07/841,646
FILING DATE: 21-FEB-1992
APPLICATION NUMBER: US 07/827,052
FILING DATE: 28-JAN-1992
APPLICATION NUMBER: US 07/579,865
FILING DATE: 7-SEP-1990
APPLICATION NUMBER: US 07/621,849
FILING DATE: 4-DEC-1990
APPLICATION NUMBER: US 07/621,988
FILING DATE: 4-DEC-1990
APPLICATION NUMBER: US 07/810,560
FILING DATE: 20-DEC-1991
APPLICATION NUMBER: US 07/569,920
FILING DATE: 20-AUG-1990
APPLICATION NUMBER: US 07/600,024
FILING DATE: 18-OCT-1990
APPLICATION NUMBER: US 07/599,543
FILING DATE: 18-OCT-1990
APPLICATION NUMBER: US 07/616,374
FILING DATE: 21-NOV-1990
APPLICATION NUMBER: US 07/483,913
FILING DATE: 22-FEB-1990
APPLICATION NUMBER: US 07/179,406
FILING DATE: 08-APR-1988
APPLICATION NUMBER: US 07/232,630
FILING DATE: 15-AUG-1988
APPLICATION NUMBER: US 07/315,342
FILING DATE: 23-FEB-1989
APPLICATION NUMBER: US 07/660,162
FILING DATE: 22-FEB-1991
APPLICATION NUMBER: US 07/422,699
FILING DATE: 17-OCT-1989
APPLICATION NUMBER: US 07/422,613
FILING DATE: 17-OCT-1989
APPLICATION NUMBER: US 07/422,623
FILING DATE: 17-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: DIANA M. STEEL
REGISTRATION NUMBER: 43,153
REFERENCE/DOCKET NUMBER: STK-001CP6C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/248-7000
TELEFAX: 617/248-7100
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1260 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
ORIGINAL SOURCE:
ORGANISM: HOMO SAPIENS
FEATURE:
NAME/KEY: CDS
LOCATION: 9..1196
OTHER INFORMATION: /function= "OSTEOGENIC PROTEIN"
/product= "CBMP2a"
/note= "CBMP2(a) (CDNA)"
SEQUENCE DESCRIPTION: SEQ ID NO: 4:

US-09-148-925C-4

Alignment Scores:

Pred. No.: 1,01e-199 Length: 1260
Score: 2092.00 Matches: 395
Percent Similarity: 99.75% Conservative: 0
Best Local Similarity: 99.75% Mismatches: 1
Query Match: 99.71% Indels: 0
DB: 3 Gaps: 0

US-10-801-648-2 (1-396) x US-09-148-925C-4 (1-1260)

| | | | |
|----|-----|--|-----|
| Qy | 1 | MetValAlaGlyThrArgCysLeuLeuAlaLeuLeuLeuProGlnValLeuLeuGlyGly | 20 |
| Db | 9 | ATGGTGGCGGACCGCTGCTCTAGCGTTGCTTCCCGCAGGTCTCTCTGGGCGGC | 68 |
| Qy | 21 | AlaAlaGlyLeuValProGluLeuGlyArgArgLysPheAlaAlaAAserSerGlyArg | 40 |
| Db | 69 | GGCGCTGGCTCTGCTCCGAGCTGGGCGCGCAGAAAGTTGGCGCGCGCTGCTGGGCGGC | 128 |
| Qy | 41 | ProSerSerGlnProSerAspGluValLeuSerGluPheGluLeuArgLeuLeuSerMet | 60 |
| Db | 129 | CCCTCATCCAGCCCTCTGACGAGTCTGAGCGAGTTCGAGTTCGGGCTGCTCAGCATG | 188 |
| Qy | 61 | PheGlyLeuLysGlnArgProThrProSerArgAspAlaValValProProThrMetLeu | 80 |
| Db | 189 | TTGGCCCTGAACAGAGACCCACCCAGCAGGAGCGCGTGGTGGCCCCCTACATGCTA | 248 |
| Qy | 81 | AspLeuTyArgArgHisSerGlyGlnProGlySerProAlaProAspHisArgLeuGlu | 100 |
| Db | 249 | GACCTGTATCGCAGGCACTCGGGTCAGCGGGCTCACCGGCCAGACCCCGGTTGGAG | 308 |
| Qy | 101 | ArgAlaAlaSerArgAlaasnThrValArgSerPheHisHisGluSerLeuGluGlu | 120 |
| Db | 309 | AGGGCAGCGCAGCGAGCCAACTGTGGCGAGCTTCCACCATGAAGAATCTTTGGAGAA | 368 |
| Qy | 121 | LeuProGluThrSerGlyLysThrThrArgArgPhePheAsnLeuSerSerIlePro | 140 |
| Db | 369 | CTACCAAGAAACGAGTGGGNAACACCCGGAGATCTCTTTAAATTAAGTTCTATCCCC | 428 |
| Qy | 141 | ThrGluGluPheIleThrSerAlaGluLeuGlnValPheArgGluGlnMetGlnAspAla | 160 |
| Db | 429 | ACGGAGGAGTTTATCACCTCAGCAGAGCTTCAGGTTTCCGAGAGACAGATGCAAGTGT | 488 |
| Qy | 161 | LeuGlyAsnAsnSerSerPheHisArgGlnLeuLeuLeuLeuLeuLeuLeuLeuLeu | 180 |
| Db | 489 | TTAGGAAACAATAGCAGTTTCCATCAGCAATTAATATATGAATCATRAAACCTGCA | 548 |
| Qy | 181 | ThrAlaAsnSerLysPheProValThrArgLeuLeuAspThrArgLeuValAsnGlnAsn | 200 |
| Db | 549 | ACAGCAACTCGAAATTTCCCGTGACAGTCTTTTGGACACAGGTTGGTGAATCAGAA | 608 |
| Qy | 201 | AlaSerArgTrpGluSerPheAspValThrProAlaValMetArgTrpThrAlaGlnGly | 220 |
| Db | 609 | GCAAGCAGGTGGAAAGTTTTGATGTGTCACCCCGCTGTGATGCGGTGGACTGCACAGGA | 668 |
| Qy | 221 | HisAlaAsnHisGlyPheValValGluValAlaHisLeuGluGluLysGlnGlyValSer | 240 |
| Db | 669 | CACGCCAACCATGATTCGTGTGGAAGTGGCCCACTTGGAGGAGAAACAAGGTCTCTCC | 728 |
| Qy | 241 | LysArgHisValArgIleSerArgSerLeuHisGlnAspGluHisSerTrpSerGlnIle | 260 |
| Db | 729 | AAGAGACATGTTAGGATTAAGCAGGTTTGTGCAACAGATGAACACAGCTGGTCAAGATA | 788 |
| Qy | 261 | ArgProLeuLeuValThrPheGlyHisAspGlyLysGlyHisProLeuHisLysArgGlu | 280 |
| Db | 789 | AGGCCATTGCTAGTAACCTTTGGCCATGATGGAAGAAGGCATCTCTCCACAAAGAGAA | 848 |
| Qy | 281 | LysArgGlnAlaLysHisGlnArgLysArgLeuLysSerSerCysLysArgHisPro | 300 |
| Db | 849 | AAACGTCAGCCAAACACAAACAGCGGAAACGCTTAAGTCCAGCTGTAAGAGACACCCCT | 908 |
| Qy | 301 | LeuTyValAspPheSerAspValGlyTrpAsnAspTrpIleValAlaProGlyTy | 320 |

Search completed: January 11, 2006, 02:12:36
Job time : 203 secs

| | | | |
|----|------|--|------|
| Db | 909 | TTGTACGTGGACTTCAGTGACCGTGGGTTGGAATGACTGCAATTTGTGGCTCCCCCGGGTAT | 968 |
| Qy | 321 | HisAlaPheTyArgCysHisGlyGluCysProPheProLeuAlaAspHisLeuAsnSerThr | 340 |
| Db | 969 | CACGCTTTTACTGCCACGGAGAAATGCCCTTTTCTCTGGCTGATCATCTGAACCTCCACT | 1028 |
| Qy | 341 | AsnHisAlaIleValGlnThrLeuValAsnSerValAsnSerLysIleProLysAlaCys | 360 |
| Db | 1029 | AATCATGCAATGTTTCAGACGTTGGTCAACTCTGTAACTCTAAGATTCTTAAGGCATGC | 1088 |
| Qy | 361 | CysValProThrGluLeuSerAlaIleSerMetLeuTyLeuAspGluAsnGluLysVal | 380 |
| Db | 1089 | TGTGTCCCGACAGAACTCAGTGCTATCTCGATGCTGTACTTTCACGAGAAATGAAAAGTT | 1148 |
| Qy | 381 | ValLeuLysAsnTyArgGlnAspMetValValGluGlyCysGlyCysArg | 396 |
| Db | 1149 | GTATTTAAAGAACTATCAGGATATGGTTGTGGAGGGTTGTGGGTGTGCG | 1196 |

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: January 10, 2006, 23:47:24 ; Search time 696 Seconds
(without alignments)

4704.991 Million cell updates/sec

Title: US-10-801-648-2

Perfect score: 2098

Sequence: 1 MVAGTRCILLALLPVLGG.....NEKVLKNYQDMVVGCGCR 396

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame_p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool/US10801648/runat_09012006_143120_14834/app_query.fasta_1.583
-DB=Published Applications NA Main -QFMT=fastap -SUFFIX=rnpbm -MINMATCH=0.1
-LOOPEXT=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blowsum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US10801648 -CGN 1 1 797 @runat_09012006_143120_14834
-NCPU=6 -ICPU=3 -NO MAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Published Applications NA.Main:*
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|--------------------------------------|
| 1 | 2098 | 100.0 | 1547 | 5 | US-10-044-716-1 Sequence 1, Appli |
| 2 | 2098 | 100.0 | 1547 | 6 | US-10-286-152A-1 Sequence 1, Appli |
| 3 | 2098 | 100.0 | 1547 | 6 | US-10-139-814-1 Sequence 1, Appli |
| 4 | 2098 | 100.0 | 1547 | 6 | US-10-366-345-10 Sequence 10, Appl |
| 5 | 2098 | 100.0 | 1547 | 6 | US-10-295-027-159 Sequence 159, App |
| 6 | 2098 | 100.0 | 1547 | 7 | US-10-302-812-19 Sequence 19, Appl |
| 7 | 2098 | 100.0 | 1547 | 7 | US-10-283-975A-403 Sequence 403, App |
| 8 | 2098 | 100.0 | 1547 | 7 | US-10-692-824-1 Sequence 1, Appli |

| | | | | | |
|----|--------|-------|--------|---|---------------------------------------|
| 9 | 2098 | 100.0 | 1547 | 8 | US-10-801-648-1 Sequence 1, Appli |
| 10 | 2098 | 100.0 | 1547 | 9 | US-10-489-740-36 Sequence 36, Appl |
| 11 | 2098 | 100.0 | 1547 | 9 | US-10-492-380-1 Sequence 1, Appli |
| 12 | 2098 | 100.0 | 1547 | 9 | US-10-917-265-1 Sequence 1, Appli |
| 13 | 2098 | 100.0 | 1547 | 9 | US-10-886-947-1 Sequence 1, Appli |
| 14 | 2098 | 100.0 | 1607 | 3 | US-03-804-625-3 Sequence 3, Appli |
| 15 | 2098 | 100.0 | 1607 | 6 | US-10-397-214-3 Sequence 3, Appli |
| 16 | 2098 | 100.0 | 1607 | 9 | US-10-397-214-3 Sequence 3, Appli |
| 17 | 2095 | 99.9 | 1607 | 6 | US-10-375-150-1 Sequence 1, Appli |
| 18 | 2092 | 99.7 | 1260 | 2 | US-08-957-425-4 Sequence 4, Appli |
| 19 | 2092 | 99.7 | 1260 | 6 | US-10-321-799-4 Sequence 4, Appli |
| 20 | 2092 | 99.7 | 1260 | 7 | US-10-428-937A-4 Sequence 4, Appli |
| 21 | 2092 | 99.7 | 2154 | 6 | US-10-210-951-45 Sequence 45, Appl |
| 22 | 2092 | 99.7 | 2154 | 6 | US-10-211-884-45 Sequence 45, Appl |
| 23 | 2092 | 99.7 | 2154 | 6 | US-10-211-858-45 Sequence 45, Appl |
| 24 | 2043.5 | 97.4 | 1314 | 3 | US-09-935-144-39 Sequence 39, Appl |
| 25 | 1929 | 91.9 | 1541 | 7 | US-10-302-812-17 Sequence 17, Appl |
| 26 | 1796.5 | 85.6 | 1233 | 3 | US-03-945-182-27 Sequence 27, Appl |
| 27 | 1796.5 | 85.6 | 1233 | 3 | US-10-779-635-27 Sequence 27, Appl |
| 28 | 1511 | 72.0 | 14759 | 3 | US-09-952-360-1 Sequence 1, Appli |
| 29 | 1511 | 72.0 | 14759 | 6 | US-10-346-723-1 Sequence 1, Appli |
| 30 | 1511 | 72.0 | 173308 | 9 | US-10-756-149-629 Sequence 629, App |
| 31 | 1338.5 | 63.8 | 1432 | 9 | US-10-169-050-63 Sequence 63, Appl |
| 32 | 1338.5 | 63.8 | 8611 | 9 | US-10-169-050-17 Sequence 17, Appl |
| 33 | 1274 | 60.7 | 1758 | 7 | US-10-152-319A-2209 Sequence 2209, Ap |
| 34 | 1269 | 60.5 | 1569 | 6 | US-10-264-049-90 Sequence 3, Appli |
| 35 | 1269 | 60.5 | 1751 | 5 | US-10-189-302-3 Sequence 3, Appli |
| 36 | 1269 | 60.5 | 1751 | 7 | US-10-240-425-1309 Sequence 1309, Ap |
| 37 | 1269 | 60.5 | 1751 | 8 | US-10-278-698-201 Sequence 201, App |
| 38 | 1269 | 60.5 | 1751 | 8 | US-10-278-698-717 Sequence 717, App |
| 39 | 1269 | 60.5 | 1788 | 2 | US-08-957-425-6 Sequence 6, Appli |
| 40 | 1269 | 60.5 | 1788 | 6 | US-10-321-799-6 Sequence 6, Appli |
| 41 | 1269 | 60.5 | 1788 | 7 | US-10-428-997A-6 Sequence 6, Appli |
| 42 | 1269 | 60.5 | 1954 | 3 | US-09-804-625-5 Sequence 5, Appli |
| 43 | 1269 | 60.5 | 1954 | 6 | US-10-375-150-3 Sequence 3, Appli |
| 44 | 1269 | 60.5 | 1954 | 6 | US-10-397-214-5 Sequence 5, Appli |
| 45 | 1269 | 60.5 | 1954 | 9 | US-10-397-214-5 Sequence 5, Appli |

ALIGNMENTS

RESULT 1
US-10-044-716-1
; Sequence 1, Application US/1004716
; Publication No. US20020159986A1
; GENERAL INFORMATION:
; APPLICANT: LANGENFELD, John
; TITLE OF INVENTION: BONE MORPHOGENETIC PROTEIN-2 IN THE TREATMENT AND DIAGNOSIS OF CP
; FILE REFERENCE: 270/0700S
; CURRENT APPLICATION NUMBER: US/10/044,716
; CURRENT FILING DATE: 2002-01-11
; PRIOR APPLICATION NUMBER: US60/261,252
; PRIOR FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1547
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: source
; LOCATION: (1)..(1547)
; OTHER INFORMATION: Homo sapiens: Taxon:9606
; NAME/KEY: gene
; LOCATION: (1)..(1547)
; OTHER INFORMATION: BMP2
; NAME/KEY: CDS
; LOCATION: (324)..(1514)
; OTHER INFORMATION:
; NAME/KEY: misc_feature
; LOCATION: (429)..(1127)
; OTHER INFORMATION: Region: TGF-beta propeptide
; NAME/KEY: variation

```

; LOCATION: (432)..(432)
; OTHER INFORMATION: Allele = "T"; Allele = "G"
; NAME/KEY: variation
; LOCATION: (584)..(584)
; OTHER INFORMATION: Allele = "A"; Allele = "G"
; NAME/KEY: variation
; LOCATION: (893)..(893)
; OTHER INFORMATION: Allele = "T"; Allele = "A"
; NAME/KEY: misc feature
; LOCATION: (1209)..(1511)
; OTHER INFORMATION: TGF-beta; Region: Transforming growth factor beta like domain
; NAME/KEY: misc feature
; LOCATION: (1209)..(1511)
; OTHER INFORMATION: TGF-beta; Region: Transforming growth factor-beta (TGF-beta) family
US-10-044-716-1

```

```

Alignment Scores:
Pred. No.: 8.92e-227 Length: 1547
Score: 2098.00 Matches: 396
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 5 Gaps: 0

US-10-801-648-2 (1-396) x US-10-044-716-1 (1-1547)

Qy 1 MetValAlaGlyThrArgCysLeuLeuAlaLeuLeuProGlnValLeuLeuGlyGly 20
Db 324 ATGTTGGCGCGGACCCGCTGCTTCTAGCGTTGCTTCCCGCAGGTCCTCTCGGGCGG 383
Qy 21 AlaAlaGlyLeuValProGluLeuGlyArgArgLysPheAlaAlaAlaSerSerGlyArg 40
Db 384 GCGGCTGGCCCTCGTTCCGGAGCTCGCGCGCAGGAGTTCCGGCGGCGTCTCGGGCGG 443
Qy 41 ProSerSerGlnProSerAspGluValLeuSerGluPheGluLeuArgLeuLeuSerMet 60
Db 444 CCTTCATCCAGCCCTCTGACGAGTCTTGACGAGTTGCGGTTGCGGCTGCTCAGCATG 503
Qy 61 PheGlyLeuLysGlnArgProThrProSerArgAspAlaValValProProTyrMetLeu 80
Db 504 TTCGGCTGAAACAGAGACCCACCCCGCAGGAGCGCGTGGTGGCCCTACATGCTA 563
Qy 81 AspLeuTyrArgArgHisSerGlyGlnProGlySerProAlaProAspHisArgLeuGlu 100
Db 564 GACCTGTATCGCAGGCACTCAGGTCAGCGCGGCTCACCCCGCCAGACCAACCGGTTGGAG 623
Qy 101 ArgAlaAlaSerArgAlaAsnThrValArgSerPheHisHisGluGluSerLeuGluGlu 120
Db 624 AGGGCAGCCAGCCAGCCACACTGTGGCAGCTTCCACCATGAGGATCTTTGGAGAA 683
Qy 121 LeuProGluThrSerGlyLysThrThrArgArgPhePheAsnLeuSerSerIlePro 140
Db 684 CTACCAGAAACGAGTGGGAAACAAACCCGAGATCTTCTTTAATTTAAGTTCTATCCCC 743
Qy 141 ThrGluGluPheIleThrSerAlaGluLeuGlnValPheArgGluGlnMetGluAspAla 160
Db 744 ACGGAGGAGTTTATCACTCTCAGCAGAGCTTCCAGGTTTTCCGAGAACAGATGCAAGATGCT 803
Qy 161 LeuGlyAsnAsnSerSerPheHisHisArgLysLeuLeuIleLeuLysProAla 180
Db 804 TTAGAAACAATAGCAGTTTCATCACCAGATTAATATTAATGAAATCATTAACCTTGCA 863
Qy 181 ThrAlaAsnSerLysPheProValThrArgLeuLeuAspThrArgLeuValAsnGlnAsn 200
Db 864 ACAGCCAACTCGAAATTCCTCCGTCACAGACTTTTGGACACACAGGTTGGTGAATCAGAT 923
Qy 201 AlaSerArgTTPGluSerPheAspValThrProAlaValMetArgTTPThrAlaGlnGly 220
Db 924 GCAAGCAGTGGGAAAGTTTGTATGTCAACCCCGCTGTGATGCGGTGGACTGCAAGGGA 983
Qy 221 HisAlaAsnHisGlyPheValValGluValAlaHisLeuGluGluLysGlnGlyValSer 240
Db 984 CACGCCAACCATGGATTCGTGGTGGAGTGGCCCACTTTGGAGGAGAAACAAGGTGTCTCC 1043

```

```

Qy 241 LysArgHisValArgIleSerArgSerLeuHisGlnAspGluHisSerTTPSerGlnIle 260
Db 1044 AAGAGACATGTTAGGATAAGCAGCTCTTTGCAACAAGATGAACACAGCTGTCACAGATA 1103
Qy 261 ArgProLeuLeuValThrPheGlyHisAspGlyLysGlyHisProLeuHisLysArgGlu 280
Db 1104 AGGCCATTTGCTAGTAATCTTTTGCCCATGATGGAAAGGGCATCTCTCCACAAAGAGAA 1163
Qy 281 LysArgGlnAlaLysHisLysGlnArgLysArgLeuLysSerSerCysLysArgHisPro 300
Db 1164 AAAGCTCAAGCCAAACACACAGCGAAGCGCTTAAGTCCAGCTGTAAAGAGACACCT 1223
Qy 301 LeuTyrValAspPheSerAspValGlyTTPAsnAspTTPileValAlaProProGlyTyr 320
Db 1224 TTGTACGTGGACTTCAGTCAGCTGGGGTGGAAATGACTGGGATTTGGCTCCCGGGGTAT 1283
Qy 321 HisAlaPheTyrCysHisGlyGluCysProPheProLeuAlaAspHisLeuAsnSerThr 340
Db 1284 CAGCCCTTTTACTGCCACGGAGATGCCCTTTTCTCTGGCTGATCATCTGAACTCCACT 1343
Qy 341 AsnHisAlaIleValGlnThrLeuValAsnSerValAsnSerLysLysIleProLysAlaCys 360
Db 1344 AATCATGCCATTTGTCAGACGTTGGTCAACTCTGTTAACTCTAAGATTCTTAAGGCATGC 1403
Qy 361 CysValProThrGluLeuSerAlaIleSerMetLeuTyrLeuAspGluAsnGluLysVal 380
Db 1404 TGTGTCCCGCAGAACTCAGTGTCTATCTCGATGCTGTACCTTGACGAGAAATGAAAGGTT 1463
Qy 381 ValLeuLysAsnTyrGlnAspMetValValGluGlyCysGlyCysArg 396
Db 1464 GTATTAAAGAACTATCAGGACATGTTTGTGGAGGTTTGTGGGTGTCG 1511

RESULT 2
US-10-286-152A-1
; Sequence 1, Application US/10286152A
; Publication No. US20030134308A1
; GENERAL INFORMATION:
; APPLICANT: Alcon Research, Ltd.
; TITLE OF INVENTION: Bone Morphogenic Proteins (BMP), BMP Receptors and BMP Binding Pr
; TITLE OF INVENTION: and Their Use in the Diagnosis and Treatment of Glaucoma
; FILE REFERENCE: 2312 US
; CURRENT APPLICATION NUMBER: US/10/286,152A
; CURRENT FILING DATE: 2002-02-28
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1547
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-286-152A-1

Alignment Scores:
Pred. No.: 8.92e-227 Length: 1547
Score: 2098.00 Matches: 396
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-801-648-2 (1-396) x US-10-286-152A-1 (1-1547)

Qy 1 MetValAlaGlyThrArgCysLeuLeuAlaLeuLeuProGlnValLeuLeuGlyGly 20
Db 324 ATGTTGGCGCGGACCCGCTGCTTCTAGCGTTGCTTCCCGCAGGTCCTCTCGGGCGG 383
Qy 21 AlaAlaGlyLeuValProGluLeuGlyArgArgLysPheAlaAlaAlaSerSerGlyArg 40
Db 384 GCGGCTGGCCCTCGTTCCGGAGCTCGCGCGCAGGAGTTCCGGCGGCGTCTCGGGCGG 443
Qy 41 ProSerSerGlnProSerAspGluValLeuSerGluPheGluLeuArgLeuLeuSerMet 60

```

Db 444 CCTCATCCAGCCCTCTGACGAGTCTGAGCGAGTTTCGAGTTTCGGCTGCTCAGCATG 503
Qy 61 PheGlyLeuLysGlnArgProThrProSerArgAspAlaValProProTyrMetLeu 80
Db 504 TTGGCCCTGAAACAGAGACCCACCCCGAGGAGCGCGTGGTCCCTTACATGCTA 563
Qy 81 AspLeuTyrArgHisSerGlyGlnProGlySerProAlaProAspHisArgLeuGlu 100
Db 564 GACCTGTATCGCAGCACTCAGGTCAGCGGGCTCACCCGCGCCAGACACCGGTTGGAG 623
Qy 101 ArgAlaLysArgAlaAsnThrValArgSerPheHisHisGluGluSerLeuGluGlu 120
Db 624 AGGGCAGCCAGCCGAGCAACACTGTGCGCAGCTTCCACCATGAAGATCTTTGGAAGA 683
Qy 121 LeuProGluThrSerGlyLysThrThrArgArgPhePheAsnLeuSerSerLeuPro 140
Db 684 CTACAGAAACGAGTGGGAAACAAACCCGGAGATCTCTTTAAATTAAGTTCATCCCC 743
Qy 141 ThrGluGluPheIleThrSerAlaGluLeuGlnValPheArgGluGlnMetGlnAspAla 160
Db 744 ACGGAGGAGTTATCACCTCAGCAGAGCTTCAGGTTTCCGAGAACAGATCGAAGTCT 803
Qy 161 LeuGlyAsnAsnSerSerPheHisHisArgIleAsnIleTyrGluIleIleLysProAla 180
Db 804 TTAGAAACAATAGCAGTTTCATCACCGAATTAATATTTATGAATCATAAACCTGCA 863
Qy 181 ThrAlaAsnSerLysPheProValThrArgLeuLeuAspThrArgLeuValAsnGlnAsn 200
Db 864 ACAGCAACTCGAAATTCGCCGTGACCAAGCTTTTGGACACACAGGTGTGTAATCAGAA 923
Qy 201 AlaSerArgTyrGluSerPheAspValThrProAlaValMetArgTyrThrAlaGlnGly 220
Db 924 GCAGCAGTGGGAAAGTTTGTATGTACCCCGCTGTGTGCGGTGACGTGCACAGGGA 983
Qy 221 HisAlaAsnHisGlyPheValValGluValAlaHisLeuGluGluLysGlnGlyValSer 240
Db 984 CACGCCAACCATGGATTCTGTGTGGAAGTGGGCCACTTTGGAGGAAACAAGGTGTCTCC 1043
Qy 241 LysArgHisValArgIleSerArgSerLeuHisGlnAspGluHisSerTyrSerGlnIle 260
Db 1044 AAGAGACATGTTAGGATAGCAGGCTTTTGCACCAAGATGAACACAGCTGTGTACAGATA 1103
Qy 261 ArgProLeuLeuValThrPheGlyHisAspGlyLysGlyHisProLeuHisLysArgGlu 280
Db 1104 AGCCATTTGCTAGTAACTTTTGGCCATGTATGGAAGAGGCATCTCTCCACAAAGAGAA 1163
Qy 281 LysArgGlnAlaLysHisLysGlnArgLysArgLeuLysSerSerCysLysArgHisPro 300
Db 1164 AAACGTCAAGCCAAACACAAACAGCGGAAACGCCCTTAAAGTCCAGCTGTAAGAGACACCT 1223
Qy 301 LeuTyrValAspPheSerAspValGlyTyrAsnAspTyrIleValAlaProProGlyTyr 320
Db 1224 TTGTACGTGGACTTCAGTGACGTGGGTGGAATGACTGGATTGTGGCTCCCGCGGGTAT 1283
Qy 321 HisAlaPheTyrCysHisGlyGluCysProPheProLeuAlaAspHisLeuAsnSerThr 340
Db 1284 CACGCCCTTTACTGTCACGGAAGTGCCTTTTCTCTGGCTGATCATCTGAACCTCACT 1343
Qy 341 AsnHisAlaIleValGlnThrLeuValAsnSerValAsnSerLysIleProLysAlaCys 360
Db 1344 AATCATGCATTTGTCAGACGTTGTCAACTCTGTAACTCTAAGATCTCTTAAGCATGC 1403
Qy 361 CysValProThrGluSerAlaIleSerMetLeuTyrLeuAspGluAsnGluLysVal 380
Db 1404 TGTGTCCGACAGAACTCAGTGCTATCTGATGCTGTACCTTGCAGAGAAATGAAAGGTT 1463
Qy 381 ValLeuLysAsnTyrGlnAspMetValValGluGlyCysGlyCysArg 396
Db 1464 GTATTAAAGAACTATCAGGACATGGTTGTGGAGGGTTGTGGGTGTGCG 1511

RESULT 3

US-10-139-814-1

; Sequence 1, Application US/10139814

Publication No. US20030134790A1
GENERAL INFORMATION:
APPLICANT: Langenfeld, John
TITLE OF INVENTION: BONE MORPHOGENETIC PROTEIN-2 IN THE TREATMENT AND DIAGNOSIS OF
TITLE OF INVENTION: CANCER
FILE REFERENCE: 273/136 Michael J. Wise
CURRENT APPLICATION NUMBER: US/10/139,814
CURRENT FILING DATE: 2002-05-02
PRIOR APPLICATION NUMBER: US60/261,252
PRIOR FILING DATE: 2001-01-12
PRIOR APPLICATION NUMBER: US10/044,716
PRIOR FILING DATE: 2002-01-11
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 1547
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: source
LOCATION: (1)..(1547)
OTHER INFORMATION: Homo sapiens: Taxon:9606
FEATURE:
NAME/KEY: gene
LOCATION: (1)..(1547)
OTHER INFORMATION: BMP2
FEATURE:
NAME/KEY: CDS
LOCATION: (324)..(1514)
OTHER INFORMATION:
FEATURE:
NAME/KEY: misc feature
LOCATION: (429)..(1127)
OTHER INFORMATION: Region: TGF-beta propeptide
FEATURE:
NAME/KEY: variation
LOCATION: (432)..(432)
OTHER INFORMATION: Allele = "T"; Allele = "G"
FEATURE:
NAME/KEY: variation
LOCATION: (584)..(584)
OTHER INFORMATION: Allele = "A"; Allele = "G"
FEATURE:
NAME/KEY: variation
LOCATION: (893)..(893)
OTHER INFORMATION: Allele = "T"; Allele = "A"
FEATURE:
NAME/KEY: misc feature
LOCATION: (1209)..(1511)
OTHER INFORMATION: TGF-beta; Region: Transforming growth factor-beta (TGF-beta) family
US-10-139-814-1

Alignment Scores:
Pred. No.: 8.92e-227 Length: 1547
Score: 2098.00 Matches: 396
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-801-648-2 (1-396) x US-10-139-814-1 (1-1547)

Qy 1 MetValAlaGlyThrArgCysLeuLeuAlaLeuLeuLeuProGlnValLeuLeuGlyGly 20
Db 384 ATGGTGGCGCGGACCCCGCTGCTTCTAGCTTGTCTCCCGAGTCTCTCTGGCGGC 383
Qy 21 AlaAlaGlyLeuValProGluLeuGlyArgArgLysPheAlaAlaAsnSerGlyArg 40
Db 384 GCGGCTGGCTCTGTTCCGAGGCTGGGCGCGAGAGTTCCGCGCGCGTCTGTCGGCGCGC 443

```
RESULT 4
US-10-366-345-10
; Sequence 10, Application US/10366345
; Publication No. US20030224501A1
; GENERAL INFORMATION:
; APPLICANT: Young, et al.
; TITLE OF INVENTION: Bone Morphogenetic Protein Polynucleotides, Polypeptides and
; FILE REFERENCE: PT189
; CURRENT APPLICATION NUMBER: US/10/366,345
; CURRENT FILING DATE: 2003-02-14
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 1547
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-366-345-10

Alignment Scores:
Pred. No.:      8.92e-227      Length:      1547
Score:          2098.00        Matches:     396
Percent Similarity: 100.00%    Conservative: 0
Best Local Similarity: 100.00% Mismatches:     0
Query Match:      100.00%      Indels:       0
DB:               6           Gaps:         0

US-10-801-648-2 (1-396) x US-10-366-345-10 (1-1547)

Qy   1  MetValAlaGlyThrArgCysLeuLeuAlaLeuLeuLeuProGlnValLeuLeuGlyGly 20
Db   324 ATGGTGGCCGGGACCCGCTGTCTTAGCGTTGCTGTCTCCACAGGTCCTCTCTGGGCGGC 383
Qy   21 AlaAlaGlyLeuValProGluLeuGlyArgArgLysPheAlaAlaSerSerGlyArg 40
Db   384 CGGCTGGCTCGTTCCGGAGCTGGGCGCGAGGAAGTTCGCGGCGGCGTCTGTCGGGCGGC 443
Qy   41 ProSerSerGlnProSerAspGluValLeuSerGluPheGluLeuArgLeuLeuSerMet 60
Db   444 CCCTCATCCAGCCCTCTGACGAGGTCCTGACGAGGTCGAGTTGCGGCTGCTCAGCATG 503
Qy   61 PheGlyLeuLysGlnArgProThrProSerArgAspAlaValValProProTyrMetLeu 80
Db   504 TTCGGCTTGAACAGAGACCCACCCCGAGGAGCGCGTGGTGCCCTACATGCTA 563
Qy   81 AspLeuTyrArgArgHisSerGlyGlnProGlySerProAlaProAspHisArgLeuGlu 100
Db   564 GACCTGTATCGCAGGCACTCAGGTCAGCGGGCTCACCCGCCCCAGACCCCGGTTGGAG 623
Qy   101 ArgAlaAlaSerArgAlaAenThrValArgSerPheHisHisGluGluSerLeuGluGlu 120
Db   624 AGGCGACCGAGCGGAGCAACACCTGCGGAGCTTCACCATGAAGAATCTTTGGAGAA 683
Qy   121 LeuProGluThrSerGlyLysThrThrArgArgPhePheAsnLeuSerSerIlePro 140
Db   684 CTACCAAGAACGAGTGGGAAAACACCCCGGAGATTCCTCTTAATTTAAGTTCTATCCCC 743
Qy   141 ThrGluGluPheLeThrSerAlaGluLeuGlnValPheArgGluGlnMetGlnAspAla 160
Db   744 ACGGAGGAGTTTATCATCTCAGCAGAGCTTCAGGTTTCCGAGAACACAGATCAAGATGCT 803
Qy   161 LeuGlyAsnAsnSerSerPheHisHisArgIleAsnIleTyrGluIleIleLysProAla 180
Db   804 TTAGGAACAAATAGCAGTTTCCATCCGAAATTAATATTATGAAATCATATAAACCTGCA 863
Qy   181 ThrAlaAsnSerLysPheProValThrArgLeuLeuAspThrArgLeuValAsnGlnAsn 200
Db   864 ACAGCCAACCTCGAAATTCCTCCGTCACAGACTTTTGGACACCCAGGTTGGTGAATCAGAT 923
Qy   201 AlaSerArgTrpGluSerPheAspValThrProAlaValMetArgTrpThrAlaGlnGly 220
Db   924 GCAAGCAGGTGGGAAAGTTTGTATGTACCCCGCTGTGATCGCGTGGCATGTCACAGGGA 983
Qy   221 HisAlaAsnHisGlyPheValValGluValAlaHisLeuGluGluLysGlnGlyValSer 240
Db   984 CACGCCAACCATGATTCGTGGTGGAAAGTGGCCCACTTGGAGGAGAAACAAGGTGTCTCC 1043
Qy   241 LysArgHisValArgIleSerArgSerLeuHisGlnAspGluHisSerTrpSerGlnIle 260
Db   1044 AAGAGACATGTTAGGATAAGCAGCTCTTTCACCAAGATGAACACAGCTGGTCACAGATA 1103
Qy   261 ArgProLeuLeuValThrPheGlyHisAspGlyLysGlyHisProLeuHisLysArgGlu 280
Db   1104 AGGCCATTGTCTAGTAACCTTTTGGCCATGATGSAAGAGGCACTCTCTCCACAAAGAGAA 1163
Qy   281 LysArgGlnAlaLysHisLysGlnArgLysArgLeuLysSerSerCysLysArgHisPro 300
Db   1164 AACGTCAGGCCAACAAACAACACGGGAACCGCTTAACTTAACTCAGCTGTAGAGACACCT 1223
Qy   301 LeuTyrValAspPheSerAspValGlyTrpAsnAspTrpIleValAlaProProGlyTyr 320
Db   1224 TTGTACGTGGACTTCAGTGAGTGGGTGGAAATGACTGGATTTGTGGTCTCCCGGGGTAT 1283
Qy   321 HisAlaPheTyrCysHisGlyGluCysProPheProLeuAlaAspHisLeuAsnSerThr 340
Db   1284 CACGCCCTTTACTGCCACCGAAGATGCCCTTTCTCTGGCTGATCATCTGAACTCCACT 1343
Qy   341 AsnHisAlaIleValGlnThrLeuValAsnSerValAsnSerLysIleProLysAlaCys 360
Db   1344 AATCATGCCATTGTTCAGACGTGGTCAACTCTCTGTAACTCTAGATTTCTTAAGGCGATGC 1403
Qy   361 CysValProThrGluLeuSerAlaIleSerMetLeuTyrLeuAspGluAsnGluLysVal 380
Db   1404 TGTGTCCCGACAGAACTCAGTGCTATCTCGATGTCTGTACCTTTGACGAGATGAAGAGTT 1463
Qy   381 ValLeuLysAsnTyrGlnAspMetValValGluGlyCysGlyCysArg 396
Db   1464 GTATTAAAGAACTATCAGGACATGGTGTGGAGGGTTGTGGGTGTGCG 1511
```

Qy 221 HisAlaAenHisGlyPheValValAlaHisLeuGluGluLysGlnGlyValSer 240
Db 984 CACCCCAACCATGATTCGTGGTGAAGTGGCCCACTTGGAGGAGAAACAAGGTGTCTCC 1043
Qy 241 LysArgHisValArgIleSerArgSerLeuHisGlnAenSerTrpSerGlnIle 260
Db 1044 AAGAGACATGTTAGGATAAGCAGGTCTTTGGCACCAGATGAACACAGCTGGTCACAGATA 1103
Qy 261 ArgProLeuLeuValThrPheGlyHisAspGlyLysGlyHisProLeuHisLysArgGlu 280
Db 1104 AGGCCATTCGTAGTAACCTTTTGGCCATGATGGAAGAGGCGCATCTCTCCACAAAGAGAA 1163
Qy 281 LysArgGlnAlaLysHisLysGlnArgLysArgLeuLysSerSerCysLysArgHisPro 300
Db 1164 AAAGCTCAGCCCAACACACACAGCGGAAACGCCTTAAGTCCAGCTGTAAAGACACCCCT 1223
Qy 301 LeuTyrValAspPheSerAspValGlyTrpAenAspTrpIleValAlaProProGlyTyr 320
Db 1224 TTGTACGTGGACTTCAGTGACGTGGGTGGATGACTGGATTGTGGCTCCCGCGGGTAT 1283
Qy 321 HisAlaPheTyrCysHisGlyGluCysProPheProLeuAlaAspHisLeuAenSerThr 340
Db 1284 CACGCCCTTTTACTGCCACGAGAAAGCCCTTTTCTCTGGCTGATCATCTGAATCTCACT 1343
Qy 341 AenHisAlaIleValGlnThrLeuValAenSerValAenSerLysIleProLysAlaCys 360
Db 1344 AATCATGCGATGTTTCAGACGTTGGTCAACTCTGTAACTCTAAGATTCTTAAGGCATGC 1403
Qy 361 CysValProThrGluLeuSerAlaIleSerMetLeuTyrLeuAspGluAenGluLysVal 380
Db 1404 TGTGTCCGACAGAACTCAGTGCTATCTCGATGCTGTACTTGCAGAGATGAAGAGTT 1463
Qy 381 ValLeuLysAenTyrGlnAspMetValValGluGlyCysGlyCysArg 396
Db 1464 GTATTAAAGAACTATCAGGACATGGTTGTGGAGGTTGTGGGTGTGCG 1511

RESULT 5

US-10-295-027-159
; Sequence 159, Application US/10295027
; Publication No. US20030232350A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Nataasha
; APPLICANT: Ginsberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glynn, Richard
; APPLICANT: Hevezi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
; FILE REFERENCE: 018501-012500US
; CURRENT APPLICATION NUMBER: US/10/295,027
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 09/663,733
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/335,394
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/332,464
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/334,393
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/340,376
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/347,211
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/347,349
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/355,250

; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/356,714
; PRIOR FILING DATE: 2002-02-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 159
; LENGTH: 1547
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-295-027-159

Alignment Scores: 8.92e-227 Length: 1547
Pred. No.: 2098.00 Matches: 396
Score: 2098.00 Conservations: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 100.00% Gaps: 0
DB: 6

US-10-801-648-2 (1-396) x US-10-295-027-159 (1-1547)

Qy 1 MetValAlaGlyThrArgCysLeuLeuAlaLeuLeuProGlnValLeuLeuGlyGly 20
Db 324 ATGCTGCGCGGACCCCGCTGTCTTAGCGTGTCTCTCCCAAGGTCTCTCGGCGGC 383
Qy 21 AlaAlaGlyLeuValProGluLeuGlyArgArgLysPheAlaAlaSerSerGlyArg 40
Db 384 CGGCTGCGCTCTGTTCCGAGCTGGCGCGCAGGAAGTTCGGCGCGGCTCGTCGGCGGC 443
Qy 41 ProSerSerGlnProSerAspGluValLeuSerGluPheGluLeuArgLeuSerMet 60
Db 444 CCCTCATCCCGAGCTCTGACGAGTCTGAGCGAGTTCGAGTTCGAGTTCGCGCTCTCAGCATG 503
Qy 61 PheGlyLeuLysGlnArgProThrProSerArgAspAlaValValProTyrMetLeu 80
Db 504 TTCGCGCTGAAACAGAGACCCACCCAGCAGGACCGCGGTGGTCCCGCTTACATGCTA 563
Qy 81 AspLeuTyrArgArgHisSerGlyGlnProGlySerProAlaProAspHisArgLeuGlu 100
Db 564 GACCTGTATCGCAGGCACTCAGGTTCAGCGCGGCTCTACCCGCGCCAGCACCAGGTGGAG 623
Qy 101 ArgAlaAlaSerArgAlaAenThrValArgSerPheHisHisGluGluSerLeuGlu 120
Db 624 AGGCGAGCCAGCGAGCCCAACACTGTGCGCAGCTTCACCATGAAGAATCTTTGGAAGAA 683
Qy 121 LeuProGluThrSerGlyLysThrArgArgPhePheAenLeuSerSerIlePro 140
Db 684 CTACCAGAAACGAGTGGGAAACCAACCCGAGATCTCTCTTTAATTTAAGTTCTATCCCC 743
Qy 141 ThrGluGluPheIleThrSerAlaGluLeuGlnValPheArgGluGlnMetGlnAspAla 160
Db 744 ACGGAGGAGTTTATCACCTCAGCAGAGTTCAGGTTTCCGAGAACACAGATGCAAGTGT 803
Qy 161 LeuGlyAenAenSerSerPheHisHisArgIleAenIleTyrGluIleIleLysProAla 180
Db 804 TTAGGAAACAATAGCAGTTTCCATCCCGAATTAATATTAATTAATTAATTAATTAATTAAT 863
Qy 181 ThrAlaAenSerLysPheProValThrArgLeuLeuAenSerArgLeuValAenGlnAen 200
Db 864 ACAGCCAACTCGAAATTCGCCGTGACCCAGTCTTTTGGACACACAGGTTGGTGAATCAGAA 923
Qy 201 AlaSerArgTyrGluSerPheAspValThrProAlaValMetArgTyrThrAlaGlnGly 220
Db 924 GCAGCAGGTGGGAAAGTTTGTATGTACCCCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 983
Qy 221 HisAlaAenHisGlyPheValValAlaHisLeuGluGluLysGlnGlyValSer 240
Db 984 CACGCCCAACCATGATTCGTGGTGAAGTGGCCCACTTGGAGGAGAAACAAGGTGTCTCC 1043
Qy 241 LysArgHisValArgIleSerArgSerLeuHisGlnAenSerTrpSerGlnIle 260
Db 1044 AAGAGACATGTTAGGATAAGCAGGTCTTTTGCACCAAGATGAACACAGCTGGTGCACAGATA 1103

Qy 261 ArgProLeuLeuValThrPheGlyHisAspGlyLysGlyHisProLeuHisLysArgGlu 280
 Db 1104 AGGCATTTGCTAGTAACCTTTTGGCCATGATGGAAGGGCATCTCTCCACAAAAGAGAA 1163
 Qy 281 LysArgGlnAlaLysHisLysGlnArgLysArgLeuLysSerSerCysLysArgHisPro 300
 Db 1164 AAACGTCAAGCAACACAAACAGCGGAACGCCCTTAAGTCCAGCTGTAGAGACACCT 1223
 Qy 301 LeuTyrValAspPheSerAspValGlyTyrPheAsnAspTrpIleValAlaProProGlyTyr 320
 Db 1224 TTGTACGTGGACTTTCAGTACGTGGGTGGAAATGACTGGATTGGCTCCCGGGGTAT 1283
 Qy 321 HisAlaPheTyrCysHisGlyGluCysProPheProLeuAlaAspHisLeuAsnSerThr 340
 Db 1284 CACGCCCTTTACTGCCACGGAGATGCCCTTTCTCTGGCTGATCATCTGAATCCACT 1343
 Qy 341 AsnHisAlaIleValGlnThrLeuValAsnSerValAsnSerLysIleProLysAlaCys 360
 Db 1344 AATCATGCCATTGTTACAGCGTTGGTCAACTCTGTTAACTTAAGATTCTTAAGGCATGC 1403
 Qy 361 CysValProThrGluLeuSerAlaIleSerMetLeuTyrLeuAspGluAsnGluLysVal 380
 Db 1404 TGTGTCCCGACAGAACTCAGTGCTATCTCGATGCTGTACCTTGACGAGAAATGAAAAGGTT 1463
 Qy 381 ValLeuLysAsnTyrGlnAspMetValValGluCysGlyCysArg 396
 Db 1464 GTATTAAAGAACTATCAGGACATGGTTGTGGAGGGTTGTGGGTGTGCG 1511

RESULT 6

US-10-302-812-19
 ; Sequence 19, Application US/10302812
 ; Publication No. US20040087016A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Keating et al.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR CELL DIFFERENTIATION AND
 ; TISSUE REGENERATION
 ; FILE REFERENCE: HYDR-P02-004
 ; CURRENT APPLICATION NUMBER: US/10/302,812
 ; CURRENT FILING DATE: 2002-11-21
 ; NUMBER OF SEQ ID NOS: 78
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 19
 ; LENGTH: 1547
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-302-812-19

Alignment Scores:

Pred. No.: 8.92e-227 Length: 1547
 Score: 2098.00 Matches: 396
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 7 Gaps: 0

US-10-801-648-2 (1-396) x US-10-302-812-19 (1-1547)

Qy 1 MetValAlaGlyThrArgCysLeuLeuAlaLeuLeuProGlnValLeuLeuGlyGly 20
 Db 324 ATGGTGGCGGAGCCCGCTGCTTCTTAGCGTTGCTGCTTCCCGAGGTCTCTCTGGGCGGC 383
 Qy 21 AlaAlaGlyLeuValProGluLeuGlyArgArgLysPheAlaAlaSerSerGlyArg 40
 Db 384 GCGGCTGGCTCGTTCCGGAGCTGGCGCGCAGGAAGTTCCGCGCGCGGTCTCTGGGCGGC 443
 Qy 41 ProSerSerGlnProSerAspGluValLeuSerGluPheGluLeuArgLeuLeuSerMet 60
 Db 444 CCTATATCCAGCCCTCTGACGAGGTCTGACGAGTTCCAGTTGCGGCTGCTCAGCATG 503
 Qy 61 PheGlyLeuLysGlnArgProThrProSerArgAspAlaValValProProTyrMetLeu 80
 Db 504 TTCGGCTGAAACAGAGACCCACCACCCCGAGGAGCGCGGTGGTGGTGGTGGTGGTGGT 563

Qy 81 AspLeuTyrArgArgHisSerGlyGlnProGlySerProAlaProAspHisArgLeuGlu 100
 Db 564 GACCTGTATCGCAGGCACTCAGGTACGCGGGTCACTCCCGCCAGACCAACCGGTTGGAG 623
 Qy 101 ArgAlaAlaSerArgAlaAsnThrValArgSerPheHisHisGluGluSerLeuGluGlu 120
 Db 624 AGGCGACCGACCGAGCAACACTGTGCGGAGCTTCCACCATGAGAAATCTTTGGAAGAA 683
 Qy 121 LeuProGluThrSerGlyLysThrThrArgArgPhePheAsnLeuSerSerIlePro 140
 Db 684 CTACCAAGAAACGAGTGGGAAAAACAACCCGAGAGTTCTCTTTAATTTAAGTTCTATCCCC 743
 Qy 141 ThrGluGluPheIleThrSerAlaGluLeuGlnValPheArgGluGlnMetGlnAspAla 160
 Db 744 ACGGAGGAGTTTATCATCCTCAGCAGAGCTTTCAGGTTTTCCGAGAACAGATGCAAGTGT 803
 Qy 161 LeuGlyAsnAsnSerSerPheHisHisArgIleAsnIleTyrGluIleLeuLysProAla 180
 Db 804 TTAGGAACAATAGAGATTTCATCCAGAAATTAATATTTATGAATCATATAAACCTTGCA 863
 Qy 181 ThrAlaAsnSerLysPheProValThrArgLeuLeuAspThrArgLeuValAsnGlnAsn 200
 Db 864 ACAGCCAACTCGAAATTTCCCGGTGACCCAGACTTTTGGACACCAAGTTGGTGAATCAGAA 923
 Qy 201 AlaSerArgTrpGluSerPheAspValThrProAlaValMetArgTrpThrAlaGlnGly 220
 Db 924 GCAAGCAGGTGGGAAAGTTTGTATGTACCCCGCTGTGATCGGTGAGACTGCACAGGGA 983
 Qy 221 HisAlaAsnHisGlyPheValValGluValAlaHisLeuGluLysGlnGlyValSer 240
 Db 984 CACGCCAACCATGGATTCTGTGGTGGAGTGGCCCACTTGGAGGAGAAACAAAGGTGTCTCC 1043
 Qy 241 LysArgHisValArgIleSerArgSerLeuHisGlnAspGluHisSerTrpSerGlnIle 260
 Db 1044 AAGAGACATGTTAGGATAAGCAGTCTTTGCCAACAGATGAACACACAGCTGTGCACAGATA 1103
 Qy 261 ArgProLeuLeuValThrPheGlyHisAspGlyLysGlyHisProLeuHisLysArgGlu 280
 Db 1104 AGGCCATTGCTAGTAACTTTTGGCCATGATGGAAGGGGCATCTCTCCACAAAGAGAA 1163
 Qy 281 LysArgGlnAlaLysHisLysGlnArgLysArgLeuLysSerSerCysLysArgHisPro 300
 Db 1164 AAACGTCAAGCAACACAAACAGCGGAACGCCCTTAAGTCCAGCTGTAGAGACACCT 1223
 Qy 301 LeuTyrValAspPheSerAspValGlyTyrPheAsnAspTrpIleValAlaProProGlyTyr 320
 Db 1224 TTGTACGTGGACTTTCAGTACGTGGGTGGAAATGACTGGATTGTGGCTCCCGGGGTAT 1283
 Qy 321 HisAlaPheTyrCysHisGlyGluCysProPheProLeuAlaAspHisLeuAsnSerThr 340
 Db 1284 CACGCCCTTTACTGCCACGGAGAAATGCCCTTTCTCTGGCTGATCATCTGAACCTCCACT 1343
 Qy 341 AsnHisAlaIleValGlnThrLeuValAsnSerValAsnSerLysIleProLysAlaCys 360
 Db 1344 AATCATGCCATTGTTACAGCTTGGTCACTCTGTTAACTCTAAGATTCTTAAGGCATGC 1403
 Qy 361 CysValProThrGluLeuSerAlaIleSerMetLeuTyrLeuAspGluAsnGluLysVal 380
 Db 1404 TGTGTCCCGACAGAACTCAGTGCTATCTCGATGCTGTACCTTGACGAGAAATGAAAAGGTT 1463
 Qy 381 ValLeuLysAsnTyrGlnAspMetValValGluCysGlyCysArg 396
 Db 1464 GTATTAAAGAACTATCAGGACATGGTTGTGGAGGGTTGTGGGTGTGCG 1511

RESULT 7

US-10-283-975A-403
 ; Sequence 403, Application US/10283975A
 ; Publication No. US20040110792A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ortho-Clinical Diagnostics, Inc.
 ; TITLE OF INVENTION: Methods For Assessing and Treating Leukemia
 ; FILE REFERENCE: CDS 293 PCT

;; CURRENT APPLICATION NUMBER: US/10/283.975A
;; CURRENT FILING DATE: 2002-10-30
;; PRIOR APPLICATION NUMBER: 60/340,938
;; PRIOR FILING DATE: 2001-10-30
;; PRIOR APPLICATION NUMBER: 60/338,997
;; PRIOR FILING DATE: 2001-10-30
;; PRIOR APPLICATION NUMBER: 60/340,081
;; PRIOR FILING DATE: 2001-10-30
;; PRIOR APPLICATION NUMBER: 60/341,012
;; PRIOR FILING DATE: 2001-10-30
;; NUMBER OF SEQ ID NOS: 900
;; SOFTWARE: Patent in version 3.1
;; SEQ ID NO 403
;; LENGTH: 1547
;; TYPE: DNA
;; ORGANISM: HUMAN
US-10-283-975A-403

Alignment Scores:

Pred. No.: 8,92e-227 Length: 1547
Score: 2098.00 Matches: 396
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 7 Gaps: 0

US-10-801-648-2 (1-396) x US-10-283-975A-403 (1-1547)

Qy 1 MetValAlaGlyThrArgCysLeuLeuAlaLeuLeuProGlnValLeuLeuGlyGly 20
Db 324 ATGTGGCGGCGGACCGCTGCTTCTAGCGTTGCTTCCAGGTCCTCTCGGCGGC 383
Qy 21 AlaAlaGlyLeuValProGluLeuGlyArgArgGlyPheAlaAlaAlaSerSerGlyArg 40
Db 384 CGCGCTGCGCTCGTTCCGAGCGTGGCGCGCGAGAGTTTCGCGCGCGCGC 443
Qy 41 ProSerSerGlnProSerAspGluValLeuSerGluPheGluLeuArgLeuLeuSerMet 60
Db 444 CCTCATCCAGCCCTCTGACGAGTCTGAGCGAGTTTCGAGTTGCGGCTGCTCAGCATG 503
Qy 61 PheGlyLeuLeuGlnArgProThrProSerArgAspAlaValValProProTyMetLeu 80
Db 504 TTGGGCTGAAACAGAGACCCACCCAGCAGGAGCGCGTGTGCTCCCTACATGCTA 563
Qy 81 AspLeuTyArgArgHisSerGlyGlnProGlySerProAlaProAspHisArgLeuGlu 100
Db 564 GACCTGTATCGCAGCACTCAGGTGAGCGGCGCTCAGCGCGCCAGACACCGGTTGAG 623
Qy 101 ArgAlaAlaSerArgAlaAsnThrValArgSerPheHisGluGluSerLeuGluGlu 120
Db 624 AGGCGAGCGCGCGGCAACACTGTGCGCAGCTTCCACCATGAAGAATCTTTGGAAGA 683
Qy 121 LeuProGluThrSerGlyLeuThrArgArgPhePheAsnLeuSerSerIlePro 140
Db 684 CTACAGAAACGAGTGGGAAACACCCGAGATCTCTTAATTAAGTTCTATCCCTCC 743
Qy 141 ThrGluGluPheIleThrSerAlaGluLeuGlnValPheArgGluGlnMetGlnAspAla 160
Db 744 ACGGAGGAGTTTATCACTCAGCAGAGCTTCCAGGTTTCCGAGAACAGATGCAATGCT 803
Qy 161 LeuGlyAsnAsnSerSerPheHisArgIleAsnIleTyArgLeuIleIleIleProAla 180
Db 804 TTAGGAAACAATAGCAGTTTCCATCAGCAATTAATATTAATGAATCATAAACCTGCA 863
Qy 181 ThrAlaAsnSerLysPheProValThrArgLeuLeuAspThrArgLeuValAsnGlnAsn 200
Db 864 ACAGCAACTCGAATTTCCCGTGACAGACTTTTGGACACAGGTTTGGTGAATCAGAT 923
Qy 201 AlaSerArgTrpGluSerPheAspValThrProAlaValMetArgTrpThrAlaGlnGly 220
Db 924 GCAAGCAGGTGGGAAAGTTTTCATGTACCCCGCTGTGATGCGGTGAGCTGCACAGGGA 983
Qy 221 HisAlaAsnHisGlyPheValValGluValAlaHisLeuGluGluGlyValSer 240

Db 984 CACGCCAACCATGATTCGTGGTGGAAAGTGGCCCACTTGGAGGAGAAACAAGGTGTCTCC 1043
Qy 241 LysArgHisValArgIleSerArgSerLeuHisGlnAspGluHisSerTrpSerGlnIle 260
Db 1044 AAGAGACATGTTAGGATAGCAGGTCTTTGACCAAGATGAACACAGCTGGTCAAGATA 1103
Qy 261 ArgProLeuLeuValThrPheGlyHisAspGlyLysGlyHisProLeuHisLysArgGlu 280
Db 1104 AGGCCATTCGTAGTAACCTTTTGGCCATGATGGAAGAGGCACTCTCCACAAAGAGAA 1163
Qy 281 LysArgGlnAlaLysHisLysGlnArgLysArgLeuLysSerSerCysLysArgHisPro 300
Db 1164 AAACGTCAGCCAAACACAAACAGCGGAACGCTTAAGTCCAGCTGTGAAGAGACACCT 1223
Qy 301 LeuTyThrValAspPheSerAspValGlyTrpAsnAspTrpIleValAlaProProGlyTy 320
Db 1224 TTGTACGTGGACTTCAGTGACGTGGGTGGAATGACTGGATTTGGCTTCCCGGGGTAT 1283
Qy 321 HisAlaPheTyTrpCysHisGlyGluCysProPheProLeuAlaAspHisLeuAsnSerThr 340
Db 1284 CACGCCCTTTACTGCCACGAGGAGATGCCCTTTCTCTGGCTGATCATCTGAACCTCCACT 1343
Qy 341 AsnHisAlaIleValGlnThrLeuValAsnSerValAsnSerLysLysIleProLysAlaCys 360
Db 1344 AATCATGCCATTTGTCAGACGTTGGTCAACTCTGTAACTCTAAGATTCTTAAGGCATGC 1403
Qy 361 CysValProThrGluLeuSerAlaIleSerMetLeuTyTrpLeuAspGluAsnGluVal 380
Db 1404 TGTGTCCCGCAGAACTCAGTGCTATCTCGATGCTGTACCTTGACGAGAAATGAAAGGTT 1463
Qy 381 ValLeuLysAsnTyTrpGlnAspMetValValGluGlyCysGlyCysArg 396
Db 1464 GTATTAAGAAGTAATCAGGACATGTTGTGGAGGTTGTGGGTGTCTGC 1511

RESULT 8

US-10-692-824-1
; Sequence 1, Application US/10692824
; Publication No. US20040126375A1
; GENERAL INFORMATION:
; APPLICANT: Langenfeld, John
; TITLE OF INVENTION: BONE MORPHOGENETIC PROTEIN-2 IN THE TREATMENT AND DIAGNOSIS OF
; TITLE OF INVENTION: CANCER
; FILE REFERENCE: 54704.8036.US03
; CURRENT APPLICATION NUMBER: US/10/692,824
; CURRENT FILING DATE: 2003-10-23
; PRIOR APPLICATION NUMBER: US60/261,252
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: US10/044,716
; PRIOR FILING DATE: 2002-01-11
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 1
; LENGTH: 1547
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: source
; LOCATION: (1)..(1547)
; OTHER INFORMATION: Homo sapiens: Taxon:9606
; FEATURE:
; NAME/KEY: gene
; LOCATION: (1)..(1547)
; OTHER INFORMATION: BMP2
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (324)..(1514)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (429)..(1127)
; OTHER INFORMATION: Region: TGF-beta propeptide
; FEATURE:
; NAME/KEY: variation

; LOCATION: (432)..(432)
 ; OTHER INFORMATION: Allele = "T"; Allele = "G"
 ; FEATURE: variation
 ; NAME/KEY: variation
 ; LOCATION: (584)..(584)
 ; OTHER INFORMATION: Allele = "A"; Allele = "G"
 ; FEATURE: variation
 ; NAME/KEY: variation
 ; LOCATION: (893)..(893)
 ; OTHER INFORMATION: Allele = "T"; Allele = "A"
 ; FEATURE: misc feature
 ; NAME/KEY: misc feature
 ; LOCATION: (1209)..(1511)
 ; OTHER INFORMATION: TGF-beta; Region: Transforming growth factor beta like domain
 ; FEATURE: misc feature
 ; NAME/KEY: misc feature
 ; LOCATION: (1209)..(1511)
 ; OTHER INFORMATION: TGF-beta; Region: Transforming growth factor-beta (TGF-beta) family
 US-10-692-824-1

Alignment Scores:
 Pred. No.: 8.92e-227 Length: 1547
 Score: 2098.00 Matches: 396
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 7 Gaps: 0

US-10-801-648-2 (1-396) x US-10-692-824-1 (1-1547)

| | | | |
|----|-----|--|-----|
| Qy | 1 | MetValAlaGlyThrArgCysLeuLeuAlaLeuLeuProGlnValLeuLeuGlyGly | 20 |
| Db | 324 | ATGTTGGCGGAGACCGCTGCTTCTAGCGTTGCTGCTTCCCGAGTCTCTCTGGCGGC | 383 |
| Qy | 21 | AlaAlaGlyLeuValProGluLeuGlyArgGlyPheAlaAlaSerSerGlyArg | 40 |
| Db | 384 | CGGCTGGCTGCTTCCGAGCTGGCGCGCAGGAAGTTCCGCGCGCGTCTCGCGCGC | 443 |
| Qy | 41 | ProSerSerGlnProSerAspGluValLeuSerGluPheGluLeuArgLeuLeuSerMet | 60 |
| Db | 444 | CCCTCATCCAGCCCTCTGACGAGTCTGACGAGTTCCAGTTGCGGCTCAGCATG | 503 |
| Qy | 61 | PheGlyLeuLysGlnArgProThrProSerArgAspAlaValValProProTyrMetLeu | 80 |
| Db | 504 | TTCCGCTGAAACAGACACCCACCCAGCAGGACCGCGTGGTGGCCCCCTCATGCTA | 563 |
| Qy | 81 | AspLeuTyrArgArgHisSerGlyGlnProGlySerProAlaProAspHisArgLeuGlu | 100 |
| Db | 564 | GACCTGTATCGAGCACTCAGGTACGCGGCTCACCGGCTCACCGCCAGACCGGTTGGAG | 623 |
| Qy | 101 | ArgAlaAlaSerArgAlaAsnThrValArgSerPheHisHisGluGluSerLeuGluGlu | 120 |
| Db | 624 | AGGCAGCAGCCGAGCCACACACTGTGCGAGCTTCCACCATGAAGAATCTTTGGAAGAA | 683 |
| Qy | 121 | LeuProGluThrSerGlyLysThrThrArgArgPhePheAsnLeuSerSerIlePro | 140 |
| Db | 684 | CTACCAAGACGATGGGAAACCAACCCGAGATCTCTTTAATTAAGTTCTATCCCC | 743 |
| Qy | 141 | ThrGluGluPheIleThrSerAlaGluLeuGlnValPheArgGluGlnMetGlnAspAla | 160 |
| Db | 744 | ACGGAGGATTATCACTCAGCAGAGCTTCAGGTTTCCGAGAACAGATGCAAGATGCT | 803 |
| Qy | 161 | LeuGlyAsnAsnSerSerPheHisHisArgIleAsnIleTyrGluIleIleLysProAla | 180 |
| Db | 804 | TTAGGAACAATAGCAGTTCCATCAGCAATTAATATATGAAATCATAAACCTGCA | 863 |
| Qy | 181 | ThrAlaAsnSerLysPheProValThrArgLeuLeuAspThrArgLeuValAsnGluAsn | 200 |
| Db | 864 | ACGCCAACTCGAAATTCGCCGTGACAGACTTTTGGACACCCAGGTTGGTGAATCAGAA | 923 |
| Qy | 201 | AlaSerArgTrpGluSerPheAspValThrProAlaValMetArgTyrThrAlaGlnGly | 220 |
| Db | 924 | GCAAGCAGTGGGAAGTTTGATGTACCCCCCTGTGATCGGTGAGCTGCACAGGA | 983 |

| | | | |
|----|------|--|------|
| Qy | 221 | HisAlaAsnHisGlyPheValValGluValAlaHisLeuGluGluLysGlnGlyValSer | 240 |
| Db | 984 | CACGCCAACCATGGATTCTGGTGGAAAGTGCCCACTTGGAGGAGAAACAGGTGTCTCC | 1043 |
| Qy | 241 | LysArgHisValArgIleSerArgSerLeuHisGlnAspGluHisSerTrpSerGlnIle | 260 |
| Db | 1044 | AAGAGACATGTTAGGATAAGCAGCTCTTTGCACCAAGATGAACACAGCTGTCACAGATA | 1103 |
| Qy | 261 | ArgProLeuLeuValThrPheGlyHisAspGlyLysGlyHisProLeuHisLysArgGlu | 280 |
| Db | 1104 | AGGCCATTGCTAGTAACCTTTTGGCCATGATGGAAGAGGCATCTCTCCCAAAAGAGAA | 1163 |
| Qy | 281 | LysArgGlnAlaLysHisLysGlnArgLysArgLeuLysSerSerCysLysArgHisPro | 300 |
| Db | 1164 | AAACGTCACGCCAACCAACACAGCGGAACGCTTAAAGTCCAGCTGTAAAGACACCCCT | 1223 |
| Qy | 301 | LeuTyrValAspPheSerAspValGlyTyrAsnAspTrpIleValAlaProProGlyTyr | 320 |
| Db | 1224 | TTGTACGTGGACTTCAGTGACGTGGGTGGATGACTGGATTGTGGCTCCCCGGGTAT | 1283 |
| Qy | 321 | HisAlaPheTyrCysHisGlyGluCysProPheProLeuAlaAspHisLeuAsnSerThr | 340 |
| Db | 1284 | CAGCCCTTTTACTGCCACGAGGAATGCCCTTTCTCTGGCTGATCATCTGAACCTCCACT | 1343 |
| Qy | 341 | AsnHisAlaIleValGlnThrLeuValAsnSerValAsnSerLysIleProLysAlaCys | 360 |
| Db | 1344 | AATCATGCCAATGTTTCAGACGTGGTCACTCTGTTAACTCTAAGATTCTTAAGGCATGC | 1403 |
| Qy | 361 | CysValProThrGluLeuSerAlaIleSerMetLeuTyrLeuAspGluAsnGluLysVal | 380 |
| Db | 1404 | TGTGTCCCGACAGAACTCAGTGCTATCTCATCTGCTGCTGCTGACGAGAAATGAAGGTT | 1463 |
| Qy | 381 | ValLeuLysAsnTyrGlnAspMetValValGluGlyCysGlyCysArg | 396 |
| Db | 1464 | GTATTAAGAACTATCAGGACATGTTGTGGAGGTTGTGGGTGTGGTGTCTGC | 1511 |

RESULT 9

US-10-801-648-1
 ; Sequence 1, Application US/10801648
 ; Publication No. US20040223953A1
 ; GENERAL INFORMATION:
 ; APPLICANT: CHEN, YAN
 ; APPLICANT: KUNG, HSIANG-FU
 ; APPLICANT: LIN, MARIE C.M.
 ; APPLICANT: LUK, K.D.K.
 ; TITLE OF INVENTION: A COMBINED ADENO-ASSOCIATED VIRUS AND ADENOVIRUS
 ; TITLE OF INVENTION: COCKTAIL GENE DELIVERY SYSTEM FOR HIGH EFFICIENCY
 ; TITLE OF INVENTION: GENE EXPRESSION WITHOUT ELICITING IMMUNE
 ; TITLE OF INVENTION: RESPONSE IN IMMUNO-COMPETENT SUBJECTS
 ; FILE REFERENCES: V9661.0074
 ; CURRENT APPLICATION NUMBER: US/10/801.648
 ; PRIOR FILING DATE: 2004-03-17
 ; PRIOR FILING DATE: 2003-03-17
 ; NUMBER OF SEQ ID NOS: 2
 ; SOFTWARE: Patent In Ver. 3.2
 ; SEQ ID NO 1
 ; LENGTH: 1547
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-801-648-1

Alignment Scores:
 Pred. No.: 8.92e-227 Length: 1547
 Score: 2098.00 Matches: 396
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 8 Gaps: 0

US-10-801-648-2 (1-396) x US-10-801-648-1 (1-1547)

Qy 1 MetValAlaGlyThrArgCysLeuLeuAlaLeuLeuProGlnValLeuLeuGlyGly 20
Db 324 ATGGTGGCGGAGCCCGCTGCTTCTAGCGTTGCTGCTTCCCGAGTCTCTCTGGCGGC 383
Qy 21 AlaAlaGlyLeuValProGluLeuGlyArgArgLysPheAlaAlaAlaSerSerGlyArg 40
Db 384 CGCGCTGGCTCGTTTCGGAGCTCGCGCGCAGGAAGTTTCGGCGGCGCTCGTTCGGCGGC 443
Qy 41 ProSerSerGlnProSerArgGluValLeuSerGluPheGluLeuArgLeuSerMet 60
Db 444 CCTCATCCCCAGCCCTCTGACGAGTCTGACGAGTTCGAGTTTCGGCTCTCAGCATG 503
Qy 61 PheGlyLeuLysGlnArgProThrProSerArgAspAlaValProProTyrMetLeu 80
Db 504 TTGGGCTGAAACAGAGACCCACCCAGCAGGAGCGCGTGGTGGCTCCCTACATGCTA 563
Qy 81 AspLeuTyrArgArgHisSerGlyGlnProGlySerProAlaProAspHisArgLeuGlu 100
Db 564 GACCTGTATCGAGCACTCAGGTGAGCGGCTCAGCGCGCTCAGCGCGCCAGACACCGGTGGAG 623
Qy 101 ArgAlaAlaSerArgAlaAsnThrValArgSerPheHisHisGluGluSerLeuGluGlu 120
Db 624 AGGGCAGCAGCCGAGGCAACACTGTGCGAGCTTCCACCATGAGAAATCTTTGGAAGA 683
Qy 121 LeuProGluThrSerGlyLysThrArgArgPhePheAsnLeuSerSerIlePro 140
Db 684 CTACAGAAACGAGTGGGAAACAAACCCGAGATCTTCTTTAATTTAAGTTCTATCCCC 743
Qy 141 ThrGluGluPheIleThrSerAlaGluLeuGlnValPheArgGluGlnMetGlnAspAla 160
Db 744 ACGGAGGAGTTTATCACCTCAGCAGAGCTTTCAGGTTTCCGAGAACAGATGCAAGATGCT 803
Qy 161 LeuGlyAsnAsnSerSerPheHisHisArgIleAsnIleTyrGluIleIleysProAla 180
Db 804 TTAGGAACAATAGCAGTTTCATCACCGAATTAATATTTATGAATCATAAACCTGCA 863
Qy 181 ThrAlaAsnSerLysPheProValThrArgLeuLeuAspThrArgLeuValAsnGlnAsn 200
Db 864 ACAGCAACTCGAAATTCCTGTCACAGACTTTTGGACACGAGTTTGGTGGATCAGAT 923
Qy 201 AlaSerArgTTPGluSerPheAspValThrProAlaValMetArgTTPThrAlaGlnGly 220
Db 924 GCAACGAGTGGGAAAGTTTGTATGTACCCCGCTGTGTATGCGGTGACTGCACAGGGA 983
Qy 221 HisAlaAsnHisGlyPheValValGluValAlaHisLeuGluGluLysGlnGlyValSer 240
Db 984 CACGCCAACCATGATTCGTGTGAGTGGCGCCACTTGGAGGAGAAACAAGGTGTCTCC 1043
Qy 241 LysArgHisValArgIleSerArgSerLeuHisGlnAspGluHiserTTPSerGlnIle 260
Db 1044 AAGAGACATGTAGGATTAAGCAGGCTTTTGCACCAAGATGACACAGTGTGTACAGATA 1103
Qy 261 ArgProLeuLeuValThrPheGlyHisAspGlyLysGlyHisProLeuHisLysArgGlu 280
Db 1104 AGGCCATGCTAGTAACCTTTTGGCCATGATGAAAGGCGCATCTCCACAAAAGAGAA 1163
Qy 281 LysArgGlnAlaLysHisLysGlnArgLysArgLeuLysSerSerCysLysArgHisPro 300
Db 1164 AAACGTCAGCCAAACACAAAACAGCGGAAACGCTTAAAGTCCAGCTGTAAGAGACACCT 1223
Qy 301 LeuTyrValAspPheSerAspValGlyTTPAsnAspTTPiLeValAlaProGlyTyr 320
Db 1224 TTGTACGTGAGCTTACGTGACGTGGGTGGATGATCTGATTTGTGGCTCCCGCGGGTAT 1283
Qy 321 HisAlaPheTyrCysHisGlyGluCysProPheProLeuAlaAspHisLeuAsnSerThr 340
Db 1284 CAGGCTTTTATGCGCAGGAGATGCTCTTTCTCTGGCTGATCACTGAACTCCACT 1343
Qy 341 AsnHisAlaIleValGlnThrLeuValAsnSerValAsnSerLysIleProLysAlaCys 360
Db 1344 AATCATGCCATTGTTTCAGACGTTGGTCAACTCTGTAACTCTAAAGTCTTAAAGCATGC 1403
Qy 361 CysValProThrGluLeuSerAlaIleSerMetLeuTyrLeuAspGluAsnGluLysVal 380

Db 1404 TGTGTCCCGCAGAACTCAGTGTCTATCTCGATGCTGTACCTTCACGAGAATGAAGGTT 1463
Qy 381 ValLeuLysAsnTyrGlnAspMetValValGluGlyCysGlyCysArg 396
Db 1464 GTATTAAAGAACTATCAGGACATGTTGTGGAGGTTGTGGGTGTCG 1511
RESULT 10
US-10-489-740-36
; Sequence 36, Application US/10489740
; Publication No. US20050112574A1
; GENERAL INFORMATION:
; APPLICANT: Biomimetics Limited
; TITLE OF INVENTION: P9
; FILE REFERENCE: Angiogenesis PCT
; CURRENT APPLICATION NUMBER: US/10/489,740
; CURRENT FILING DATE: 2004-03-15
; NUMBER OF SEQ ID NOS: 216
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 36
; LENGTH: 1547
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-489-740-36
Alignment Scores:
Pred. No.: 8,92e-227 Length: 1547
Score: 2098.00 Matches: 396
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0
US-10-801-648-2 (1-396) x US-10-489-740-36 (1-1547)
Qy 1 MetValAlaGlyThrArgCysLeuLeuAlaLeuLeuProGlnValLeuLeuGlyGly 20
Db 324 ATGGTGGCGGAGCCCGCTGCTTCTAGCGTTGCTGCTTCCCGAGTCTCTCTGGCGGC 383
Qy 21 AlaAlaGlyLeuValProGluLeuGlyArgArgLysPheAlaAlaAlaSerSerGlyArg 40
Db 384 CGCGCTGGCTCGTTTCGGAGCTGGCGCGCAGGAAGTTTCGGCGGCGCTCGTTCGGCGGC 443
Qy 41 ProSerSerGlnProSerAspGluValLeuSerGluPheGluLeuArgLeuLeuSerMet 60
Db 444 CCTCATCCCCAGCCCTCTGACGAGTCTGACGAGTTCGAGTTTCGGCTGCTCAGCATG 503
Qy 61 PheGlyLeuLysGlnArgProThrProSerArgAspAlaValProProTyrMetLeu 80
Db 504 TTGGGCTGAAACAGAGACCCACCCAGCAGGAGCGCGTGGTGGCTCCCTACATGCTA 563
Qy 81 AspLeuTyrArgArgHisSerGlyGlnProGlySerProAlaProAspHisArgLeuGlu 100
Db 564 GACCTGTATCGAGCACTCAGGTGAGCGGCTCAGCGCGCTCAGCGCGCCAGACACCGGTGGAG 623
Qy 101 ArgAlaAlaSerArgAlaAsnThrValArgSerPheHisHisGluGluSerLeuGluGlu 120
Db 624 AGGGCAGCAGCCGAGGCAACACTGTGCGAGTTCACCATGAGAAATCTTTGGAAGA 683
Qy 121 LeuProGluThrSerGlyLysThrArgArgPhePheAsnLeuSerSerIlePro 140
Db 684 CTACAGAAACGAGTGGGAAACAAACCCGAGATCTTCTTTAATTTAAGTTCTATCCCC 743
Qy 141 ThrGluGluPheIleThrSerAlaGluLeuGlnValPheArgGluGlnMetGlnAspAla 160
Db 744 ACGGAGGAGTTTATCACCTCAGCAGAGCTTTCAGGTTTCCGAGAACAGATGCAAGATGCT 803
Qy 161 LeuGlyAsnAsnSerSerPheHisHisArgIleAsnIleTyrGluIleIleysProAla 180
Db 804 TTAGGAACAATAGCAGTTTCATCACCGAATTAATATTTATGAATCATAAACCTGCA 863
Qy 181 ThrAlaAsnSerLysPheProValThrArgLeuLeuAspThrArgLeuValAsnGlnAsn 200

```
Db      864 ACAGCCAACTCGAAATTCCTCCGTCAGCAGACTTTTGGACACAGAGTTGGTGAATCAGAAT 923
Qy      201 AlaSerArgTTrpGluSerPheAspValThrProAlaValMetArgTrpThrAlaGlnGly 220
Db      924 GCAAGCAGGTGGGAAAGTTTGTGATGTACCCCGCTGTGATGCGGTGGACTGCAAGGGA 983
Qy      221 HisAlaAsnHisGlyPheValValAlaHisIleuGluValHisGlnGlyValSer 240
Db      984 CACGCCAACCACTGGATTCGTGGTGAAGTGGCCCACTTGGAGGAGAAACAAGTGTCTCC 1043
Qy      241 LysArgHisValArgIleSerArgSerLeuHisGlnAspGluHisSerTrpSerGlnIle 260
Db      1044 AAGAGACATGTTAGGATAAGCAGGTCTTTGGCCATGATGGAAGAGGCACTCTCTCCACAAAGAGAA 1163
Qy      261 ArgProIleuLeuValThrPheGlyHisAspGlyLysGlyHisIleProLeuHisIleArgGlu 280
Db      1104 AGGCCATTTGCTAGTAACATTTTGGCCATGATGGAAGAGGCACTCTCTCCACAAAGAGAA 1163
Qy      281 LysArgGlnAlaLysHisIleSerArgLysGlnArgLysArgLeuLysSerSerCysLysArgHisPro 300
Db      1164 AAACGTCAAGCCAAACACAAACAGCGGAAACGCTTAAAGTCCAGCTGTAAGAGACACCT 1223
Qy      301 LeuTyrValAspPheSerAspValGlyTrpAsnAspTrpIleValAlaProProGlyTyr 320
Db      1224 TTGTACGTGGACTTCAGTGACGTGGGTGGAAATGACTGGATTGGCTCCCGGGGTAT 1283
Qy      321 HisAlaPheTyrCysHisGlyGluCysProPheProLeuAlaAspHisLeuAsnSerThr 340
Db      1284 CACGCCTTTTACTGTCACGGAGAAATGCCCTTTTCTCTGGCTGATCATCTGAATCCACT 1343
Qy      341 AsnHisAlaIleValGlnThrLeuValAsnSerValAsnSerIleProLysAlaCys 360
Db      1344 AATCATGCCATTGTTCAGACGTTGGTCAACTCTGTAACTCTAAGATTCTTAAGGCATGC 1403
Qy      361 CysValProThrGluLeuSerAlaIleSerMetLeuTyrLeuAspGluAsnGluLysVal 380
Db      1404 TGTGTCGCGACAGAACTCAGTGCTATCTCGATGCTGTACCTTGACGAGAAATGAAAGGTT 1463
Qy      381 ValLeuLysAsnTyrGlnAspMetValValGluGlyCysGlyCysArg 396
Db      1464 GTATTAAAGAACTATCAGGACATGGTTGTGGAGGGTTGTGGGTGTGCG 1511

RESULT 11
US-10-492-380-1
; Sequence 1, Application US/10492380
; Publication No. US20050118585A1
; GENERAL INFORMATION:
; APPLICANT: Alcon Research, Ltd.
; APPLICANT: Clark, Abbot P.
; TITLE OF INVENTION: Bone Morphogenic Proteins (BMP), BMP Receptors and BMP Binding
; TITLE OF INVENTION: Proteins and their Use in the Diagnosis and Treatment of Glaucom
; FILE REFERENCE: 2312 US
; CURRENT APPLICATION NUMBER: US/10/492,380
; CURRENT FILING DATE: 2004-04-12
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
; LENGTH: 1547
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-492-380-1

Alignment Scores:
Pred. No.:      8,92e-227      Length:      1547
Score:          2098.00      Matches:      396
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:      100.00%      Indels:      0
DB:              9          Gaps:      0

US-10-801-648-2 (1-396) x US-10-492-380-1 (1-1547)
Qy      1 MetValAlaGlyThrArgCysLeuLeuAlaLeuLeuProGlnValLeuLeuGlyGly 20
```

```
Db      324 ATGTTGCGCGGGACCCCGCTGTCTTCTAGCGTTGCTGTCTTCCCGAGGTCCTCTCTCGGGCGGC 383
Qy      21 AlaAlaGlyLeuValProGluLeuGlyArgArgLysPheAlaAlaLaserSerGlyArg 40
Db      384 GCGGCTGGCTCGTTCCGAGCTGGCGCGCAGGAAGTTTCGCGCGCGCTGCTCGGGCGGC 443
Qy      41 ProSerSerGlnProSerAspGluValIleuSerGluPheGluLeuArgLeuLeuSerMet 60
Db      444 CCCTCATTCCTCCAGCCCTCTGACGAGTCTTGAGCGAGTTCGAGTTGCGGCTGCTCAGCATG 503
Qy      61 PheGlyLeuLysGlnArgProThrProSerArgAspAlaValValProProTyrMetLeu 80
Db      504 TTGCGCTGAAACAGAGACCCACCCCGACGAGGACCGCTGTGTGTCCTCCCTACATGCTA 563
Qy      81 AspLeuTyrArgArgHisSerGlyGlnProGlySerProAlaProAspHisArgLeuGlu 100
Db      564 GACCTGTATCGAGGCACTCAGGTTCAGCGGGCTCACCCGCCCCAGACACCCGGTGGAG 623
Qy      101 ArgAlaAlaSerArgAlaAsnThrValArgSerPheHisIleGluGluSerLeuGluGlu 120
Db      624 AGGCACCCACGAGCCAGCCAACTGTGCGCAGCTTCCACCATGAAGAATCTTTTGGAGAA 683
Qy      121 LeuProGluThrSerGlyLysThrThrArgArgPhePheAsnLeuSerSerIlePro 140
Db      684 CTACCAGAAACGAGTGGGAAACAAACCCGAGATCTTCTTTAATTTAAGTTCTATCCCC 743
Qy      141 ThrGluGluPheIleThrSerAlaGluLeuGlnValPheArgGluGlnMetGlnAspAla 160
Db      744 ACGGAGGAGTTTATCCTCCTCAGCAGAGCTTCAGGTTTTCCGAGAACAGATGCAAGATGCT 803
Qy      161 LeuGlyAsnAsnSerSerPheHisArgIleAsnIleTyrGluIleIleLysProAla 180
Db      804 TTAGGAAACAAATAGCAGTTTCCATCACCGAATTAATAATTTTGAATCATAAAAACCTGCA 863
Qy      181 ThrAlaAsnSerLysPheProValThrArgLeuLeuAspThrArgLeuValAsnGlnAsn 200
Db      864 ACAGCCAACTCGAAATTTCCCGTGACCAAGCTTTTGGACACAGGTTGGTGAATCAGAAT 923
Qy      201 AlaSerArgTrpGluSerPheAspValThrProAlaValMetArgTrpThrAlaGlnGly 220
Db      924 GCAAGCAGGTGGGAAAGTTTGTATGTCAACCCCGCTGTGATGCGTGGATGCAAGGGA 983
Qy      221 HisAlaAsnHisGlyPheValValGluValAlaHisIleuGluLysGlnGlyValSer 240
Db      984 CACGCCAAACCATGGATTCGTGGTGGAGTGGCCCACTTGGAGGAGAAACAAGTGTCTCC 1043
Qy      241 LysArgHisValArgIleSerArgSerLeuHisGlnAspGluHisSerTrpSerGlnIle 260
Db      1044 AAGAGACATGTTAGGATAAGCAGTCTTTGGCCATGATGGAAGAGGCACTCTCTCCACAAAGAGAA 1163
Qy      261 ArgProLeuLeuValThrPheGlyHisAspGlyLysGlyHisProLeuHisLysArgGlu 280
Db      1104 AGGCCATTTGCTAGTAACATTTTGGCCATGATGGAAGAGGCACTCTCTCCACAAAGAGAA 1163
Qy      281 LysArgGlnAlaLysHisIleSerArgLysGlnArgLysArgLeuLysSerSerCysLysArgHisPro 300
Db      1164 AAACGTCAAGCCAAACACAAACAGCGGAAACGCTTAAAGTCCAGCTGTAAGAGACACCT 1223
Qy      301 LeuTyrValAspPheSerAspValGlyTrpAsnAspTrpIleValAlaProProGlyTyr 320
Db      1224 TTGTACGTGGACTTCAGTGACGTGGGTGGAAATGACTGGATTGGCTCCCGGGGTAT 1283
Qy      321 HisAlaPheTyrCysHisGlyGluCysProPheProLeuAlaAspHisLeuAsnSerThr 340
Db      1284 CACGCCTTTTACTGCCACGGAGAAATGCCCTTTTCTCTGGCTGATCATCTGAATCCACT 1343
Qy      341 AsnHisAlaIleValGlnThrLeuValAsnSerValAsnSerIleProLysAlaCys 360
Db      1344 AATCATGCCATTGTTCAGACGTTGGTCAACTCTGTAACTCTAAGATTCTTAAGGCATGC 1403
Qy      361 CysValProThrGluLeuSerAlaIleSerMetLeuTyrLeuAspGluAsnGluLysVal 380
```

Db 1404 TGTGTCCGACAGAACTCAGTGCTATCTCGATGCTGTGACCTTGACGAGAAATGAAAAAGGTT 1463
Qy 381 ValLeuLysAsnTyrGlnAspMetValValGluGlyCysGlyCysArg 396
Db 1464 GTATTAAAGAACTATCAGGACATGTTGTGGAGGTTGTGGGTGTGCG 1511
RESULT 12
US-10-917-265-1
; Sequence 1, Application US/10917265
; Publication No. US20050136042A1
; GENERAL INFORMATION:
; APPLICANT: BETZ, OLIVER B.
; APPLICANT: EVANS, CHRISTOPHER H.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TISSUE REPAIR
; FILE REFERENCE: BWY-004.01
; CURRENT APPLICATION NUMBER: US/10/917,265
; CURRENT FILING DATE: 2004-08-11
; PRIOR APPLICATION NUMBER: 60/494,484
; PRIOR FILING DATE: 2003-08-12
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patent In Ver. 3.3
; SEQ ID NO 1
; LENGTH: 1547
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-917-265-1
Alignment Scores:
Pred. No.: 8,92e-227 Length: 1547
Score: 2098.00 Matches: 396
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
US-10-801-648-2 (1-396) x US-10-917-265-1 (1-1547)
Qy 1 MetValAlaGlyThrArgCysLeuLeuAlaLeuLeuProGlnValLeuLeuGlyGly 20
Db 324 ATGTGGCGCGGACCGCTGCTTCTTAGCGTTGCTGTCCCGACGGTCTCTCTGGGCGGC 383
Qy 21 AlaAlaGlyLeuValProGluLeuGlyArgArgLysPheAlaAlaAlaSerSerGlyArg 40
Db 384 CGGGTGGCGCTGTTCCGAGCTGGCGCCGACAGAAAGTTCCGCGCGCGCTGTCGGGCGCG 443
Qy 41 ProSerSerGlnProSerAspGluValLeuSerGluPheGluLeuArgLeuSerMet 60
Db 444 CCTCATCCAGCCCTCTGACGAGTCTCTGACGAGTCTGAGCGAGTTCCGAGTTCGGCTGCTCAGCATG 503
Qy 61 PheGlyLeuLysGlnArgProThrProSerArgAspAlaValValProProTyrMetLeu 80
Db 504 TTCGGCCTGAAACAGAGACCCACCCCGACGAGCGCGCTGCTGCGCCCTTACATGCTA 563
Qy 81 AspLeuTyrArgArgHisSerGlyGlnProGlySerProAlaProAspHisArgLeuGlu 100
Db 564 GACCTGTATCGAGGACCTCAGGTGAGCGGGCTCACCAGCGCCAGACCCAGCGTTGAG 623
Qy 101 ArgAlaAlaSerArgAlaAsnThrValArgSerPheHisGluGluSerLeuGluGlu 120
Db 624 AGGGCAGCGCGGAGCCACACTGTGCGCAGTCTCCACCATGAAGATCTTTGGAGAA 683
Qy 121 LeuProGluThrSerGlyLysThrThrArgArgPhePheAsnLeuSerSerIlePro 140
Db 684 CTACAGAAACAGTGGGAAACACACCCGAGATCTCTTTAAATTAAGTTCTATCCGC 743
Qy 141 ThrGluGluPheIleThrSerAlaGluLeuGlnValPheArgGluGlnMetGlnAspAla 160
Db 744 ACGGAGGAGTTTATCATCTCCTCAGAGCTTTCAGGTTTCCGAGAAACAGATGATGCT 803
Qy 161 LeuGlyAsnAsnSerSerPheHisArgGlnLeuIleLeuLysProAla 180
Db 804 TTAGGAAACATAGCAGGTTTCCATCCGAAATTAATTTATGAAATCATAAACCTGCA 863

Qy 181 ThrAlaAsnSerLysPheProValThrArgLeuLeuAspThrArgLeuValAsnGlnAsn 200
Db 864 ACAGCAACTCGAAATTCCTCCGTCGACAGACTTTTGGACACACAGGTTGGTGAATCAGAA 923
Qy 201 AlaSerArgTTPGluSerPheAspValThrProAlaValMetArgTTPThrAlaGlnGly 220
Db 924 GCAAGCAGGTGGGAAAGTTTGTATGTCACTCCCTCTGTATGCGGTGGACTGCAAGGGA 983
Qy 221 HisAlaAsnHisGlyPheValValGluValAlaHisLeuGluGluLysGlnGlyValSer 240
Db 984 CACGCCAACCATGATTCGTGGTGAAGTGGCCCACTTGGAGGAGAAACAGAGTGTCTCC 1043
Qy 241 LysArgHisValArgIleSerArgSerLeuHisGlnAspGluHisSerTrpSerGlnIle 260
Db 1044 AAGAGACATGTTAGGATAAGCAGGCTCTTGCACCAAGATGAACACAGCTGCTGCAGATA 1103
Qy 261 ArgProLeuLeuValThrPheGlyHisAspGlyLysGlyHisProLeuHisLysArgGlu 280
Db 1104 AGGCCATTGCTAGTAACCTTTTGGCCATGATGAAAGGGCATCTCTCTCCACAAAGAGAA 1163
Qy 281 LysArgGlnAlaLysHisLysGlnArgLysArgLeuLysSerSerCysLysArgHisPro 300
Db 1164 AACGTCAGCCAAACAAACACAGCGAAGCCCTTAAGTCCAGCTGTAAAGACACCT 1223
Qy 301 LeuTyrValAspPheSerAspValGlyTrpAsnAspTrpIleValAlaProProGlyTyr 320
Db 1224 TTGTACGTGGACTTCAGTGAGCTGGGTGGAATGACTGATTTGTGGCTCCCGGGGTAT 1283
Qy 321 HisAlaPheTyrCysHisGlyGluCysProPheProLeuAlaAspHisLeuAsnSerThr 340
Db 1284 CACGCTTTTACTGCCAGGAGAAATGCGCTTTCTCTGGCTGATCATCTGAACCTCCACT 1343
Qy 341 AsnHisAlaIleValGlnThrLeuValAsnSerValAsnSerLysIleProLysAlaCys 360
Db 1344 AATCATGCCATTGTTCCAGACGTTGGTCAACTCTGTAACTCTAAGATTCTTAAGCAATGC 1403
Qy 361 CysValProThrGluLeuSerAlaIleSerMetLeuTyrLeuAspGluAsnGluLysVal 380
Db 1404 TGTGTCCGACAGAACTCAGTGTCTATCTCGATGCTGTACCTTGACGAGAAATGAAAGGTT 1463
Qy 381 ValLeuLysAsnTyrGlnAspMetValValGluGlyCysGlyCysArg 396
Db 1464 GTATTAAAGAACTATCAGGACATGTTGTGGAGGTTGTGGGTGTGCG 1511

RESULT 13

US-10-886-947-1
; Sequence 1, Application US/10886947
; Publication No. US20050197304A1
; GENERAL INFORMATION:
; APPLICANT: New York University School of Medicine
; APPLICANT: Dicesare, Paul
; TITLE OF INVENTION: Nucleic Acid Therapy To Enhance Cartilage Repair
; FILE REFERENCE: 1049-1-037N
; CURRENT APPLICATION NUMBER: US/10/886,947
; CURRENT FILING DATE: 2004-07-08
; PRIOR APPLICATION NUMBER: 60/485,669
; PRIOR FILING DATE: 2003-07-08
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patent In version 3.1
; SEQ ID NO 1
; LENGTH: 1547
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-886-947-1

Alignment Scores:
Pred. No.: 8,92e-227 Length: 1547
Score: 2098.00 Matches: 396
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
DB:

US-10-801-648-2 (1-396) x US-10-886-947-1 (1-1547)

Qy 1 MetValAlaGlyThrArgCysLeuLeuAlaLeuLeuProGlnValLeuLeuGlyGly 20
Db 324 ATGGTGGCGGAGACCGCTGTCTTCTAGCGTTGCTGTCTCCAGGTCCTCTGGGCGGC 383

Qy 21 AlaAlaGlyLeuValProGluLeuGlyArgGlyPheAlaAlaLeuSerSerGlyArg 40
Db 384 GCGGCTGCGCTGCTTTCGGAGCTGGCGCGAGGAGTTTCGGCGGCGCTGCTCGGCGCGC 443

Qy 41 ProSerSerGlnProSerAspGluValLeuSerGluPheGluLeuLeuArgLeuSerMet 60
Db 444 CCCTCATCCAGCCCTCTGACAGAGTCTGAGCGAGTTGAGTTGCGGCTGCTCAGCATG 503

Qy 61 PheGlyLeuLysGlnArgProThrProSerArgPheAlaValValProProTyrMetLeu 80
Db 504 TTCGGCTGMAAACAGAGACCCACCCAGCAGGAGCGCGTGGTGCCTACATGCTA 563

Qy 81 AspLeuTyrArgArgHisSerGlyGlnProGlySerProAlaProAspHisArgLeuGlu 100
Db 564 GACCTGTATCCAGGCATCTAGGTACGCGGCTCACCGGCCAGACCCAGCCGCTTGAG 623

Qy 101 ArgAlaLeuSerArgAlaAsnThrValArgSerPheHisHisGluGluSerLeuGluGlu 120
Db 624 AGGCGAGCCAGCCGAGCCAACTGTGCGCAGCTTCCACCATGAAGATCTTTGGAGAA 683

Qy 121 LeuProGluThrSerGlyLysThrThrArgArgPhePheAsnLeuSerSerIlePro 140
Db 684 CTACAGAAACGAGTGGGMAAACCAACCCGAGATCTCTCTTAATTTAAGTTCTATCCCC 743

Qy 141 ThrGluGluPheIleThrSerAlaGluLeuGlnValPheArgGluGlnMetGlnAspAla 160
Db 744 ACGGAGAGTTTATCACTTCAGCAGAGCTTCAGGTTTCGAGAGAACAGATGCT 803

Qy 161 LeuGlyAsnAsnSerSerPheHisHisArgIleAsnIleTyrGluIleIleLysProAla 180
Db 804 TTAGGMAACAATAGCAGTTCCATCACCGAATTATATATGAATCATATAAACCTGCA 863

Qy 181 ThrAlaAsnSerLysPheProValThrArgLeuLeuAspThrArgLeuValAsnGlnAsn 200
Db 864 ACAGCCAACTCGAAATTCCTCGTACCAGACTTTTGGACACACAGTTGGTGAATCAGAT 923

Qy 201 AlaSerArgTrpGluSerPheAspValThrProAlaValMetArgTrpThrAlaGlnGly 220
Db 924 GCAAGCAGGTGGGAAAGTTTGTATGTACCCCTGTGTATGCGGTGAGTGCACAGGGA 983

Qy 221 HisAlaAsnHisGlyPheValValGluValAlaHisLeuGluGluLysGlnGlyValSer 240
Db 984 CACGCCAACCATGGATTGCTGGTGGAGTGGCCCACTTGGAGGAGAAACAGGTGTCTCC 1043

Qy 241 LysArgHisValArgIleSerArgSerLeuHisGlnAspGluHisSerTrpSerGlnIle 260
Db 1044 AAGAGCATGTTAGGATAAGCAGTCTTTTGCAACAGATGAACACAGCTGCTCACAGATA 1103

Qy 261 ArgProLeuLeuValThrPheGlyHisAspGlyLysGlyHisProLeuHisLysArgGlu 280
Db 1104 AGGCCATGTCTAGTAATCTTTGGCCATGATGGAAGGCGCATCTCTCCACAAAGAGAA 1163

Qy 281 LysArgGlnAlaLysHisLysGlnArgLysArgLeuLysSerSerCysLysArgHisPro 300
Db 1164 AAAGCTCAGCCAAACACAAACACGCGGAAACGCTTAAGTCCAGCTGTAGAGACACCT 1223

Qy 301 LeuTyrValAspPheSerAspValGlyTrpAsnAspTrpIleValAlaProProGlyTyr 320
Db 1224 TTGTACGTGGACTTCAGTGACGTGGGTGGAAATGACTGGATTGGTCTCCCGGGGTAT 1283

Qy 321 HisAlaPheTyrCysHisGlyGluCysProPheProLeuAlaAspHisLeuAsnSerThr 340
Db 1284 CACGCCCTTTACTGCCACGGAATGCCCTTTCTCTGGCTGATCATCTGAATCCACT 1343

Qy 341 AsnHisAlaIleValGlnThrLeuValAsnSerValAsnSerLysIleProLysAlaCys 360

Db 1344 AATCATGCCATTGTCAGACGTTGGTCAACTCTGTTAACTCTTAAGATTCTTAAGGCATGC 1403

Qy 361 CysValProThrGluLeuSerAlaIleSerMetLeuTyrLeuAspGluAsnGluLysVal 380
Db 1404 TGTGTCCCGCAGAACTCAGTGTCTATCTCGATGCTGTACCTTGACGAGAATGAAGGTT 1463

Qy 381 ValLeuLysAsnTyrGlnAspMetValValGluGlyCysGlyCysArg 396
Db 1464 GTATTAAAGAACTATCAGGACATGTTGTGGAGGGTTGTGGGTGTCTGC 1511

RESULT 14

US-09-804-625-3
; Sequence 3, Application US/09804625
; Publication No. US20030049826A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Elizabeth A.
; Rosen, Vicki A.
; Wozney, John M.
; TITLE OF INVENTION: No. US20030049826A1el BMP Products
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LEGAL AFFAIRS, GENETICS INSTITUTE, INC.
; STREET: 87 CAMBRIDGE PARK DRIVE
; CITY: CAMBRIDGE
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/804,625
; FILING DATE: 09-Mar-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/925,779
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Kapinos, Ellen J.
; REGISTRATION NUMBER: 32,245
; REFERENCE/DOCKET NUMBER: 5160C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-876-1170
; TELEFAX: 617-876-5851
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1607 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo Sapiens
; CELL TYPE: Osteosarcoma Cell Line
; CELL LINE: U-2OS
; IMMEDIATE SOURCE:
; LIBRARY: U2OS cDNA in Lambda GT10
; CLONE: Lambda U2OS-39
; POSITION IN GENOME:
; UNITS: bp
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 356..1546
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 1202..1543
; FEATURE:
; NAME/KEY: mRNA
; LOCATION: 14..1607

FEATURE:
; NAME/KEY: sig peptide
; LOCATION: 356-424
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-804-625-3

Alignment Scores:
Pred. No.: 9,43e-227 Length: 1607
Score: 2098.00 Matches: 396
Percent Similarity: 100.00% Conservat: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-10-801-648-2 (1-396) x US-09-804-625-3 (1-1607)

Qy 1 MetValAlaGlyThrArgCysLeuLeuAlaLeuLeuLeuProGlnValLeuLeuGlyGly 20
Db 356 ATGGTGGCGGAGCCCGCTGCTTCTAGCGTTGCTGCTTCCCGAGGTCCTCTCGGGCGGC 415

Qy 21 AlaAlaGlyLeuValProGluLeuGlyArgGlyPheAlaAlaAlaSerSerGlyArg 40
Db 416 GCGGCTGCGGCTGCTTCCGAGCTGGCGCGCAGGAAGTTCCGCGCGGCTGCTCGGGCGGC 475

Qy 41 ProSerSerGlnProSerAspGluValLeuSerGluPheGluLeuArgLeuSerMet 60
Db 476 CCTCATCCAGCCCTCTGAGGAGTCTGAGCGAGTTGCGAGTTGCGGCTGCTCAGCATG 535

Qy 61 PheGlyLeuLysGlnArgProThrProSerArgAspAlaValValProProTyrMetLeu 80
Db 536 TTGGCGCTGAAACAGACAGACCCACCCAGCAGGAGCGCGTGGTGGTCCCGCTTACATGCTA 595

Qy 81 AspLeuTyrArgArgHisSerGlyGlnProGlySerProAlaProAspHisArgLeuGlu 100
Db 596 GACCTGTATCGAGGACATCTAGGTGAGCGGCGCTCAGCGCGGCTCAGCGCGGCTGAG 655

Qy 101 ArgAlaAlaSerArgAlaAsnThrValArgSerPheHisHisGluGluSerLeuGluGlu 120
Db 656 AGGCGAGCGAGCGGAGCCACACTGTGGCAGCTTCCACCATGAAGATCTTTGGAAGA 715

Qy 121 LeuProGluThrSerGlyLysThrThrArgArgPhePheAsnLeuSerSerIlePro 140
Db 716 CTACAGAAACGAGTGGGAAACACACCGGAGATCTCTTTAAATTAAGTTCTATCCCC 775

Qy 141 ThrGluGluPheIleThrSerAlaGluLeuGlnValPheArgGluGluMetGlnAspAla 160
Db 776 ACGGAGGAGTTATCACTCAGCAGAGCTTACGGTTTCCGAGAACAGATGCAAGATGCT 835

Qy 161 LeuGlyAsnAsnSerSerPheHisHisArgIleAsnIleTyrGluIleLeuLysProAla 180
Db 836 TTAGGAACAATAGCAGTTTCCATCCGAAATTAATATTAATTAATTAATTAATTAATTA 895

Qy 181 ThrAlaAsnSerLysPheProValThrArgLeuLeuAspThrArgLeuValAsnGlnAsn 200
Db 896 ACAGCCAACTCGAAATTCCTCCGTGACAGACTTTTGGACACAGGTTGGTGAATCAGAAT 955

Qy 201 AlaSerArgTTPGluSerPheAspValThrProAlaValMetArgTTPThrAlaGlnGly 220
Db 956 GCAAGCAGGTGGGAAAGTTTGTATGTACCCCGCTGTGATCGGTGAGTGCACAGGGA 1015

Qy 221 HisAlaAsnHisGlyPheValValGluValAlaHisLeuGluGluLysGlnGlyValSer 240
Db 1016 CAGCGCAACCATGGATTCGTGGTGGAGTGGCCACTTGGAGAGAGAACAGGTGTCTCC 1075

Qy 241 LysArgHisValArgIleSerArgSerLeuHisGlnAspGluHisSerTrpSerGlnIle 260
Db 1076 AAGAGACATGTTAGGATAGCAGGCTTTTGGACCAAGATGAACAGCTGGTGCACAGATA 1135

Qy 261 ArgProLeuLeuValThrPheGlyHisAspGlyLysGlyHisProLeuHisLysArgGlu 280
Db 1136 AGGCCATTTGCTAGTAACCTTTTGGCCATGATGGAAGGGCATCTCTCCACAAAAAGAAA 1195

Qy 281 LysArgGlnAlaLysHisLysGlnArgLysArgLeuLysSerSerCysLysArgHisPro 300

Db 1196 AAACGTCAAGCAAAACACAAACAGCGGAAACGCCTTAAGTCAGCTGTAAAGACACCCCT 1255

Qy 301 LeuTyrValAspPheSerAspValGlyTTPAsnAspTTPileValAlaProProGlyTyr 320
Db 1256 TTGTACGTGGAGCTTCAGTGACGTGGGTGGGAATGACTGGATGTGGCTCCCGGGGTAT 1315

Qy 321 HisAlaPheTyrCysHisGlyGluCysProPheProLeuAlaAspHisLeuAsnSerThr 340
Db 1316 CACGCCTTTACTGCCACGGAGATGCCCTTTCTCTGGCTGATCATCTGAACCTCACT 1375

Qy 341 AsnHisAlaIleValGlnThrLeuValAsnSerValAsnSerLysIleProLysAlaCys 360
Db 1376 AATCATGCCATTGTTTCAGACGTTGGTCAACTCTGTTAACCTCTAAGATTCTTAAGCATGC 1435

Qy 361 CysValProThrGluLeuSerAlaIleSerMetLeuTyrLeuAspGluAsnGluLysVal 380
Db 1436 TGTGTCCCGACAGAACTCAGTGCTATCTCGATGCTGTACCTTACGAGATGAAGAGTT 1495

Qy 381 ValLeuLysAsnTyrGlnAspMetValValGluGlyCysGlyCysArg 396
Db 1496 GTATTAAAGAACTATCAGGACATGTTGTGGAGGTTGTGGGTGTGCG 1543

RESULT 15
US-10-397-214-3
; Sequence 3, Application US/10397214
; Publication No. US20040009916A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Elizabeth A.
; APPLICANT: Rosen, Vicki A.
; APPLICANT: Wozney, John M.
; TITLE OF INVENTION: NO. US20040009916A1el BMP Products
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LEGAL AFFAIRS, GENETICS INSTITUTE, INC.
; STREET: 87 CAMBRIDGE PARK DRIVE
; CITY: CAMBRIDGE
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/10/397,214
; FILING DATE: 27-MARCH-2003
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/721,847A
; FILING DATE: 14-JUN-1991
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Kapinos, Ellen J.
; REGISTRATION NUMBER: 32,245
; REFERENCE/DOCKET NUMBER: 5160C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-876-1170
; TELEFAX: 617-876-5851
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1607 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo Sapiens
; CELL TYPE: Osteosarcoma Cell Line
; CELL LINE: U-2OS

```

; IMMEDIATE SOURCE:
; LIBRARY: U2OS cDNA in Lambda GT10
; CLONE: Lambda U2OS-39
; POSITION IN GENOME:
; UNITS: bp
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 356..1546
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 1202..1543
; FEATURE:
; NAME/KEY: mRNA
; LOCATION: 14..1607
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 356..424
; US-10-397-214-3
Alignment Scores:
Pred. No.: 9.43e-227 Length: 1607
Score: 2098.00 Matches: 396
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-10-801-648-2 (1-396) x US-10-397-214-3 (1-1607)
Qy 1 MetValAlaGlyThrArgCysLeuLeuAlaLeuLeuProGlnValLeuLeuGlyGly 20
Db 356 ATGTTGGCCGGAGACCCGCTGCTTCTAGCGTGTGCTTCTCCAGGTCCTCTCTGGGCGGC 415
Qy 21 AlaAlaGlyLeuValProGluLeuGlyArgGlyPheAlaAlaLeuSerSerGlyArg 40
Db 416 GCGGCTGGCCCTGTTCCGGAGCTGGCGCGCAGGAAGTTCCGCGCGGCTGCTCGGCGCGC 475
Qy 41 ProSerSerGlnProSerAspGluValLeuSerGluPheGluLeuLeuArgLeuLeuSerMet 60
Db 476 CCCTCATCCCCAGCCCTCTGACGAGGTCTCTGAGCGAGTTCGAGTTGCGGCTGCTCAGCATG 535
Qy 61 PheGlyLeuLysGlnArgProThrProSerArgAspAlaValValProProTyrMetLeu 80
Db 536 TTCGGCTTGAAACAGAGACCCACCCCGCAGCGGAGCGCCGTTGGTGCCTCATGCTA 595
Qy 81 AspLeuTyrArgArgHisSerGlyGlnProGlySerProAlaProAspHisArgLeuGlu 100
Db 596 GACCTGTATCGACGCACTCAGGTTCAGCGCGGCTCACCGCCCGCCAGACCCCGGTTGGAG 655
Qy 101 ArgAlaAlaSerArgAlaAsnThrValArgSerPheHisHisGluGluSerLeuGluGlu 120
Db 656 AGGCGAGCCAGCCGAGCCCAACACTGTGCGCAGCTTCCACCATGAAGAATCTTTGGAGAA 715
Qy 121 LeuProGluThrSerGlyLysThrThrArgArgPhePheAsnLeuSerSerIlePro 140
Db 716 CTACAGAAACGATGGGAAACAAACCCGAGATCTCTTTAAATTAAGTTCTATCCCC 775
Qy 141 ThrGluGluPheIleThrSerAlaGluLeuGlnValPheArgGluGlnMetGlnAspAla 160
Db 776 ACGGAGGAGTTTATCACTCAGCAGAGCTTCAGGTTCGAGAACAGATGCAAGATGCT 835
Qy 161 LeuGlyAsnAsnSerSerPheHisHisArgIleAsnIleTyrGluIleIleLysProAla 180
Db 836 TTAGGAACCAATAGCAGTTTCATCAGCAATTAATATTTATGAATCATAAACCTGCA 895
Qy 181 ThrAlaAsnSerLysPheProValThrArgLeuLeuAspThrArgLeuValAsnGlnAsn 200
Db 896 ACACCCAACCTCGAAATTTCCCGGTGACCAGACTTTTGGACACACAGTTGGTGAATCAGAA 955
Qy 201 AlaSerArgTrpGluSerPheAspValThrProAlaValMetArgTrpThrAlaGlnGly 220
Db 956 GCAAGCAGGTGGGAAAGTTTTTGATGTACACCCCGCTGTGTATGCGGTGGCTGCACAGGA 1015

```

```

Qy 221 HisAlaAsnHisGlyPheValValGluValAlaHisLeuGluGluLysGlnGlyValSer 240
Db 1016 CAGCCCAACCATGATTCTGGTGGAGTGGCCACCTTGGAGGAGAAACAAGGTGTCTCC 1075
Qy 241 LysArgHisValArgIleSerArgSerLeuHisGlnAspGluHisSerTrpSerGlnIle 260
Db 1076 AAGAGACATGTTAGGATAAGCAGGTCTTTGACCAACAGATGACACAGCTGGTGCAGATA 1135
Qy 261 ArgProLeuLeuValThrPheGlyHisAspGlyLysGlyHisProLeuHisLysArgGlu 280
Db 1136 AGGCCATTGCTAGTAACCTTTTGGCCATGATGGAAGAGGCATCTCTCCACAAAGAGAA 1195
Qy 281 LysArgGlnAlaLysHisLysGlnArgLysArgLeuLysSerSerCysLysArgHisPro 300
Db 1196 AAACGTCAAGCCAAACACAAACAGCGGAAACGCCCTTAAGTCCAGCTGTAAAGAGACACCC 1255
Qy 301 LeuTyrValAspPheSerAspValGlyTyrAsnAspTrpIleValAlaProProGlyTyr 320
Db 1256 TTGTACGTGGACTTCAGTACGTGGGTGGAAATGACTGGATTGTGGCTCCCCGGGTAT 1315
Qy 321 HisAlaPheTyrCysHisGlyGluCysPheProPheProLeuAlaAspHisLeuAsnSerThr 340
Db 1316 CAGCCCTTTTACTGCCACGAGAAATGCCCTTTTCTCTGGCTGATCATCTGAACCTCCACT 1375
Qy 341 AsnHisAlaIleValGlnThrLeuValAsnSerValAsnSerLysIleProLysAlaCys 360
Db 1376 AATCATGCCATTGTTGACAGCTTGGTCAACTCTGTAACTCTAAGATTCTTAAGGCAATGC 1435
Qy 361 CysValProThrGluLeuSerAlaIleSerMetLeuTyrLeuAspGluAsnGluLysVal 380
Db 1436 TGTGTCCCGACAGAACTCAGTGTCTATCTCGATGCTGTACTTGCACGAGATGAAGAAGTT 1495
Qy 381 ValLeuLysAsnTyrGlnAspMetValValGluGlyCysGlyCysArg 396
Db 1496 GTATTAAAGAACTATCAGGACATGTTTGTGGAGGGTTGTGGGTGTCTGC 1543

```

Search completed: January 11, 2006, 02:24:24
Job time : 721 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model
Run on: January 10, 2006, 23:57:41 ; Search time 207 Seconds
(without alignments)
1394.733 Million cell updates/sec

Title: US-10-801-648-2
Perfect score: 2038
Sequence: 1 MVAGTRCILLALLPQLVLLG.....NEKVLKNYQDMVVGCGCR 396

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4637633 seqs, 364532575 residues

Total number of hits satisfying chosen parameters: 9275266

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame_plus_p2n_model -DEV=xlh
-Q=/cgn2_1/USPTO_spool/US10801648/runat_09012006_143121_14860/app_query.fasta_1.583
-DB=Published Applications NA New -QFMT=fastap -SUFFIX=rnpbn -MINMATCH=0.1
-LOOPEXT=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=US10801648 @CGN 1 1 117 @runat 09012006 143121_14860
-NCPU=6 -ICPU=3 -NO MAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DRV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA New.*
1: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
2: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
3: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
4: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
5: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
6: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
7: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
8: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
9: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
10: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|--------|-------------|--------|----|--------------------------------------|
| 1 | 2098 | 100.0 | 1547 | 6 | US-10-650-326B-10 Sequence 10, Appl |
| 2 | 2092 | 99.7 | 1260 | 7 | US-11-051-568-4 Sequence 4, Appl |
| 3 | 1927.5 | 91.9 | 2738 | 7 | US-11-136-527-2371 Sequence 2371, Ap |
| 4 | 1269 | 60.5 | 1751 | 6 | US-10-650-326B-11 Sequence 11, Appl |
| 5 | 1269 | 60.5 | 1788 | 7 | US-11-051-568-6 Sequence 6, Appl |
| 6 | 1259 | 59.8 | 1900 | 7 | US-11-136-527-2142 Sequence 2142, Ap |
| 7 | 1179 | 56.2 | 1586 | 7 | US-11-051-568-18 Sequence 18, Appl |
| 8 | 561.5 | 26.8 | 525 | 7 | US-11-051-568-16 Sequence 16, Appl |

| | | | | | |
|----|-------|------|------|---|--------------------------------------|
| 9 | 554.5 | 26.4 | 1505 | 7 | US-11-051-568-12 Sequence 12, Appl |
| 10 | 546 | 26.0 | 1277 | 7 | US-11-051-568-14 Sequence 14, Appl |
| 11 | 544.5 | 26.0 | 1822 | 6 | US-10-816-768-38 Sequence 38, Appl |
| 12 | 544.5 | 26.0 | 1822 | 6 | US-10-650-326B-17 Sequence 17, Appl |
| 13 | 544.5 | 26.0 | 1822 | 7 | US-11-051-568-1 Sequence 1, Appl |
| 14 | 544.5 | 26.0 | 1878 | 7 | US-11-186-284-9 Sequence 9, Appl |
| 15 | 542 | 25.8 | 1873 | 6 | US-10-650-326B-18 Sequence 18, Appl |
| 16 | 542 | 25.8 | 1873 | 7 | US-11-051-568-24 Sequence 24, Appl |
| 17 | 534 | 25.5 | 2943 | 7 | US-11-000-688-1535 Sequence 1535, Ap |
| 18 | 534 | 25.5 | 5801 | 7 | US-11-000-463-580 Sequence 580, App |
| 19 | 525.5 | 25.0 | 600 | 7 | US-11-136-527-6238 Sequence 6238, Ap |
| 20 | 489.5 | 23.3 | 1926 | 6 | US-10-650-326B-22 Sequence 22, Appl |
| 21 | 489.5 | 23.3 | 1926 | 7 | US-11-051-568-26 Sequence 26, Appl |
| 22 | 487 | 23.2 | 1723 | 6 | US-10-650-326B-20 Sequence 20, Appl |
| 23 | 483 | 23.0 | 1723 | 7 | US-11-051-568-28 Sequence 28, Appl |
| 24 | 466 | 22.2 | 1459 | 7 | US-11-136-527-607 Sequence 607, App |
| 25 | 456.5 | 21.8 | 1004 | 7 | US-11-051-568-10 Sequence 10, Appl |
| 26 | 456 | 21.7 | 1400 | 7 | US-11-136-527-4703 Sequence 4703, Ap |
| 27 | 443.5 | 21.1 | 2703 | 7 | US-11-191-072-1 Sequence 1, Appl |
| 28 | 423 | 20.2 | 1252 | 6 | US-10-131-826A-341 Sequence 341, App |
| 29 | 421 | 20.1 | 3197 | 7 | US-11-000-463-538 Sequence 538, App |
| 30 | 421 | 20.1 | 3283 | 7 | US-11-000-463-66 Sequence 66, Appl |
| 31 | 418 | 19.9 | 1212 | 9 | US-11-091-334-1 Sequence 1, Appl |
| 32 | 397 | 18.9 | 314 | 7 | US-11-051-568-33 Sequence 33, Appl |
| 33 | 395 | 18.8 | 405 | 6 | US-10-816-768-90 Sequence 90, Appl |
| 34 | 385 | 18.4 | 1764 | 7 | US-11-136-527-3392 Sequence 3392, Ap |
| 35 | 383.5 | 18.3 | 2158 | 7 | US-11-136-527-3797 Sequence 3797, Ap |
| 36 | 375.5 | 17.9 | 516 | 7 | US-11-051-568-8 Sequence 8, Appl |
| 37 | 370.5 | 17.7 | 1840 | 7 | US-11-186-284-88 Sequence 88, Appl |
| 38 | 370.5 | 17.7 | 2017 | 6 | US-10-821-234-107 Sequence 107, App |
| 39 | 361.5 | 17.2 | 1419 | 7 | US-11-092-353-7 Sequence 7, Appl |
| 40 | 357.5 | 17.0 | 647 | 6 | US-10-816-768-99 Sequence 99, Appl |
| 41 | 336 | 16.0 | 1437 | 7 | US-11-092-353-8 Sequence 8, Appl |
| 42 | 329 | 15.7 | 745 | 7 | US-11-136-527-1322 Sequence 1322, Ap |
| 43 | 327.5 | 15.6 | 600 | 7 | US-11-136-527-5418 Sequence 5418, Ap |
| 44 | 326.5 | 15.6 | 2429 | 7 | US-11-136-527-2792 Sequence 2792, Ap |
| 45 | 326 | 15.5 | 1400 | 7 | US-11-136-527-6467 Sequence 6467, Ap |

ALIGNMENTS

RESULT 1
US-10-650-326B-10
; Sequence 10, Application US/10650326B
; Publication No. US20050272649A1
; GENERAL INFORMATION:
; APPLICANT: Hruska, Keith A.
; APPLICANT: McCartney, John B.
; APPLICANT: Charette, Marc F.
; TITLE OF INVENTION: CONJOINT ADMINISTRATION OF MORPHOGENS AND ACE INHIBITORS IN
; FILE REFERENCE: JJJ-P01-599
; CURRENT APPLICATION NUMBER: US/10/650,326B
; PRIOR FILING DATE: 2003-08-28
; PRIOR APPLICATION NUMBER: 60/406,431
; FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 1547
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-650-326B-10

| | | | |
|--|-----------|---------------|------|
| Alignment Scores: | | | |
| Pred. No.: | 2,32e+200 | Length: | 1547 |
| Score: | 2098.00 | Matches: | 396 |
| Percent Similarity: | 100.00% | Conservative: | 0 |
| Best Local Similarity: | 100.00% | Mismatches: | 0 |
| Query Match: | 100.00% | Indels: | 0 |
| DB: | 6 | Gaps: | 0 |
| US-10-801-648-2 (1-396) x US-10-650-326B-10 (1-1547) | | | |

Qy 1 MetValalaGlyThrArgCysLeuLeuAlaLeuLeuLeuProGlnValLeuLeuGlyGly 20
Db 324 ATGGTGGCCGGAGACCCGCTGCTTCTAGCGTGTGCTTCTCCAGGTCCTCTGGGGCGC 383
Qy 21 AlaAlaGlyLeuValProGluLeuGlyArgArgLysPheAlaAlaAlaSerSerGlyArg 40
Db 384 CGGCTGGCCCTCGTTCCGGAGTCGGCCGAGGAGTTCCGGCGGGCGTCTGGGGCGC 443
Qy 41 ProSerSerGlnProSerAspGluValLeuSerGluPheGluLeuArgLeuLeuSerMet 60
Db 444 CCTCATCCAGCCCTCTGACAGGCTCTGACAGGTTCCAGGAGTTCCAGTTGGCGCTGCTCAGCATG 503
Qy 61 PheGlyLeuLysGlnArgProThrProSerArgAspAlaValValProProTyrrMetLeu 80
Db 504 TTCGGCTGAAACAGACAGACCCACCCAGCAGGAGACCGCGTGGTCCCTCATGCTA 563
Qy 81 AspLeuTyrrArgArgHisSerGlyGlnProGlySerProAlaProAspHisArgLeuGlu 100
Db 564 GACCTGTATCGACGCACTCAGTTCAGCGGGCTCACCCGCCAGACACCGGTTGGAG 623
Qy 101 ArgAlaAlaSerArgAlaAsnThrValArgSerPheHisGluGluSerLeuGluGlu 120
Db 624 AGGCAGCCAGCCGAGCAACACTGTGCGCAGCTTCCACCATGAAGAATCTTTGGAAGA 683
Qy 121 LeuProGluThrSerGlyLysThrArgArgPhePheAsnLeuSerSerIlePro 140
Db 684 CTACCAAGACGATGGGAAACAAACCCGGAGATCTCTTTTAATTTAAGTTCTATCCCC 743
Qy 141 ThrGluGluPheIleThrSerAlaGluLeuGlnValPheArgGluGlnMetGlnAspAla 160
Db 744 ACGAGAGTTTATCACTCAGCAGAGCTTCAGGTTTCCGAGAACAGATGCAGATGCT 803
Qy 161 LeuGlyAsnAsnSerSerPheHisArgIleAsnIleTyrrGluIleLysProAla 180
Db 804 TTAGGAAACAATAGCAGTTTCCATCAGCAATTAATATTTATGAATCATAAAACTGCA 863
Qy 181 ThrAlaAsnSerLysPheProValThrArgLeuLeuAspThrArgLeuValAsnGlnAsn 200
Db 864 ACAGCCAACTCGAAATTTCCCGTCGACAGACTTTTGGACACCAAGTTGGTGAATCAGAAT 923
Qy 201 AlaSerArgTTPGluSerPheAspValThrProAlaValMetArgTTPThrAlaGlnGly 220
Db 924 GCAGCAGTGGGAAAGTTTGTATGTACCCCGCTGTGATCGCGTGCAGTGCACAGGA 983
Qy 221 HisAlaAsnHisGlyPheValValGluValAlaHisLeuGluGluLysGlnGlyValSer 240
Db 984 CAGCCCAACCATGATTCGTGTGGAAGTGGCCCACTTGGAGGAGAAACAAGGTGTCTCC 1043
Qy 241 LysArgHisValArgIleSerArgSerLeuHisGlnAspGluHisSerTrpSerGlnIle 260
Db 1044 AAGACATGTTAGGTAAGCAGGTCTTTGACCAAGATGAACAGCTGGTCTCAGATA 1103
Qy 261 ArgProLeuLeuValThrPheGlyHisAspGlyLysGlyHisProLeuHisLysArgGlu 280
Db 1104 AGGCATTTGTAGTAATCTTTGGCCATGATGAAAGGCGATCTCTCCACAAAGAGAA 1163
Qy 281 LysArgGlnAlaLysHisLysGlnArgLysArgLeuLysSerSerCysLysArgHisPro 300
Db 1164 AAAGCTCAAGCCAAACAAACAGCGGAAACGCCTTAAGTCCAGCTGTAGAGACACCCCT 1223
Qy 301 LeuTyrrValAspPheSerAspValGlyTrpAsnAspTrpIleValAlaProProGlyTyrr 320
Db 1224 TTGTACGTGGACTTTCAGTACGTGGGTGGATGACTGGAATTTGGTCTCCCGGGGTAT 1283
Qy 321 HisAlaPheTyrrCysHisGlyGluCysProPheProLeuAlaAspHisLeuAsnSerThr 340
Db 1284 CAGCCCTTTACTGCCACGGAGATGCCCTTTCTCTGGCTGATCATCTGAACTCCACT 1343
Qy 341 AsnHisAlaIleValGlnThrLeuValAsnSerValAsnSerTyrrIleProTyrrAlaCys 360
Db 1344 AATCATGCCATTGTTACAGCGTTGCTCACTCTGTTAACTCTAAGATTCCTTAAGGCATGC 1403

Qy 361 CysValProThrGluLeuSerAlaIleSerMetLeuTyrrLeuAspGluAsnGluLysVal 380
Db 1404 TGTGTCCGAGAGACTCAGTCTATCTCATGCTGTACTTGTACGAGATGAAAAGTT 1463
Qy 381 ValLeuLysAsnTyrrGlnAspMetValValGluGlyCysGlyCysArg 396
Db 1464 GTATTAAAGAACTATCAGGACATGTTGTGGAGGGTTGTGGGTGTCGC 1511

RESULT 2
US-11-051-568-4
; Sequence 4, Application US/11051568
; Publication No. US20050255141A1
; GENERAL INFORMATION:
; APPLICANT: OPPERMAN, HERMANN
; OZKAYNAK, ENGIN
; KUBERASAMPATH, THANGAVEL
; RUEGER, DAVID C.
; PANG, ROY H.L.
; TITLE OF INVENTION: OSTEOGENIC DEVICES
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TESTA, HURWITZ & THIBEAULT
; STREET: 125 HIGH STREET
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: U.S.A.
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/051.568
; FILING DATE: 04-Feb-2005
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 10/321,799
; FILING DATE: 17-DEC-2002
; APPLICATION NUMBER: US 09/148,925
; FILING DATE: 8-SEP-1998
; APPLICATION NUMBER: US 08/449,699
; FILING DATE: 24-MAY-1995
; APPLICATION NUMBER: US 08/147,023
; FILING DATE: 1-NOV-1993
; APPLICATION NUMBER: US 07/841,646
; FILING DATE: 21-FEB-1992
; APPLICATION NUMBER: US 07/827,052
; FILING DATE: 28-JAN-1992
; APPLICATION NUMBER: US 07/579,865
; FILING DATE: 7-SEP-1990
; APPLICATION NUMBER: US 07/621,849
; FILING DATE: 4-DEC-1990
; APPLICATION NUMBER: US 07/621,988
; FILING DATE: 4-DEC-1990
; APPLICATION NUMBER: US 07/810,560
; FILING DATE: 20-DEC-1991
; APPLICATION NUMBER: US 07/569,920
; FILING DATE: 20-AUG-1990
; APPLICATION NUMBER: US 07/600,024
; FILING DATE: 18-OCT-1990
; APPLICATION NUMBER: US 07/599,543
; FILING DATE: 18-OCT-1990
; APPLICATION NUMBER: US 07/616,374
; FILING DATE: 21-NOV-1990
; APPLICATION NUMBER: US 07/483,913
; FILING DATE: 22-FEB-1990
; APPLICATION NUMBER: US 07/179,406
; FILING DATE: 08-APR-1988
; APPLICATION NUMBER: US 07/232,630
; FILING DATE: 15-AUG-1988
; APPLICATION NUMBER: US 07/315,342
; FILING DATE: 23-FEB-1989

APPLICATION NUMBER: US 07/660,162
 FILING DATE: 22-FEB-1991
 APPLICATION NUMBER: US 07/422,699
 FILING DATE: 17-OCT-1989
 APPLICATION NUMBER: US 07/422,613
 FILING DATE: 17-OCT-1989
 APPLICATION NUMBER: US 07/422,623
 FILING DATE: 17-OCT-1989
 ATTORNEY/AGENT INFORMATION:
 NAME: DIANA M. STEEL
 REGISTRATION NUMBER: 43,153
 REFERENCE/DOCKET NUMBER: STR-001CP6C3
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617/248-7000
 TELEFAX: 617/248-7100
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1260 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: HOMO SAPIENS
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 9..1196
 OTHER INFORMATION: /function= "OSTEOGENIC PROTEIN"
 /product= "CBMP2A"
 /note= "CBMP2A (CDNA)"
 SEQUENCE DESCRIPTION: SEQ ID NO: 4:

US-11-051-568-4
 Alignment Scores:
 Pred. No.: 6,9e-200 Length: 1260
 Score: 2092.00 Matches: 395
 Percent Similarity: 99.75% Conservatives: 0
 Best Local Similarity: 99.75% Mismatches: 1
 Query Match: 99.71% Indels: 0
 Gaps: 0
 US-10-801-648-2 (1-396) x US-11-051-568-4 (1-1260)

Qy 141 ThrGluGluPheLeuThrSerAlaGluLeuGlnValPheArgGluGlnMetGlnAspAla 160
 Db 429 ACGGAGGAGTTTATCACTCAGCAGAGCTTCAGGTTTTCGAGAACAGATGCAAGTCT 488
 Qy 161 LeuGlyAsnAsnSerSerPheHisArgIleAsnIleTyrGluIleIleLeuProAla 180
 Db 489 TTAGGAACAATAGCAGTTTCCATCCAGAAATTAATATTATTAAGAAATCATAAACCTGCA 548
 Qy 181 ThrAlaAsnSerLysPheProValThrArgLeuLeuAspThrArgLeuValAsnGlnAsn 200
 Db 549 ACAGCCAACTCGAAATTCCTCGTGCAGCAGCTTTTGGACACACAGGTTGGTGAATCAGAT 608
 Qy 201 AlaSerArgTrpGluSerPheAspValThrProAlaValMetArgTrpThrAlaGlnGly 220
 Db 609 GCAAGCAGGTGGGAAAGTTTGTATGTCACTCCCTGTGATCGGTGACATGCAACAGGA 668
 Qy 221 HisAlaAsnHisGlyPheValValGluValAlaHisIleGluGluValGlnGlyValSer 240
 Db 669 CACGCCAACCATGATTCGTGTGGTGGAGTGGCCCACTTGGAGGAGAAACAAGGTGTCTCC 728
 Qy 241 LysArgHisValArgIleSerArgSerLeuHisGlnAspGluHisSerTrpSerGlnIle 260
 Db 729 AAGAGACATGTAGATAGCAGGCTCTTGCACCAAGATGAACACAGCTGTGTACAGATA 788
 Qy 261 ArgProLeuValThrPheGlyHisAspGlyLysGlyHisProLeuHisLysArgGlu 280
 Db 789 AGGCCATTGCTAGTAACCTTTTGGCCATGATGGAAGAGGGCATCTCTCCACAAAGAGAA 848
 Qy 281 LysArgGlnAlaLysHisLysGlnArgLysArgLysSerSerSerCysLysArgHisPro 300
 Db 849 AAACGTCAAGCCAAACACAAACACGCGGAAACCGCTTAAGTCCAGCTGTGAAGAGACACCT 908
 Qy 301 LeuTyrValAspPheSerAspValGlyTrpAsnAspTrpIleValAlaProGlyTyr 320
 Db 909 TTGTACGTGGACTTCAGTGACGTGGGTGGAGTGAATGATGATGTGGTCTCCCGGGGTAT 968
 Qy 321 HisAlaPheTyrCysHisGlyGluCysProPheProLeuAlaAspHisLeuAsnSerThr 340
 Db 969 CACGCCCTTTTACTGCCAGGAGATGCCCTTTCTCTGGCTGATCATCTGAACCTCCACT 1028
 Qy 341 AsnHisAlaIleValGlnThrLeuValAsnSerValAsnSerLysIleProLysAlaCys 360
 Db 1029 AATCATGCCATTGTTTCAGACCGTTGTCCAACTCTGTTAACCTCTAAGATTCTTAAGGCATGC 1088
 Qy 361 CysValProThrGluLeuSerAlaIleSerMetLeuTyrLeuAspGluAsnGluLysVal 380
 Db 1089 TGTGTCCCGACAGAACTCAGTGCTATCTCGATGCTGTACCTTGACGAGAAATGAAGGTT 1148
 Qy 381 ValLeuLysAsnTyrGlnAspMetValValGluGlyCysGlyCysArg 396
 Db 1149 GTATTAAAGAACTATCAGGATATGGTTGTGGAGGGTTGTGGGTGTCTGC 1196
 RESULT 3
 US-11-136-527-2371
 ; Sequence 2371, Application US/11136527
 ; Publication No. US20050287570A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wyeth
 ; APPLICANT: Mounts, William M
 ; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
 ; FILE REFERENCE: 031896-041000 (AM101086)
 ; CURRENT APPLICATION NUMBER: US/11/136,527
 ; CURRENT FILING DATE: 2005-05-25
 ; PRIOR APPLICATION NUMBER: US 60/574,294
 ; PRIOR FILING DATE: 2005-05-26
 ; NUMBER OF SEQ ID NOS: 362830
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 2371
 ; LENGTH: 2738
 ; TYPE: DNA
 ; ORGANISM: Rattus norvegicus
 US-11-136-527-2371

Qy 1 MetValAlaGlyThrArgCysLeuLeuAlaLeuLeuProGlnValLeuLeuGlyGly 20
 Db 9 ATGGTGGCGCGACCGCTGCTTCTAGCGTTGCTCTTCCCGAGGCTCTCTCGGGCGGC 68
 Qy 21 AlaAlaGlyLeuValProGluLeuGlyArgArgLysPheAlaAlaAsnSerSerGlyArg 40
 Db 69 GCGGCTGGCCTCGTTCCGAGCTGGCGCGCAGGAAAGTTTCGCGCGCGCGCTGTCGCGCGCGC 128
 Qy 41 ProSerSerGlnProSerAspGluValLeuSerGluPheGluLeuArgLeuLeuSerMet 60
 Db 129 CCTCATTCACCCCTCTGACAGAGGTCTGACGAGTTCGAGTTCGGGCTGCTGACATG 188
 Qy 61 PheGlyLeuLysGlnArgProThrProSerArgAspAlaValProProTyrMetLeu 80
 Db 189 TTCCGCGCTGAACACAGACACCCACCCAGCAGCGCGCTGCTGCGCGCGCTACATGCTA 248
 Qy 81 AspLeuTyrArgArgHisSerGlnProGlySerProAlaProAspHisArgLeuGlu 100
 Db 249 GACCTGTATCGCAGGCACTCGGGTCAGCGCGGCTCACCCGCGCCAGACCCAGCGTTGGAG 308
 Qy 101 ArgAlaAlaSerArgAlaAsnThrValArgSerPheHisGluGluSerLeuGluGlu 120
 Db 309 AGGCGACG 368
 Qy 121 LeuProGluThrSerGlyLysThrArgArgPhePheAsnLeuSerSerIlePro 140
 Db 369 CTACCGAAGACGAGTGGGAAACACACCCCGAGATCTCTTTAAATTAAGTCTATCC 428

Alignment Scores:

| | | | |
|------------------------|-----------|---------------|------|
| Pred. No.: | 7,038-183 | Length: | 2738 |
| Score: | 1927.50 | Matches: | 361 |
| Percent Similarity: | 95.71% | Conservative: | 18 |
| Best Local Similarity: | 91.16% | Mismatches: | 16 |
| Query Match: | 91.87% | Indels: | 3 |
| DB: | 7 | Gaps: | 2 |

US-10-801-648-2 (1-396) x US-11-136-527-2371 (1-2738)

| | | | |
|----|------|---|------|
| Qy | 1 | MetValAlaGlyThrArgCysLeuLeuAlaLeuLeuLeuProGlnValLeuLeuGlyGly | 20 |
| Db | 348 | ATGTGGCGGGACCGCTGCTCTTCTAGTGTGTGCTTCCACAGTCTCTCTGGCGCGC | 407 |
| Qy | 21 | AlaAlaGlyLeuValProGluLeuGlyVArgArgLysPheAlaAlaAAserSerGlyArg | 40 |
| Db | 408 | CGGCGCGGCTCATTTCCGGAGCTGGCGCGCAAGAAGTTCCGCGGGCATCSGGC | 461 |
| Qy | 41 | ProSerSerGlnProSerAspGluValLeuSerGluPheGluLeuArgLeuLeuSerMet | 60 |
| Db | 462 | CCCTTATCCCGGCTCTCGAGGACGCTCTCAGCGAGTTTGAGTTGAGGCTGCTCAGCATG | 521 |
| Qy | 61 | PheGlyLeuLysGlnArgProThrProSerArgAspAlaValValProProTyrMetLeu | 80 |
| Db | 522 | TTTGGCCTGAAGCAGAGACCCACCCCGCAAGGACGTCGTGTGTCGCCCTTATATGCTC | 581 |
| Qy | 81 | AspLeuTyrArgArgHisSerGlyGlnProGlySerProAlaProAspHisArgLeuGlu | 100 |
| Db | 582 | GACCTGTACCCCGGCATCTCGGCGCAGCAGGCGCTCGCCCCAGACACCGGCTGGAG | 641 |
| Qy | 101 | ArgAlaAlaSerArgAlaAsnThrValArgSerPheHisGluGluSerLeuGluGlu | 120 |
| Db | 642 | AGGCGAGCAGCGCGCCAAACACCGTGCTCAGCTTCCATCAGAGAAGCCATCGAGAA | 701 |
| Qy | 121 | LeuProGluThrSerSerGlyLysThrThrArgArgPhePheAsnLeuSerSerIlePro | 140 |
| Db | 702 | CTTTTCAGAAATAGATGGGAAACTTTCCGACGCTTCTTCTTCAATTTAAGTTCTGTCCCT | 761 |
| Qy | 141 | ThrGluGluPheIleThrSerAlaGluLeuGlnValPheArgGluGluMetGlnAspAla | 160 |
| Db | 762 | ACTGATGAGTTTCTCACATCTGCAGAGCTCCAGATTTTTCGGGAACAAATGAGGAAGCT | 821 |
| Qy | 161 | LeuGlyAsnAsnSerSerPheHisArgIleAsnIleTyrGluIleIleLysProAla | 180 |
| Db | 822 | TTGGGA--AATAGTAGTTTCCAGCACCGAATTAATATTTATGAAATTTAAGCGCTGCC | 878 |
| Qy | 181 | ThrAlaAsnSerLysPheProValThrArgLeuLeuAspThrArgLeuValAsnGlnAsn | 200 |
| Db | 879 | ACAGCCAGCTCAAAATTTCTGTGTACACAGACTATTGGACACAGGTTAGTGACTCAGAAC | 938 |
| Qy | 201 | AlaSerArgTyrGluSerPheAspValThrProAlaValMetArgTyrThrAlaGlnGly | 220 |
| Db | 939 | ACAAGTCAGTGGGAGAGCTTTGATGTACCCCGGCTGTGATGCGATGGACACACAGGA | 998 |
| Qy | 221 | HisAlaAsnHisGlyPheValValGluValAlaHisLeuGluGluLysGlnGlyValSer | 240 |
| Db | 999 | CACACCAACCATGGTTTGTGGTGGAGTGCGCCACTTAGAGGAGAGCCAGGTGTCTCC | 1058 |
| Qy | 241 | LysArgHisValArgIleSerArgSerLeuHisGlnAspGluHisSerTrpSerGlnIle | 260 |
| Db | 1059 | AAGAGACATGTGAGGATTTAGCAGGTCTTTTGACCAAGATGAACACAGCTGGTCTCAGGTA | 1118 |
| Qy | 261 | ArgProLeuLeuValThrPheGlyHisAspGlyLysGlyHisProLeuHisLysArgGlu | 280 |
| Db | 1119 | AGACCATGTGTAGTGACTTTTGGCCACGACCGGTAAAGACATCACTCCAACACGAGA | 1178 |
| Qy | 281 | LysArgGlnAlaLysHisLysGlnArgLysArgLeuLysSerSerCysLysArgHisPro | 300 |
| Db | 1179 | AAGCGTCAAGCCAAACAAACACGCGAAGCGTCTTAAGTCCAGCTGCAAAAGCACCCCT | 1238 |
| Qy | 301 | LeuTyrValAspPheSerAspValGlyTyrPasnAspTrpIleValAlaProProGlyTyr | 320 |
| Db | 1239 | TTGTATGTGGACTTCAGTGATGTGGGTGGAAATGACTGATCGTGGGCCCTCCAGGCTAT | 1298 |


```

;
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: HOMO SAPIENS
; TISSUE TYPE: HIPPOCAMPUS
;
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 403..1626
; IDENTIFICATION METHOD: experimental
; OTHER INFORMATION: /function= "OSTEOGENIC PROTEIN"
; /product= "CMP2B"
; /evidence= EXPERIMENTAL
; /note= "CMP2B (CDNA)"
;
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-11-051-568-6

Alignment Scores:
Pred. No.: 5.29e-117 Length: 1788
Score: 1269.00 Matches: 258
Percent Similarity: 73.19% Conservative: 45
Best Local Similarity: 62.32% Mismatches: 87
Query Match: 60.49% Indels: 24
DB: 7 Gaps: 10

US-10-801-648-2 (1-396) x US-11-051-568-6 (1-1788)

Qy 1 MetValAlaGlyThrArgCysLeuAlaLeuLeuProGlnValLeuLeuGlyGly 20
Db 403 ATGATTCTGTGTACCGAATGCTGATGCTGTTTATTATGCTCAAGTCTCTAGAGGC 462

Qy 21 Ala-----AlaGlyLeuValProGluLeuGlyArgArgLysPheAla-----Ala 35
Db 463 GCGAGCCATGCTAGTTTGATACCTGAGACGGGGAGAAAAGTCCGCGAGATTTCAGGGC 522

Qy 36 AlaSerSerGlyArgProSerSerGlnProSerAspGluValLeuSerGluPheGluLeu 55
Db 523 CACCGGGAGGACCGCGCTCAGGGCAG---AGCCATGAGTCTCTGCGGAGCTTCGAGGCG 579

Qy 56 ArgLeuLeuSerMetPheGlyLeuLysGlnArgProThrProSerArgAspAlaValVal 75
Db 580 ACATTCTGCGAGATGTTGGCTGCGCGCGCGCGCGAGCTTAGCAAGATGCGCTCAT 639

Qy 76 ProProTyrMetLeuAspLeuTyrArgArgHisSerGlyGln----- 89
Db 640 CCGGACTACATCGCGGATCTTTACCGGCTTCAGTCTGGGAGGAGGAGGAGAGCAGATC 699

Qy 90 -----ProGlySerProAlaProAspHisArgLeuGluArgAlaAlaSerArgAlaAsn 107
Db 700 CACAGCACTGCTCTTGAGTATCTCT-----GAGCGCGCGCGCGAGCGCGGCGCAAC 747

Qy 108 ThrValArgSerPheHisHisGluGluSerLeuGluGluProGluThrSerGlyLys 127
Db 748 ACCGTGAGGAGCTTCCACCAGAGACATCTGGAGAACATCCCGAGGACCATGTGAAAC 807

Qy 128 ThrThrArgArgPhePheAsnLeuSerSerIleProThrGluGluPheIleThrSer 147
Db 808 TCTGCTTTCTCTCTCTTTAACTCAGCAGCATCTCCAGAGAGTCTCCAGAGAGTCTCTCT 867

Qy 148 AlaGluLeuGlnValPheArgGluGlnMetGlnAspAlaLeuGlyAsnAsnSerPhe 167
Db 868 GCAGAGCTTCGGCTCTTCCGGGAGGAGGTGACCGAGGCGCTGATTTGGAAAGGGGCTTC 927

Qy 168 HisHisArgIleAsnIleTyrGluIleIleLys---ProAlaThrAlaAsnSerLysPhe 186
Db 928 ---CACCGTATAACATTATGAGTTATGAGCCCGCCAGCAGAGTGGTCCCTGGGCAC 984

Qy 187 ProValThrArgLeuLeuAspThrArgLeuValAsnGlnAsnAlaSerArgTyrPgluSer 206
Db 985 CTCATCACGACTACTGACACGAGCTGGTCCACCAATGTGACACGCGTGGGAAACT 1044

Qy 207 PheAspValThrProAlaValMetArgTrpThrAlaGlnGlyHisAlaAsnHisGlyPhe 226

```

```

Db 1045 TTTGATGTGAGCCTCGGTCCTTCGCTGGACCGGAGAGAGCCAAATATGGGCTA 1104
Qy 227 ValValGluValAlaHisLeuGluGluLysGlnGlyValSerLysArgHisValArgIle 246
Db 1105 GCCATTGAGGTGACTACCTCCATCAGACTCGGACCCACAGGGCCAGCATGTCCAGGATT 1164
Qy 247 SerArgSerLeuHisGlnAspGluHisSerTrpSerGlnIleArgProLeuLeuValThr 266
Db 1165 AGCCGATCGTTTACCTCAAGGAGTGGGAATTTGGGCCCGAGCTCCGCCCTCTCTGTCACC 1224
Qy 267 PheGlyHisAspGlyLysGlyHisProLeu-----HisLysArgGluLysArgGlnAla 284
Db 1225 TTTGGCCATGATGGCGGGCCATGCTTGACCGACCGCGAGGGCCAGCGTAGCCCT 1284
Qy 285 Lys---HisLysGlnArgLysArgLeuLysSer---SerCysLysArgHisProLeuTyr 302
Db 1285 AAGCATCACTCACAGCGGGCCAGGAAGAATAAGAACTGCCGGCGCCACTCGCTCTAT 1344
Qy 303 ValAspPheSerAspValGlyTrpAsnAspTrpIleValAlaProGlyTyrHisAla 322
Db 1345 GTGGACTTCAGCGATGTGGGCTGGAATGACTGGATTTGTGCCCCACAGGCTACCGGCC 1404
Qy 323 PheTyrCysHisGlyGluCysProPheProLeuAlaAspHisLeuAsnSerThrAsnHis 342
Db 1405 TTCTACTGCCATGGGAGTGCCTTCCACTGGCTGACCACTCAACTCAACCAACCAT 1464
Qy 343 AlaIleValGlnThrLeuValAsnSerValAsnSerLysIleProLysAlaCysCysVal 362
Db 1465 GCCATTGTGCAGACCTTGTTCATTTCTCAATTTCCAGTATCCCAAGCCGTGTTGTG 1524
Qy 363 ProThrGluLeuSerAlaIleSerMetLeuTyrLeuAspGluAsnGluLysValValLeu 382
Db 1525 CCCACTGAACGTGAGTGCATCTCCATGCTGTACCTGATGATGATAGTGGTACTG 1584
Qy 383 LysAsnTyrGlnAspMetValValGluGlyCysGlyCysArg 396
Db 1585 AAAAATTATCAGGAGATGGTAGTAGAGGATGTGGGTGCCGC 1626

RESULT 6
US-11-136-527-2142
; Sequence 2142, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2142
; LENGTH: 1900
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-2142

Alignment Scores:
Pred. No.: 1.47e-115 Length: 1900
Score: 1255.00 Matches: 256
Percent Similarity: 72.46% Conservative: 44
Best Local Similarity: 61.84% Mismatches: 90
Query Match: 59.82% Indels: 24
DB: 7 Gaps: 10

US-10-801-648-2 (1-396) x US-11-136-527-2142 (1-1900)

Qy 1 MetValAlaGlyThrArgCysLeuLeuAlaLeuLeuProGlnValLeuLeuGlyGly 20
Db 401 ATGATTCTGTGTACCGAATGCTGATGCTGTTTATTATGCTCAAGTCTCTAGAGGC 460

```



```

; APPLICATION NUMBER: US 07/660,162
; FILING DATE: 22-FEB-1991
; APPLICATION NUMBER: US 07/422,699
; FILING DATE: 17-OCT-1989
; APPLICATION NUMBER: US 07/422,613
; FILING DATE: 17-OCT-1989
; APPLICATION NUMBER: US 07/422,623
; FILING DATE: 17-OCT-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: DIANA M. STEEL
; REGISTRATION NUMBER: 43,153
; REFERENCE/DOCKET NUMBER: STK-001CP6C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/248-7000
; TELEFAX: 617/248-7100
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1586 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1257
; OTHER INFORMATION: /function= "OSTEOGENIC PROTEIN"
; /product= "CBMP2B-2"
; /note= "CBMP2B-2 - FUSION"
; SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-11-051-568-18

Alignment Scores:
Pred. No.: 4,88e-108 Length: 1586
Score: 1179.00 Matches: 233
Percent Similarity: 74.86% Conservative: 38
Best Local Similarity: 64.36% Mismatches: 73
Query Match: 56.20% Indels: 18
DB: 7 Gaps: 7

US-10-801-648-2 (1-396) x US-11-051-568-18 (1-1586)

Qy 48 GluValLeuSerGluPheGluLeuArgLeuSerMetPheGlyLeuLysGlnArgPro 67
Db |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 187 GAGCTCTCGGGAGCTTCGAGCGGACACTTCGAGATGTTTGGGCTGCGCGCGCGCG 246
Db |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 68 ThrProSerArgAspAlaValProProTyrMetLeuAspLeuTyrArgArgHisSer 87
Db |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 247 CAGCTAGCAGAGTGGCGTCACTTCGGGACTACATGCGGATCTTTACCGGCTTCAGTCT 306
Db |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 88 GlyGln-----ProGlySerProAlaProAspHisArgLeu 99
Db |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 307 GGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 354
Db |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 100 GluArgAlaAlaSerArgAlaAsnThrValArgSerPheHisGluGluSerLeuGlu 119
Db |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 355 GAGCGCGCGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 414
Db |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 120 GluLeuProGluThrSerGlyLysThrThrArgArgPhePheAsnLeuSerSerIle 139
Db |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 415 AACATCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 474
Db |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 140 ProThrGluGluPheIleThrSerAlaGluLeuGlnValPheArgGluGlnMetGlnAsp 159
Db |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 475 CCTGAGAACGAGGCGATCTCTCTCGAGAGCTTCGGCTCTTCGGGAGGAGGAGGAGGAG 534
Db |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 160 AlaLeuGlyAsnAsnSerSerPheHisArgIleAsnIleTyrGluIleLys--- 178
Db |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 535 GGCCCTGATTGGGAAAGGGGCTTC---CACGATATAACATTATGAGGTTATGAGGCC 591
Db |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 179 ProAlaThrAlaAsnSerLysPheProValThrArgLeuLeuAspThrArgLeuValAsn 198
Db |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

```

```

Db 592 CCAGCAGAGTGGTGCTGGGCGACCTCATCACAGCACTACTGGACACAGAGACTGGTCCAC 651
Qy 199 GlnAsnAlaSerArgTyrGluSerPheAspValThrProAlaValMetArgTyrThrAla 218
Db |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 652 CACAATGTGACAGCGTGGGAAACTTTTGTGAGCCCTCGGTCCTTCGCTGAGCCCGG 711
Db |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 219 GlnGlyHisAlaAsnHisGlyPheValValGluValAlaHisLeuGluLysGlnGly 238
Db |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 712 GAGAGCAGCAGCAACTATGGCTAGCCATTGAGGTGACTCACCTCCATCAGACTCGGACC 771
Qy 239 ValSerLysArgHisValArgIleSerArgSerLeuHisGlnAspGluHisSerTyrSer 258
Db |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 772 CACGAGGCGCAGCATGTGAGGATTAGCGATCGTTACTCAAGGAGTGGGAATTGGGCC 831
Qy 259 GlnIleArgProLeuLeuValThrPheGlyHisAspGlyLysGlyHisProLeu----- 276
Db |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 832 CAGCTCGGCGCCCTCTCTGGTCACTTTGGCCATGATGGCGGCGGCGCATGCCCTTACCCGA 891
Qy 277 HisLysArgGluLysArgGlnAlaLys---HisLysGlnArgLysArgLeuLysSer--- 294
Db |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 892 CGCGGAGGCGCAGCGTAGCCCTTACGATCACTCACAGCGGCGCAGAGAGAGATAAG 951
Qy 295 SerCysLysArgHisProLeuTyrValAspPheSerAspValGlyTyrAsnAspTyrIle 314
Db |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 952 AACTGCGCGCGCACCTCGCTCTATGTGACTTCAGCGATGTGGCTGGAATGACTGGATT 1011
Qy 315 ValAlaProGlyTyrHisAlaPheTyrCysHisGlyGluCysProPheProLeuAla 334
Db |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 1012 GTGGCGCCACAGCTACAGGCGCTTCTACTGCGCATGGGACTGCCCTTTCCACTGGCT 1071
Qy 335 AspHisLeuAsnSerThrAsnHisAlaIleValGlnThrLeuValAsnSerValAsnSer 354
Db |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 1072 GACCACCTCAACTCAACCAACCATGCCATTGTGAGACCTTGGTCAATTCGTCAATTC 1131
Qy 355 LysIleProLysAlaCysCysValProThrGluLeuSerAlaIleSerMetLeuTyrLeu 374
Db |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 1132 AGTATCCCAAGCGCTGTGTGCGCCACTGAAGTGAAGTGCATCTCCATGCTGACTGTG 1191
Qy 375 AspGluAsnGluLysValValLeuLysAsnTyrGlnAspMetValValGluGlyCysGly 394
Db |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 1192 GATGAGTATGATAAGGTGGTACTGAAATAATATCAGGAGATGGTAGTAGAGGATGTGGG 1251
Qy 395 CysArg 396
Db 1252 TGCGCG 1257

RESULT 8
US-11-051-568-16
; Sequence 16, Application US/11051568
; Publication No. US20050255141A1
; GENERAL INFORMATION:
; APPLICANT: OPPERMANN, HERMANN
; OZKAYNAK, ENGIN
; KUBERASAMPATH, THANGAVEL
; RUEGER, DAVID C.
; PANG, ROY H.L.
; TITLE OF INVENTION: OSTEOGENIC DEVICES
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TESTA, HURWITZ & THIBEAULT
; STREET: 125 HIGH STREET
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: U.S.A.
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/051,568
; FILING DATE: 04-Feb-2005

```


CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
FILING DATE: 17-DEC-2002
APPLICATION NUMBER: US 09/148,925
FILING DATE: 8-SEP-1998
APPLICATION NUMBER: US 08/449,699
FILING DATE: 24-MAY-1995
APPLICATION NUMBER: US 08/147,023
FILING DATE: 1-NOV-1993
APPLICATION NUMBER: US 07/841,646
FILING DATE: 21-FEB-1992
APPLICATION NUMBER: US 07/827,052
FILING DATE: 28-JAN-1992
APPLICATION NUMBER: US 07/579,865
FILING DATE: 7-SEP-1990
APPLICATION NUMBER: US 07/621,849
FILING DATE: 4-DEC-1990
APPLICATION NUMBER: US 07/621,988
FILING DATE: 4-DEC-1990
APPLICATION NUMBER: US 07/810,560
FILING DATE: 20-DEC-1991
APPLICATION NUMBER: US 07/569,920
FILING DATE: 20-AUG-1990
APPLICATION NUMBER: US 07/600,024
FILING DATE: 18-OCT-1990
APPLICATION NUMBER: US 07/599,543
FILING DATE: 18-OCT-1990
APPLICATION NUMBER: US 07/616,374
FILING DATE: 21-NOV-1990
APPLICATION NUMBER: US 07/483,913
FILING DATE: 22-FEB-1990
APPLICATION NUMBER: US 07/179,406
FILING DATE: 08-APR-1988
APPLICATION NUMBER: US 07/232,630
FILING DATE: 15-AUG-1988
APPLICATION NUMBER: US 07/315,342
FILING DATE: 23-FEB-1989
APPLICATION NUMBER: US 07/660,162
FILING DATE: 22-FEB-1991
APPLICATION NUMBER: US 07/422,699
FILING DATE: 17-OCT-1989
APPLICATION NUMBER: US 07/422,613
FILING DATE: 17-OCT-1989
APPLICATION NUMBER: US 07/422,623
FILING DATE: 17-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: DIANA M. STEEL
REGISTRATION NUMBER: 43,153
REFERENCE/DOCKET NUMBER: STK-001CP6C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/248-7000
TELEFAX: 617/248-7100
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 525 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: YES
FEATURE:
NAME/KEY: CDS
LOCATION: 1..516
OTHER INFORMATION: /function= "OSTEOGENIC PROTEIN"
/product= "CBMP2B-1"
/note= "CBMP2B-1 - FUSION"
SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-11-051-568-16

Alignment Scores: 1.05e-46 Length: 525
Pred. No.: 561.50 Matches: 105
Score:

Percent Similarity: 82.84% Conservative: 6
Best Local Similarity: 78.36% Mismatches: 14
Query Match: 26.76% Indels: 9
DB: 7 Gaps: 2
US-10-801-648-2 (1-396) x US-11-051-568-16 (1-525)
Qy 264 LeuValThrPheGlyHisAspGlyHisProLeuHisLysArgGluLysArgGln 283
Db 139 ATCGTTACTCCGGGTCTCGTTACGTTGCGGATCCTAAGCAT----- 180
Qy 284 AlaLysHisLysGlnArgLysArgLeuLysSer---SerCysLysArgHisProLeuTyr 302
Db 181 -----CACTCACAGCGGCCAGGAAGAATAAGAACTCCGCGCCCATCGCTCTAT 234
Qy 303 ValAspPheSerAspValGlyTyrAsnAspTrpIleValAlaProProGlyTyrHisAla 322
Db 235 GTGGACTTCAGCGATGGGCTGGATGACTGGATTGTGGCCCAACAGGCTACCGGCC 294
Qy 323 PheTyrCysHisGlyGluCysProPheProLeuAlaAspHisLeuAsnSerThrAsnHis 342
Db 295 TTCTACTGCCATGGGAATGCCCTTCCCGCTAGCGGATCACTTCAACAGCACCAACCAC 354
Qy 343 AlaIleValGlnThrLeuValAsnSerValAsnSerLysIleProLysAlaCysCysVal 362
Db 355 GCCGTGGTGCAGACCTCGTGAACCTCTGTCAACTCCAGATCCCTAAGGCTTGCTGCGTG 414
Qy 363 ProThrGluLeuSerAlaIleSerMetLeuTyrLeuAspGluAsnGluLysValValLeu 382
Db 415 CCCACCGAGCTGTCCGCCATCAGCATGCTGTACCTGGACGAGATGAGAGTGTGTGCTG 474
Qy 383 LysAsnTyrGlnAspMetValValGluGlyCysGlyCysArg 396
Db 475 AAGAACTACAGGAGATGGTAGAGGGCTGCGGCTGCGGC 516
RESULT 9
US-11-051-568-12
; Sequence 12, Application US/11051568
; Publication No. US20050255141A1
; GENERAL INFORMATION:
; APPLICANT: OPPERMAN, HERMANN
; OZKAYNAK, ENGIN
; KUBERASAMPATH, THANGAVEL
; RUEGER, DAVID C.
; PANG, ROY H.L.
; TITLE OF INVENTION: OSTEOGENIC DEVICES
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TESTA, HURWITZ & THIBEAULT
; STREET: 125 HIGH STREET
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: U.S.A.
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/051,568
; FILING DATE: 04-Feb-2005
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 10/321,799
; FILING DATE: 17-DEC-2002
; APPLICATION NUMBER: US 09/148,925
; FILING DATE: 8-SEP-1998
; APPLICATION NUMBER: US 08/449,699
; FILING DATE: 24-MAY-1995
; APPLICATION NUMBER: US 08/147,023
; FILING DATE: 1-NOV-1993
; APPLICATION NUMBER: US 07/841,646

QY 322 aPheTyrCysHisGlyGluCysProPheProLeuAlaAspHisLeuAenSerThrAsnHi 342
 Db 1227 CTACTACTGTGAGGGGAGTGTGCTTCCCTCTGAACCTCTACATGAGCCACCAACA 1286
 QY 342 sAlaIleValGlnThrLeuValAsnSerValAsnSerLys---IleProLysAlaCysCy 361
 Db 1287 CCCCATCGTCGAGAGCTGTCCACTTCTATCAACCGGAAACGGTGCACAGCCCTGTG 1346
 QY 361 sValProThrGluLeuSerAlaIleSerMetLeuTyrLeuAspGluAenGluLysValVa 381
 Db 1347 TCGGCCACGAGCTCAATGCCATCTCGTCTCTACTTCGATGACAGTCCACGTCAT 1406
 QY 381 lleuLysAsnTyrGlnAspMetValValGluGlyCysGlyCys 395
 Db 1407 CCGTGAAGAAATACAGAAACATGTGTGTCGGGCGCTGTGGCTGC 1449

RESULT 10

US-11-051-568-14
 ; Sequence 14, Application US/11051568
 ; Publication No. US20050255141A1
 ; GENERAL INFORMATION:
 ; APPLICANT: OPPERMANN, HERMANN
 ; OZKAYNAK, ENGIN
 ; KUBERASAMPATH, THANGAVEL
 ; RUEGER, DAVID C.
 ; PANG, ROY H.L.
 ; TITLE OF INVENTION: OSTEOGENIC DEVICES
 ; NUMBER OF SEQUENCES: 33
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: TESTA, HURWITZ & THIBEAULT
 ; STREET: 125 HIGH STREET
 ; CITY: BOSTON
 ; STATE: MASSACHUSETTS
 ; COUNTRY: U.S.A.
 ; ZIP: 02110
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/11/051,568
 ; FILING DATE: 04-Feb-2005
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 10/321,799
 ; FILING DATE: 17-DEC-2002
 ; APPLICATION NUMBER: US 09/148,925
 ; FILING DATE: 8-SEP-1998
 ; APPLICATION NUMBER: US 08/449,699
 ; FILING DATE: 24-MAY-1995
 ; APPLICATION NUMBER: US 08/147,023
 ; FILING DATE: 1-NOV-1993
 ; APPLICATION NUMBER: US 07/841,646
 ; FILING DATE: 21-FEB-1992
 ; APPLICATION NUMBER: US 07/827,052
 ; FILING DATE: 28-JAN-1992
 ; APPLICATION NUMBER: US 07/579,865
 ; FILING DATE: 7-SEP-1990
 ; APPLICATION NUMBER: US 07/621,849
 ; FILING DATE: 4-DEC-1990
 ; APPLICATION NUMBER: US 07/621,988
 ; FILING DATE: 4-DEC-1990
 ; APPLICATION NUMBER: US 07/810,560
 ; FILING DATE: 20-DEC-1991
 ; APPLICATION NUMBER: US 07/569,920
 ; FILING DATE: 20-AUG-1990
 ; APPLICATION NUMBER: US 07/600,024
 ; FILING DATE: 18-OCT-1990
 ; APPLICATION NUMBER: US 07/599,543
 ; FILING DATE: 18-OCT-1990
 ; APPLICATION NUMBER: US 07/616,374
 ; FILING DATE: 21-NOV-1990

APPLICATION NUMBER: US 07/483,913
 FILING DATE: 22-FEB-1990
 APPLICATION NUMBER: US 07/179,406
 FILING DATE: 08-APR-1988
 APPLICATION NUMBER: US 07/232,630
 FILING DATE: 15-AUG-1988
 APPLICATION NUMBER: US 07/315,342
 FILING DATE: 23-FEB-1989
 APPLICATION NUMBER: US 07/660,162
 FILING DATE: 22-FEB-1991
 APPLICATION NUMBER: US 07/422,699
 FILING DATE: 17-OCT-1989
 APPLICATION NUMBER: US 07/422,613
 FILING DATE: 17-OCT-1989
 APPLICATION NUMBER: US 07/422,623
 FILING DATE: 17-OCT-1989
 ATTORNEY/AGENT INFORMATION:
 NAME: DIANA M. STEEL
 REGISTRATION NUMBER: 43,153
 REFERENCE/DOCKET NUMBER: STK-001CP6C3
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617/248-7000
 TELEFAX: 617/248-7100
 INFORMATION FOR SEQ ID NO: 14:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1277 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 HYPOTHETICAL: YES
 ANTI-SENSE: NO
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 1..1224
 OTHER INFORMATION: /function= "OSTEOGENIC PROTEIN"
 /product= "Op1D"
 /note= "Op1D - FUSION"
 SEQUENCE DESCRIPTION: SEQ ID NO: 14:
 US-11-051-568-14
 Alignment Scores:
 Pred. No.: 1,368-44 Length: 1277
 Score: 546.00 Matches: 130
 Percent Similarity: 46.45% Conservative: 60
 Best Local Similarity: 31.78% Mismatches: 123
 Query Match: 26.02% Indels: 96
 DB: 7 Gaps: 12
 US-10-801-648-2 (1-396) x US-11-051-568-14 (1-1277)
 QY 52 GluPheGluLeuArgLeuLeuSerMetPheGlyLeuLysGlnArgProThrPro----- 69
 Db 88 GAGATGACGCGGAGATCTCTCCATTTTGGGCTTGCCTCCACCGCGCGCGCGCACCTC 147
 QY 70 ---SerArgAspAlaValProProTyrMetLeuAspLeuTyrArgArgHisSerGly 88
 Db 148 CAGGCAAGACAACTCGGCAACCCCATGTTTCATGCTGACCTGTACAAACCCCATGCGGT 207
 QY 89 -----GlnProGlySer----- 92
 Db 208 GGAGGAGGCGT 267
 QY 93 -----ProAlaProAspHisArgLeuGluArgAlaAlaSerArgAlaSerThr 108
 Db 268 ACCCAGGGCATG 327
 QY 109 ValArgSerPhe-----His 113
 Db 328 GTCATGAGCTTCGTCAACCTCGTGGAAACATGACAAAGGAATTTTCCACCCACGCTACCC 387
 QY 114 HisGluGluSerLeuGluLeuProGluThrSerGlyLysThrArgArgPhePhe 133

```
Db 388 CAT-----CGAGATTCCGG 402
Qy 134 PheAenLeuSerSerIleProThrGluGluPheIleThrSerAlaGluLeuValPhe 153
Db 403 TTTGATCTTTCAAGATCCCAAGAGGGGAAGCTGTACGCGCAGCGCAATTCGGATCTAC 462
Qy 154 ArgGluGlnMetGlnAspAlaLeuGlyAsnAsnSerSerPheHisHisArgIleAsnIle 173
Db 463 AAGGACTATACATCCCGGAGCGTTTCGACATGAGACG-----TTCCGGATCAGCGTT 513
Qy 174 TyrGluIleIleLysPro-----AlaThrAlaAsnSerLysPheProValThrArgLeu 191
Db 514 TATCAGGTGCTCCAGGAGCACTTGGCGAGGAATCGGATCTCTTC-----CTG 561
Qy 192 LeuAspThrArgLeuValAsnGlnAsnAlaSerArgTrpGluSerPheAspValThrPro 211
Db 562 CTCACAGCCGTCACCTCTGGCGCTCGGAGGAGGCGTGGTGTGTGTGATCATCACAGCC 621
Qy 212 AlaValMetArgTrpThrAlaGlnGlyHisAlaAsnHisGlyPheValValGluValAla 231
Db 622 ACCAGCAACCACTGGGTGGTCAATCCGCGGCACAACTGGGCGCTCGAGCTCTCGGTGGAG 681
Qy 232 HisLeuGluGlnLysGlnGlyValSerLysArgHisValArgIleSerArgSerLeuHis 251
Db 682 ACGTGGATGGCGAGAGCATCAACCCAGTTGGCGGCGCTGATTTGGCGG-----732
Qy 252 GlnAspGluHisSerTrpSerGlnIleArgProLeuLeuValThrPheGlyHisAspGly 271
Db 733 -----CACGGGCCCCAGAACAGCAGCCCTTCATGGTGGCTTC-----TTC 774
Qy 272 LysGlyHisProLeuHisLysArgGluLysArgGlnAlaLysHisLysGlnArgLysArg 291
Db 775 AAGGCCAGGAGGTCCACTTCCGAGCATCCGGTCCACGGGAGCAACAGCGCAGCAG 834
Qy 292 LeuLysSer-----294
Db 835 AACGCTCCAGAGCGCCCAAGAACCCAGGAGCCCTCGGATGGCCACAGTGGCAGAGAAC 894
Qy 295 -----SerCysLysArgHisProLeuTyrValAspPheSerAsp 307
Db 895 AGCAGCAGCGCAGAGCAGCGCTGTAAAGAACAGCAGCTGTATGTTCAGCTTCGAGAC 954
Qy 308 ValGlyTrpAsnAspTrpIleValAlaProProGlyTyrHisAlaPheTyrCysHisGly 327
Db 955 CTGGGTGGCAGGACTGTGATCATCGCGCTGAAGGCTACGCGCTACTACTGTGAGGGG 1014
Qy 328 GluCysProPheProLeuAlaAspHisLeuAsnSerThrAsnHisAlaIleValGlnThr 347
Db 1015 GAGTGTGCTTCCCTCTGAATCTCTACATGACGCCACCAACAGCCATCGTCGACAGC 1074
Qy 348 LeuValAsnSerValAsnSerLys---IleProLysAlaCysCysValProThrGluLeu 366
Db 1075 CTGGTCCACTTCATCAACCCGGAACGGTGCCCAAGCCCTGTGTGGCCCAACAGCTC 1134
Qy 367 SerAlaIleSerMetLeuTyrLeuAspGlnAsnGlnLysValValLeuLysAsnTyrGln 386
Db 1135 AATGCCATCTCCGCTCTACTTCGATGACAGCTCCAAACGTCATCCTCGAAGAAATACAGA 1194
Qy 387 AspMetValValGluGlyCysGlyCys 395
Db 1195 AACATGTGTGTCGGGCTGTGGTGTG 1221
```

RESULT 11

```
US-10-816-768-38
; Sequence 38, Application US/10816768
; Publication No. US20050250936A1
; GENERAL INFORMATION:
; APPLICANT: Oppermann, Hermann
; APPLICANT: Tai, Mei-Sheng
; APPLICANT: McCartney, John
; TITLE OF INVENTION: Modified TGF-beta Superfamily Proteins
; FILE REFERENCE: STK-075
; CURRENT APPLICATION NUMBER: US/10/816,768
```

```
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: PatentIn version 2.0
; SEQ ID NO 38
; LENGTH: 1822
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURES:
; NAME/KEY: CDS
; LOCATION: (49)..(1341)
; OTHER INFORMATION: Morphogenic Protein OP1
US-10-816-768-38
```

Alignment Scores:

| | | | |
|------------------------|----------|---------------|------|
| Pred. No.: | 3,21e-44 | Length: | 1822 |
| Score: | 544.50 | Matches: | 147 |
| Percent Similarity: | 45.39% | Conservative: | 60 |
| Best Local Similarity: | 32.24% | Mismatches: | 136 |
| Query Match: | 25.95% | Indels: | 114 |
| DB: | 6 | Gaps: | 14 |

US-10-801-648-2 (1-396) x US-10-816-768-38 (1-1822)

| | | | |
|----|-----|--|-----|
| Qy | 20 | GlyAlaAlaGlyLeuValProGluLeuGlyArgArgLysPheAlaAlaSerSerGly | 39 |
| Db | 75 | GGCGCCGACACAGCTTCGTGGCGCTTCGGGACCCCTCTTCTGCTGCGCTCCGCCCTGGC | 134 |
| Qy | 40 | ArgProSerSerGlnPro-SerAspGluValLeuSerGluPhe | 53 |
| Db | 135 | CGA-----CTTCAGCTTGGCAACAGAGTGCACTCGAGCTTCATCCACCGGCGCTCCG | 188 |
| Qy | 54 | -----GluLeuArgLeuLeuSerMetPheGlyLeuLysGlnAr | 66 |
| Db | 189 | CAGCCAGGAGCGCGGAGATGCAGCGCAGATCTCTCCATTTTGGGCTTGGCCACCG | 248 |
| Qy | 66 | gProThrPro-----SerArgAspAlaValProProTyrMetLeuAspLeuTy | 83 |
| Db | 249 | CCCGCGCCCGACCTCCAGGGCAAGCAAACTCGGCGCCCATGTTTCATGCTGGACCTGTA | 308 |
| Qy | 83 | rArgArgHisSerGly | 88 |
| Db | 309 | CAA-CGCCATGGCGTGGAGGAGCGCGCGCGCGCGCGGCTTCTCTACCCCT | 367 |
| Qy | 89 | -----GlnProGlySerProAlaProAsp | 96 |
| Db | 368 | ACAAAGCCGTCTTCAGTACCCAGCGGCCCTCTTGGCCAGCTGCAAGATAGCATTTCC | 427 |
| Qy | 97 | -HisArg-LeuGluArgAlaAlaSerArgAlaAsnThrValArg | 110 |
| Db | 428 | TCACCGACCGGCATCGTTCATGAGCTTCGTCACCTCGTGAACATGACAGGAATTC | 487 |
| Qy | 111 | -----SerPheHisHisGluSerLeuGluGluLeuProGluThrSerGlyLysT | 128 |
| Db | 488 | TCCACCCACGCTACCACAT | 507 |
| Qy | 128 | hrThrArgArgPhePhePheAsnLeuSerSerIleProThrGluGluPheIleThrSerA | 148 |
| Db | 508 | -----CGAGAGTTCGGGTTTGATCTTTCCAAGATCCCAAGAGGGAAGCTGTACGGCAG | 562 |
| Qy | 148 | laGluLeuGlnValPheArgGluGlnMetGlnAspAlaLeuGlyAsnAsnSerSerPheH | 168 |
| Db | 563 | CCGAATTCGGATCTCAAGGACTACATCCGGGACGCTTCGACAGATGAGACG | 615 |
| Qy | 168 | ishisArgIleAsnIleTyrGluIleIleLysPro-----AlaThrAlaAsnSerLysP | 186 |
| Db | 616 | --TTCCGGATCAGCGTTTATCAGGTGCTCCAGGAGCACTTGGCGAGGAATCGGATCTCT | 673 |
| Qy | 186 | heProValThrArgLeuLeuAspThrArgLeuValAsnGlnAsnAlaSerArgTrpGluS | 206 |
| Db | 674 | TC-----CTGCTCGACACGCGTACCTCTCGGCGCTCGGAGGAGGCGTGGTGG | 721 |
| Qy | 206 | erPheAspValThrProAlaValMetArgTrpThrAlaGlnGlyHisAlaAsnHisGlyP | 226 |

Db 722 TGTTGACATCATACAGCCACCAACCACTGGGTGGTCAATCCGGGCACCAACCTGGGCC 781
Qy 226 heValValGluValAlaHisLeuGluGluLysGlnGlyValSerLysArgHisValArgI 246
Db 782 TCAGCTCTCGGTGGAGAGCGTGGATGGGAGAGCATCAACCCCAAGTTGGGGCCCTGA 841
Qy 246 leSerArgSerLeuHisGlnAspGluHisSerTrpSerGlnIleArgProLeuLeuValT 266
Db 842 TTGGGGCGG-----CACGGGCCCCAGAACCAAGCAGCCCTTCATGGTGG 883
Qy 266 hrPheGlyHisAspGlyLysGlyHisProLeuHisLysArgGlnLysArgGlnAlaLysH 286
Db 884 CTTTTC-----TTCAAGGCCACCGAGGTCCACTTCGGCAGCATCCGGTCCACGGGGA 934
Qy 286 leLysGlnArgLysArgLeuLysSer----- 294
Db 935 GCMAACGGCGACGACGAGACCGCTCAAGACGCCCAAGAACCAAGAGCCCTGGGGATGG 994
Qy 295 -----SerCysLysArgHisProLeuT 302
Db 995 CCAAGCTGGCAGAGAAACAGCAGCAGCAGCAGCGCTGTAAAGAACGACGAGCTGT 1054
Qy 302 yrValAspPheSerAspValGlyTrpAsnAspTrpIleValAlaProProGlyTyrHisA 322
Db 1055 ATGTGAGCTTCGAGACCTGGGCTGGCAGGACTGGATCATCGCGCTGAAGGCTACGCGC 1114
Qy 322 laPheTyrCysHisGlyGluCysProPheProLeuAlaAspHisLeuAsnSerThrAsnH 342
Db 1115 CTTACTACTGTGAGGGGAGTGTGCTTCCCTCTGACTCTTACATGAACGCCCAAC 1174
Qy 342 isAlaIleValGlnThrLeuValAsnSerValAsnSerLys---IleProLysAlaCysC 361
Db 1175 ACGCCATGTGCAGACGCTGTGTCCACTTCATCAACCGGAAACGGTGGCCAGCCCTGCT 1234
Qy 361 ysValProThrGluLeuSerAlaIleSerMetLeuTyrLeuAspGluAsnGluLysValV 381
Db 1235 GTGCCGCCACGCGCATCAATGCCATCTCGTCTCTACTTCCATGACAGCTCCCAACGTCA 1294
Qy 381 alLeuLysAsnTyrGlnAspMetValValGluGlyCysGlyCys 395
Db 1295 TCCTGAGAAATACAGAAACATGGTGGTCCGGGGCTGTGGGTGC 1338

RESULT 12
US-10-650-326B-17
; Sequence 17, Application US/10650326B
; Publication No. US20050272649A1
; GENERAL INFORMATION:
; APPLICANT: Hruska, Keith A.
; APPLICANT: McCartney, John E.
; APPLICANT: Charette, Marc F.
; TITLE OF INVENTION: CONJOINT ADMINISTRATION OF MORPHOGENS AND ACE INHIBITORS IN
; TITLE OF INVENTION: TREATMENT OF CHRONIC RENAL FAILURE
; FILE REFERENCE: JJJ-P01-599
; CURRENT APPLICATION NUMBER: US/10/650,326B
; CURRENT FILING DATE: 2003-08-28
; PRIOR APPLICATION NUMBER: 60/406,431
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17
; LENGTH: 1822
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-650-326B-17

Alignment Scores:
Pred. No.: 3,21e-44 Length: 1822
Score: 544.50 Matches: 147
Percent Similarity: 45.33% Conservative: 60
Best Local Similarity: 32.24% Mismatches: 136
Query Match: 25.95% Indels: 114
DB: 6 Gaps: 14

US-10-801-648-2 (1-396) x US-10-650-326B-17 (1-1822)
Qy 20 GlyValAlaGlyLeuValProGluLeuGlyValArgLysPheAlaAlaSerSerGly 39
Db 75 GCGCGCGCACAGCTTCGTGGCGCTCTGGGACCCCTGTCTCTGCTGCGCTCGCCCTGCG 134
Qy 40 ArgProSerSerGlnPro-SerAspGluValLeuSerGluPhe----- 53
Db 135 CGA-----CTTCAGCCTGGACAACGAGGTGCACCTCGAGCTTCATCCACCGCGCCTCG 188
Qy 54 -----GluLeuArgLeuLeuSerMetPheGlyLeuLysGlnAr 66
Db 189 CAGCAGGAGCGCGGAGATGCAGCGCAGATCCTCTCCATTTTGGGCTTGGCCACCG 248
Qy 66 gProThrPro-----SerArgAspAlaValProProTyrMetLeuAspLeuTy 83
Db 249 CCGCGCGCGCACCTCCAGGGCAAGCAACTCGGCACCCATGTTTCATGCTGGACCTGTA 308
Qy 83 rArgArgHisSerGly----- 88
Db 309 CAA-CGCCATGCGGTGGAGGAGGCGCGCGCGCGCGCGCTTCTCTACCCCT 367
Qy 89 -----GlnProGlySerProAlaProAsp----- 96
Db 368 ACAAGCGCGCTTTCAGTACCCAGGGCGCCCTCTGCGCCAGCCTGCAAGATAGCCATTTCC 427
Qy 97 -HisArg-LeuGluArgAlaAlaSerArgAlaAsnThrValArg----- 110
Db 428 TCACCGCGCGCAGCATGTCATGAGCTTCGTCAACCTCGTGAACATGACAGGAATCT 487
Qy 111 -----SerPheHisGlyGluSerLeuGluLeuProGluThrSerGlyLysT 128
Db 488 TCCACCCACGCTACCCAT----- 507
Qy 128 hrThrArgArgPhePhePheAsnLeuSerSerIleProThrGluGluPheIleThrSerA 148
Db 508 -----CGAGAGTTCGGTTTCATCTTTCCAAAGATCCCAAGAGGGAGAGTGTGACGCG 562
Qy 148 laGluLeuGlnValPheArgGluGlnMetGlnAspAlaLeuGlyAsnAsnSerSerPheH 168
Db 563 CCGAATTCGGATCTTCAAGAGACTATCCCGGGAACGCTTCGACAAATGAGAG----- 615
Qy 168 isHisArgIleAsnIleTyrGluIleIleLysPro-----AlaThrAlaAsnSerLysP 186
Db 616 --TTCCGGATCAGCGTTTATCAGGTGCTTCAGAGCAGCTTGGGCGAGGAGATCGATCTCT 673
Qy 186 heProValThrArgLeuLeuAspThrArgLeuValAsnGlnAsnAlaSerArgTrpGluS 206
Db 674 TC-----CTGCTCGACAGCGCTACCTCTGGGCGCTCGGAGGAGGGCTGGCTGG 721
Qy 206 erPheAspValThrProAlaValMetArgTTrpThrAlaGlnGlyHisAlaAsnHisGlyP 226
Db 722 TGTTTGATCATCACAGCCACCAGCAACCACTGGGTGGTCAATCCGCGGCGCAACCTGGGCC 781
Qy 226 heValValGluValAlaHisLeuGluGluLysGlnGlyValSerLysArgHisValArgI 246
Db 782 TGCAGCTCTCGGTGGAGAGCGTGGATGGGAGAGCATCAACCCCAAGTTGGCGGCGCTGA 841
Qy 246 leSerArgSerLeuHisGlnAspGluHisSerTrpSerGlnIleArgProLeuLeuValT 266
Db 842 TTGGGCGG-----CACGGGCCCCAGAACCAAGCAGCCCTTCATGGTGG 883
Qy 266 hrPheGlyHisAspGlyLysGlyHisProLeuHisLysArgGlnLysArgGlnAlaLysH 286
Db 884 CTTTTC-----TTCAAGGCCACCGAGGTCCACTTCGGCAGCATCCGGTCCACGGGGA 934
Qy 286 isLysGlnArgLysArgLeuLysSer----- 294
Db 935 GCMAACGGCGACGACGAGACCGCTCAAGACGCCCAAGAACCAAGAGCCCTGGGGATGG 994
Qy 295 -----SerCysLysArgHisProLeuT 302
Db 995 CCAAGCTGGCAGAGAAACAGCAGCAGCAGCAGCGCTGTAAAGAACGACGAGCTGT 1054

```
Qy 302 yrValaspPheSeraspValGlyTrpAenAspTrpIleValalaproProGlyTyrHisA 322
Db 1055 AIGCAGCTTCGAGACCTGGCGTGCAGGACTGATCATCGCGCTGAAGGCTACGCCG 1114
Qy 322 laPheTyrCysHisGlyGluCysProPheProLeuAlaAspHisLeuAsnSerThrAenH 342
Db 1115 CCTACTACTGTGAGGGGAGTGGCTTCCCTCTGAACTCTTACATGACGCCACCAACC 1174
Qy 342 isAlalleValGlnThrLeuValAenSerValAenSerLys---IleProLysAlaCysC 361
Db 1175 ACGGCATCGTCAGACGCTGCTCCACTTCATCAACCCGAAACGGTGCCCAAGCCCTGCT 1234
Qy 361 ysValProThrGluLeuSerAlaIleSerMetLeuTyrLeuAspGluAsnGluLysValV 381
Db 1235 GTGGCCCAACGAGCTCAATCCATCTCCGCTCTTACTTCGATGACAGCTCCCAACGTCA 1294
Qy 381 alLeuLysAsnTyrGlnAspMetValValGluGlyCysGlyCys 395
Db 1295 TCCTGAGAATAACAGAAACATGTGTGTCGGGCTGTGGTGC 1338

RESULT 13
US-11-051-568-1
; Sequence 1, Application US/11051568
; Publication No. US20050255141A1
; GENERAL INFORMATION:
; APPLICANT: OPPERMANN, HERMANN
; OZKATNAK, ENGIN
; KUBERASAMPATH, THANGAVEL
; RUEGER, DAVID C.
; PANG, ROY H.L.
; TITLE OF INVENTION: OSTEOGENIC DEVICES
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TESTA, HURWITZ & THIBEAULT
; STREET: 125 HIGH STREET
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: U.S.A.
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/051,568
; FILING DATE: 04-Feb-2005
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 10/321,799
; FILING DATE: 17-DEC-2002
; APPLICATION NUMBER: US 09/148,925
; FILING DATE: 8-SEP-1998
; APPLICATION NUMBER: US 08/449,699
; FILING DATE: 24-MAY-1995
; APPLICATION NUMBER: US 08/147,023
; FILING DATE: 1-NOV-1993
; APPLICATION NUMBER: US 07/841,646
; FILING DATE: 21-FEB-1992
; APPLICATION NUMBER: US 07/827,052
; FILING DATE: 28-JAN-1992
; APPLICATION NUMBER: US 07/579,865
; FILING DATE: 7-SEP-1990
; APPLICATION NUMBER: US 07/621,849
; FILING DATE: 4-DEC-1990
; APPLICATION NUMBER: US 07/621,988
; FILING DATE: 4-DEC-1990
; APPLICATION NUMBER: US 07/810,560
; FILING DATE: 20-DEC-1991
; APPLICATION NUMBER: US 07/569,920
; FILING DATE: 20-AUG-1990
; APPLICATION NUMBER: US 07/600,024
```

```
;
; FILING DATE: 18-OCT-1990
; APPLICATION NUMBER: US 07/599,543
; FILING DATE: 18-OCT-1990
; APPLICATION NUMBER: US 07/616,374
; FILING DATE: 21-NOV-1990
; APPLICATION NUMBER: US 07/483,913
; FILING DATE: 22-FEB-1990
; APPLICATION NUMBER: US 07/179,406
; FILING DATE: 08-APR-1988
; APPLICATION NUMBER: US 07/232,630
; FILING DATE: 15-AUG-1988
; APPLICATION NUMBER: US 07/315,342
; FILING DATE: 23-FEB-1989
; APPLICATION NUMBER: US 07/660,162
; FILING DATE: 22-FEB-1991
; APPLICATION NUMBER: US 07/422,699
; FILING DATE: 17-OCT-1989
; APPLICATION NUMBER: US 07/422,613
; FILING DATE: 17-OCT-1989
; APPLICATION NUMBER: US 07/422,623
; FILING DATE: 17-OCT-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: DIANA M. STEEL
; REGISTRATION NUMBER: 43,153
; REFERENCE/DOCKET NUMBER: STK-001CP6C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/248-7000
; TELEFAX: 617/248-7100
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1822 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: HOMO SAPIENS
; TISSUE TYPE: HIPPOCAMPUS
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 49..1341
; IDENTIFICATION METHOD: experimental
; OTHER INFORMATION: /function= "OSTEOGENIC PROTEIN"
; /product= "OPI"
; /evidence= EXPERIMENTAL
; /standard name= "OPI"
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-11-051-568-1

Alignment Scores:
Pred. No.: 3,21e-44 Length: 1822
Score: 544.50 Matches: 147
Percent Similarity: 45.39% Conservative: 60
Best Local Similarity: 32.24% Mismatches: 136
Query Match: 25.95% Indels: 114
DB: 7 Gaps: 14

US-10-801-648-2 (1-396) x US-11-051-568-1 (1-1822)
Qy 20 GlyAlaalaGlyLeuValProGluLeuGlyArgArgLysPheAlaAlaAlaSerSerGly 39
Db 75 GCGCGCGACAGCTTCGTGGCGCTCTGGGACCCCTGTTCTCTGCTGCGCTCGCGCTGCG 134
Qy 40 ArgProSerSerGlnPro-SerAspGluValLeuSerGluPhe----- 53
Db 135 CGA-----CTTCAGCTTGGACACGAGGTGCATCTCGAGCTTCATCCACCGCGCTCCG 188
Qy 54 -----GluLeuArgLeuSerMetPheGlyLeuLysGlnAr 66
Db 189 CAGCCAGGAGCGCGGAGATGCACGCGAGATCTCTCCATTTTGGGCTTGGCCCAACCG 248
```


This Page Blank (uspio)

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: January 10, 2006, 23:27:45 ; Search time 3445 Seconds

(without alignments)
5378.138 Million cell updates/sec

Title: US-10-801-648-2

Perfect score: 2098

Sequence: 1 MVAGTRCILLALLPQLVIGG.....NEKVLKNYQDMVVGCGCR 396

Scoring table:

BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODE=frame+ p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool/SUPPIX-rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-DB=EST -QFMT=fastap -SUPPIX-rst -TRANS=human40.cdi -LIST=45
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pclo -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10801648.@CGN 1_1_4015@runat_09012006_143119_14778 -NCPU=6 -ICPU=3
-NO MMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOF=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST:*
1: gb_est1.*
2: gb_est2.*
3: gb_est3.*
4: gb_hc.*
5: gb_est4.*
6: gb_est5.*
7: gb_est6.*
8: gb_est7.*
9: gb_gss1.*
10: gb_gss2.*
11: gb_gss3.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|-------------|----------------------|
| 1 | 2098 | 100.0 | 2394 | 4 CR618407 | CR618407 full-length |
| 2 | 1732 | 82.6 | 983 | 10 AY418812 | AY418812 Homo sapi |
| 3 | 1568 | 75.7 | 977 | 10 AY418814 | AY418814 Mus muscu |
| 4 | 1444 | 68.8 | 903 | 5 BX431362 | BX431362 BX431362 |
| 5 | 1339 | 63.8 | 841 | 8 DN117475 | DN117475 1117145 M |
| 6 | 1269 | 60.5 | 1227 | 10 AY409113 | AY409113 Homo sapi |
| 7 | 1269 | 60.5 | 1676 | 4 CR595138 | CR595138 full-length |

| | | | | | |
|----|--------|------|------|-------------|--------------------|
| 8 | 1269 | 60.5 | 1692 | 4 CNSLTI18E | BX161438 human ful |
| 9 | 1269 | 60.5 | 1705 | 4 CNSLTI18D | BX161385 human ful |
| 10 | 1268 | 60.4 | 1227 | 10 AY409115 | AY409115 Mus muscu |
| 11 | 1254.5 | 59.8 | 1636 | 8 CX354839 | CX354839 ssalrgb53 |
| 12 | 1234 | 58.8 | 724 | 8 CV804617 | CV804617 AGENCOURT |
| 13 | 1232 | 58.7 | 711 | 10 AY418813 | AY418813 Pan trogl |
| 14 | 1229 | 58.6 | 881 | 5 BU444424 | BU444424 60313309 |
| 15 | 1167 | 55.6 | 727 | 5 BU625617 | BU625617 UI-H-FGI- |
| 16 | 1106 | 52.7 | 715 | 7 CK940908 | CK940908 4064444 B |
| 17 | 1077 | 51.3 | 1227 | 10 AY409114 | AY409114 Pan trogl |
| 18 | 1056 | 50.3 | 581 | 3 BP276858 | BP276858 BP276858 |
| 19 | 1045 | 49.8 | 1001 | 5 BX432994 | BX432994 BX432994 |
| 20 | 1042 | 49.7 | 649 | 3 BQ184625 | BQ184625 UI-B-EJ1- |
| 21 | 1039 | 49.5 | 642 | 3 BM929343 | BM929343 UI-B-EJ1- |
| 22 | 1038 | 49.5 | 648 | 3 BM683313 | BM683313 UI-B-EJ1- |
| 23 | 1035 | 49.3 | 711 | 7 CN396138 | CN396138 170004241 |
| 24 | 1029 | 49.0 | 666 | 1 AW332667 | AW332667 XZ89F02.X |
| 25 | 1021 | 48.7 | 782 | 5 BX728232 | BX728232 BX728232 |
| 26 | 1015 | 48.4 | 761 | 5 BX728231 | BX728231 BX728231 |
| 27 | 1014 | 48.3 | 649 | 3 BQ186599 | BQ186599 UI-B-EJ1- |
| 28 | 1010.5 | 48.2 | 830 | 8 DN117122 | DN117122 1116761 M |
| 29 | 1008 | 48.0 | 674 | 3 BM674840 | BM674840 UI-B-EJ0- |
| 30 | 999.5 | 47.6 | 867 | 8 CX315415 | CX315415 JGI_XZT55 |
| 31 | 998.5 | 47.6 | 780 | 6 CF286367 | CF286367 AGENCOURT |
| 32 | 970 | 46.2 | 908 | 5 BX757756 | BX757756 BX757756 |
| 33 | 964 | 45.9 | 912 | 8 CX490118 | CX490118 JGI_XZG33 |
| 34 | 958.5 | 45.7 | 904 | 7 CN157350 | CN157350 946052 MA |
| 35 | 958 | 45.7 | 632 | 8 CX593098 | CX593098 CT020004A |
| 36 | 956 | 45.6 | 1002 | 11 CNS041FG | AL292165 Tetraodon |
| 37 | 948.5 | 45.2 | 656 | 3 B1400982 | B1400982 MI-P-Ayl- |
| 38 | 946 | 45.1 | 617 | 1 AL864240 | AL864240 AL864240 |
| 39 | 946 | 45.1 | 802 | 5 BU244511 | BU244511 603781223 |
| 40 | 940 | 44.8 | 614 | 9 AZ655571 | AZ655571 1M0530C11 |
| 41 | 934 | 44.5 | 1115 | 5 BU114214 | BU114214 603130312 |
| 42 | 930.5 | 44.4 | 821 | 7 CR433599 | CR433599 CR433599 |
| 43 | 928.5 | 44.3 | 898 | 6 CA454850 | CA454850 AGENCOURT |
| 44 | 921 | 43.9 | 533 | 7 CO610202 | CO610202 DGB-90H16 |
| 45 | 917 | 43.7 | 526 | 6 CB132019 | CB132019 K-EST0182 |

RESULT 1

CR618407
LOCUS full-length cDNA clone CS0DE003YB10 of Placenta of Homo sapiens
DEFINITION 2394 bp mRNA linear HTC 21-JUL-2004
(human).

ACCESSION CR618407

VERSION CR618407.1 GI:50499214

KEYWORDS HTC; CNSLT cDNA.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 2394)

AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished

REMARK Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ Invitrogen Corporation 1600

Paradise Avenue

REFERENCE 2 (bases 1 to 2394)

Genoscope.

AUTHORS Direct Submission

TITLE Submitted (20-JUL-2004) Genoscope - Centre National de Sequençage :

BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.

```

FEATURES
source      Location/Qualifiers
1. .2394
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DE003YB10"
/tissue_type="Placenta"
/plasmid="PCMVSPORT_6"

ORIGIN
Alignment Scores:
Pred. No.:      5.6e-201      Length:      2394
Score:          2098.00      Matches:    396
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:     100.00%      Indels:     0
DB:              4              Gaps:       0

US-10-801-648-2 (1-396) x CR618407 (1-2394)

Qy 1 MetValAlaGlyThrArgCysLeuLeuAlaLeuLeuProGlnValLeuLeuGlyGly 20
Db 360 ATGTGCGCGGAGCCCGCTGCTTCTAGCGTGTCTGCTTCCCGAGGTCTCTCGGGCGGC 419
Qy 21 AlaAlaGlyLeuValProGluLeuGlyArgArgLysPheAlaAlaLaSerSerGlyArg 40
Db 420 GCGGCTGGCCTCGTTCGGAGCTGGCGCGAGGAAGTTCGGCGGCGGTCTCGGGCGGC 479
Qy 41 ProSerSerGlnProSerAspGluValLeuSerGluPheGluLeuLeuArgLeuLeuSerMet 60
Db 480 CCCTCATCCAGCCCTCTGACGAGTCTGAGCGAGTTCGAGTTCGCGTCTCAGCATG 539
Qy 61 PheGlyLeuLysGlnArgProThrProSerArgAspAlaValProProTyTrMetLeu 80
Db 540 TTCGGCCTGAAACAGAGACCCACCCCGCAGCAGGACCGCGTGTGGTCCCGCTACATGCTA 599
Qy 81 AspLeuTyTrArgArgHisSerGlyGlnProGlySerProAlaProAspHisArgLeuGlu 100
Db 600 GACCTGTATCCAGGCACTAGGTTCAGCCGGGCTCACCCGCCCGCAGACCAGCGGTGGAG 659
Qy 101 ArgAlaLaSerArgAlaAsnThrValArgSerPheHisHisGluGluSerLeuGluGlu 120
Db 660 AGGCGAGCCAGCCAGCCACACTGTGCGCAGCTTCACCATGAAGAATCTTTTGAAGAA 719
Qy 121 LeuProGluThrSerGlyLysThrThrArgArgPhePheAsnLeuSerSerIlePro 140
Db 720 CTACCAGAAACGAGTGGGAAACAAACCCGGAGATCTCTTTTAATTTTAAGTTCATCCCC 779
Qy 141 ThrGluGluPheIleThrSerAlaGluLeuGlnValPheArgGluGlnMetGlnAspAla 160
Db 780 ACGGAGGAGTTTATCACTCTAGCAGAGCTTCAGGTTTTCGAGAACAGATGCAAGATGCT 839
Qy 161 LeuGlyAsnAsnSerSerPheHisHisArgIleAsnIleTyGluIleIleLysProAla 180
Db 840 TTAGGAAACATAGCAGTTTCATCCACCGAATTAATATTTATGAATCATATAAACCTGCA 899
Qy 181 ThrAlaAsnSerLysPheProValThrArgLeuLeuAspThrArgLeuValAsnGlnAsn 200
Db 900 ACAGCCAACTCGAAATTTCCCGCGTACCCAGACTTTTGGACACACAGTGTGGTGAATCAGAAT 959
Qy 201 AlaSerArgTTPGluSerPheAspValThrProAlaValMetArgTTPThrAlaGlnGly 220
Db 960 GCAAGCAGGTGGGAAAGTTTGTGATGTCCACCCCGCTGTGATCGGTGAGCTGCACAGGA 1019
Qy 221 HisAlaAsnHisGlyPheValValGluValAlaHisLeuGluGluLysGlnGlyValSer 240
Db 1020 CACGCCAACCATGATTCTGTGTGGAGTGGCCCACTTGGAGGAGAAACAAAGGTGTCTCC 1079
Qy 241 LysArgHisValArgIleSerArgSerLeuHisGlnAspGluHisSerTrpSerGlnIle 260
Db 1080 AAGAGACATGTTAGGATAAGCAGGTCTTTGACCAGATGAACACAGCTGTGTCAAGATA 1139
Qy 261 ArgProLeuLeuValThrPheGlyHisAspGlyLysGlyHisProLeuHisLysArgGlu 280

```

```

Db 1140 AGGCATTGCTAGTAACCTTTTGCCATGATGGAAAGGGCATCTCTCCCAAGAGAA 1199
Qy 281 LysArgGlnAlaLysHisLysGlnArgLysArgLeuLysSerSerCysLysArgHisPro 300
Db 1200 AAACGTCACAGCCAAACACAAACAGCGGAAACGCGCTTAAGTCCAGCTGTAAAGAGACACCT 1259
Qy 301 LeuTyTrValAspPheSerAspValGlyTrpAsnAspTrpIleValAlaProProGlyTyTr 320
Db 1260 TTGTACGTGGACTTCAGTGACGTGGGTGGAATGACTGGATTGTGGTCCCGGGGTAT 1319
Qy 321 HisAlaPheTyTrCysHisGlyGluCysProPheProLeuAlaAspHisLeuAsnSerThr 340
Db 1320 CACGCTTTTACTGCCACGAGAGATGCCCTTTTCTCTGCTGATCATCTGAATCCACT 1379
Qy 341 AsnHisAlaIleValGlnThrLeuValAsnSerValAsnSerLysLysIleProLysAlaCys 360
Db 1380 AATCATGCCATTGTTTCAGACGTTGGTCAACTCTGTTAACTCTAAGATTCTTAAGGCATGC 1439
Qy 361 CysValProThrGluLeuSerAlaIleSerMetLeuTyTrLeuAspGluAsnGluLysVal 380
Db 1440 TGTGTCCCGACAGAACTCAGTGCTATCTCGATGCTGTACCTTGACGAGAAATGAAGGTT 1499
Qy 381 ValLeuLysAsnTyTrGlnAspMetValValGluGlyCysGlyCysArg 396
Db 1500 GTATTAAAGAACTATCAGGACATGTTGTGAGGGTTGTGGTGTCTGC 1547

RESULT 2
AY418812      983 bp      DNA      linear      GSS 17-DEC-2003
LOCUS        Homo sapiens BMP2 gene, VIRTUAL TRANSCRIPT, partial sequence,
DEFINITION   genomic survey sequence.
ACCESSION    AY418812
VERSION      AY418812.1 GI:39774772
KEYWORDS     GSS.
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE    1 (bases 1 to 983)
AUTHORS     Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Perriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
            Adams,M.D. and Cargill,M.
            Inferring nonneutral evolution from human-chimp-mouse orthologous
            gene trios
            Science 302 (5652), 1960-1963 (2003)
JOURNAL      14671302
PUBMED
REFERENCE    2 (bases 1 to 983)
AUTHORS     Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferreria,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
            Direct Submission
            Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
            These sequences were made by sequencing genomic exons and ordering
            them based on alignment.
FEATURES     Location/Qualifiers
source       1. .983
            /organism="Homo sapiens"
            /mol_type="genomic DNA"
            /db_xref="taxon:9606"
            <1. .>983
            /gene="BMP2"
            /locus_tag="HCM6682"
gene
ORIGIN
Alignment Scores:
Pred. No.:      1.82e-164      Length:      983
Score:          1732.00      Matches:    326
Percent Similarity: 99.69%      Conservative: 0

```

```
Best Local Similarity: 99.69% Mismatches: 1
Query Match: 82.55% Indels: 0
DB: 10 Gaps: 0

US-10-801-648-2 (1-396) x AY418812 (1-983)

Qy 4 GlyThrArgCysLeuLeuAlaLeuLeuLeuProGlnValLeuLeuGlyGlyAlaAlaGly 23
Db 3 GGGACCGCGTCTCTTACGCTTCTCTTCCAGGTCCTCTCTGGGCGGCGCGCTGGC 62

Qy 24 LeuValProGluLeuGlyArgArgLysPheAlaAlaAlaSerSerGlyArgProSerSer 43
Db 63 CTCGTCGCGAGCTGGCGCGAGAGTTCGCGCGGCTCGTCTGGGCGGCGCGCTCATCC 122

Qy 44 GlnProSerAspGluValLeuSerGluPheGluLeuArgLeuLeuSerMetPheGlyLeu 63
Db 123 CAGCCCTCTGACGAGTCTCTGACGAGTTCAGTTGCGGCTGCTCAGCAGTTTGGCCCTG 182

Qy 64 LysGlnArgProThrProSerArgAspAlaValValProProTyrMetLeuAspLeuTyr 83
Db 183 AAACAGAGACCCACCCAGCAGGAGCGCGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 242

Qy 84 ArgArgHisSerGlyGlnProGlySerProAlaProAspHisArgLeuGluAlaAla 103
Db 243 CGCAGGCACTCAGGTCAGCGGCTCACCCGCGCCAGACACCGGTTGGAGGCGCAGCC 302

Qy 104 SerArgAlaAanThrValArgSerPheHisGluGluSerLeuGluGluLeuProGlu 123
Db 303 AGCGAGGCAACACTGTCGCGAGCTTCACCATGAAGAATCTTTGGAGAAGACTACCAGAA 362

Qy 124 ThrSerGlyLysThrThrArgArgPhePheAsnLeuSerSerIleProThrGluGlu 143
Db 363 ACAGTGGGAAACACACCGCGAGATCTCTTTAAATTAAGTTCTATCCCGCAGGAG 422

Qy 144 PheIleThrSerAlaGluLeuGlnValPheArgGluGlnMetGlnAspAlaLeuGlyAsn 163
Db 423 TTTATCACTCAGCAGAGCTTCAGGTTTTCGAGAACACAGATGCTTTAGGAAAC 482

Qy 164 AsnSerSerPheHisArgIleAsnIleTyrGluIleIleLysProAlaThrAlaAsn 183
Db 483 AATAGCAGTTTCCATCACCGAATTATATTAATTAATTAATTAATTAATTAATTAAT 542

Qy 184 SerLysPheProValThrArgLeuLeuAspThrArgLeuValAsnGlnAsnAlaSerArg 203
Db 543 TCGAAATTCCTCCGTCAGCAGCTTTTGGACACAGGTTGGTGAATCAGATGCAAGCAG 602

Qy 204 TrpGluSerPheAspValThrProAlaValMetArgTrpThrAlaGlnGlyHisAlaAsn 223
Db 603 TGGGAAAGTTTGTATGTACCCCGCTGTGATGCGGTGACTGTCACAGGACACGCGCAAC 662

Qy 224 HisGlyPheValValGluValAlaHisLeuGluGluLysGlnGlyValSerLysArgHis 243
Db 663 CATGATTCGTTGGTGAAGTGCCACCTTGGAGGAGAAACAGGTTCTCAAGAGACAT 722

Qy 244 ValArgIleSerArgSerLeuHisGlnAspGluHisSerTrpSerGlnIleArgProLeu 263
Db 723 GTTAGTAAGCAGAGTCTTTGACCAACAGATGACACAGCTGCTCAGATTAAGCCATTG 782

Qy 264 LeuValThrPheGlyHisAspGlyLysGlyHisProLeuHisLysArgGluLysArgGln 283
Db 783 CTAGTAACTTTTGGCCATGATGGAAGAGGCGATCTCTCCACAAAGAGAGAAACGTCAA 842

Qy 284 AlaLysHisLysGlnArgLysArgLeuLysSerSerCysLysArgHisProLeuTyrVal 303
Db 843 GCCAACAACAACACGCGAAACGCTTAAGTCCAGCTGTAAAGAGACACCCCTTTGTACGTG 902

Qy 304 AspPheSerAspValGlyTrpAsnAspTrpIleValAlaProProGlyTyrHisAlaPhe 323
Db 903 GACTTCAGTACGTTGGGTGGAAATGACTGATTTGGCTTCCCGGGGTATACACCCCTTT 962

Qy 324 TyrCysHisGlyGluCysPro 330
Db 963 TACTGCCACGAGAAATGCCCT 983
```

```
RESULT 3
AV418814
LOCUS Mus musculus BMP2 gene, VIRTUAL TRANSCRIPT, partial sequence, 977 bp DNA linear GSS 17-DEC-2003
DEFINITION Mus musculus BMP2 gene, VIRTUAL TRANSCRIPT, partial sequence, 977 bp DNA linear GSS 17-DEC-2003
ACCESSION AY418814
VERSION AY418814.1 GI:39774774
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 977)
AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 977)
AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
COMMENT These sequences were made by sequencing genomic exons and ordering them based on alignment.
FEATURES
source location/Qualifiers
1..977
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
<1..>977
/gene="BMP2"
/locus_tag="HCN6682"
gene
ORIGIN
Alignment Scores:
Pred. No.: 6.99e-150 Length: 977
Score: 1588.00 Matches: 295
Percent Similarity: 95.41% Conservative: 17
Best Local Similarity: 90.21% Mismatches: 13
Query Match: 75.69% Indels: 2
DB: 10 Gaps: 2
US-10-801-648-2 (1-396) x AY418814 (1-977)
Qy 4 GlyThrArgCysLeuLeuAlaLeuLeuLeuProGlnValLeuLeuGlyGlyAlaAlaGly 23
Db 3 GGGACCGCGTCTCTTACGCTTCTCTTCCAGGTCCTCTCTGGGCGGCGCGCTGGC 62
Qy 24 LeuValProGluLeuGlyArgArgLysPheAlaAlaAlaSerSerGlyArgProSerSer 43
Db 63 CTCATTCAGAGCTGGCGCGAGAGTTCGCGCGGCTCGTCTGGGCGGCGCGCTCATCC 119
Qy 44 GlnProSerAspGluValLeuSerGluPheGluLeuArgLeuLeuSerMetPheGlyLeu 63
Db 120 CGGCTTCGGAAGAGCTCTCTCAGGAATTTGATTTGAGGCTGCTCAGCATGTTGGCCCTG 179
Qy 64 LysGlnArgProThrProSerArgAspAlaValValProProTyrMetLeuAspLeuTyr 83
Db 180 AAGCAGAGACCCACCCAGCAGCAGCTCGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 239
Qy 84 ArgArgHisSerGlyGlnProGlySerProAlaProAspHisArgLeuGluAlaAla 103
Db 240 CGCAGGCACTCAGGCGCAGGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCC 299
```

Qy 104 SerArgAlaAenThrValArgSerPheHisHisGluSerLeuGluLeuProGlu 123
 Db 300 AGCCGCGCCACACCGTGGCGAGCTTCATCACAAGAAAGCGTGGAGAACTTCCAGAG 359
 Qy 124 ThrSerGlyLysThrThrArgArgPhePheAsnLeuSerSerIleProThrGluGlu 143
 Db 360 ATGAGTGGGAAACGCGCGCGCTCTCTTCAATTAAAGTTCTGTCCCGCAGTGACGAG 419
 Qy 144 PheIleThrSerAlaGluLeuGlnValPheArgGluGlnMetGlnAspAlaLeuGlyAsn 163
 Db 420 TTTCTCATCTGCAGAACTCCAGATCTCCGGAACAGATACAGAGAGCTTTGGGA--- 476
 Qy 164 AsnSerSerPheHisHisArgIleAsnIleTyrGluIleLeuLysProAlaThrAlaAsn 183
 Db 477 AACAGTATTTCCAGCACCGAATTAATATTATGAATTTAAGCTTGCAGAGCCCAAC 536
 Qy 184 SerLysPheProValThrArgLeuLeuAspThrArgLeuValAsnGlnAsnAlaSerArg 203
 Db 537 TTGAAATTTCTGTGACCACTATTGGACACCAAGTTAGTGATCAGAACACAACTCAG 596
 Qy 204 TrpGluSerPheAspValThrProAlaValMetArgTrpThrAlaGlnGlyHisAlaAsn 223
 Db 597 TGGAGAGAGCTTCGACGTCACCCAGCTGTGTATGCGGTGGACACACAGGGCACACCAAC 656
 Qy 224 HisGlyPheValValAlaHisLeuGluGlnLysGlnGlyValSerLysArgHis 243
 Db 657 CATGGGTTTGGTGGAGTGGCCCATTTAGAGAGAACCCAGGTGTCTCCAGAGACAT 716
 Qy 244 ValArgIleSerArgSerLeuHisGlnAspGluHisSerTrpSerGlnIleArgProLeu 263
 Db 717 GTGAGGATTAGCAGTCTTTGCCACCAAGATGAACACAGCTGTGTACAGATTAAGCCATTG 776
 Qy 264 LeuValThrPheGlyHisAspGlyLysGlyHisProLeuHisLysArgGluLysArgGln 283
 Db 777 CTAGTGACTTTTGGACATGATGGAAGAAGCATCCGCTCCACAAACGAGAAACGCTCAA 836
 Qy 284 AlaLysHisLysGlnArgLysArgLeuLysSerSerCysLysArgHisProLeuTyrVal 303
 Db 837 GCCAAACACAAACAGCGAAGCGCTCAAGTCCAGCTGCAAGAGACACCCCTTTGTATGTG 896
 Qy 304 AspPheSerAspValGlyTrpAsnAspTrpIleValAlaProProGlyTyrHisAlaPhe 323
 Db 897 GACTTCAGTGATGGGTGGATGACTGGATCGTGGCACCTCCGGGCTATCATGCTCTT 956
 Qy 324 TyrCysHisGlyLysGluCysPro 330
 Db 957 TACTGCCATGGGAGTGTCTCT 977

RESULT 4
 BX431362
 LOCUS BX431362 903 bp mRNA linear EST 04-MAY-2004
 DEFINITION BX431362 Homo sapiens PLACENTA Homo sapiens cDNA clone CS0DE003YB10
 5-PRIME, mRNA sequence.
 ACCESSION BX431362
 VERSION BX431362.2 GI:47009531
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Homo.
 1 (bases 1 to 903)
 L4,W.B., Gruber,C., Jessee,J. and Polayes,D.
 Full-length cDNA libraries and normalization
 Unpublished (2001)
 On May 15, 2003 this sequence version replaced gi:30781021.
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 2 rue Gaston Crémieux, Cp 5706 - 91057 EVRY cedex - FRANCE
 Email: seqreg@genoscope.cns.fr, Web : www.genoscope.cns.fr
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
 end enriched, double-strand cDNA was digested with Not I and cloned
 into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library

was not normalized. Library was constructed by Life Technologies, a
 division of Invitrogen.
 This sequence belongs to sequence cluster 10041.f
 For more information about this cluster, see
 http://www.genoscope.cns.fr/cdna?s=CS0BAG0112G10_CS01039_1&c=10041.f.

FEATURES

source

Location/Qualifiers
 1..903
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0DE003YB10"
 /tissue_type="PLACENTA"
 /clone_lib="Homo sapiens PLACENTA"
 /notes="vector: pCMVSPORT 6; 1st strand cDNA was primed
 with a NotI-oligo(dT) primer. Five prime end enriched,
 double-strand cDNA was digested with Not I and cloned into
 the Not I and EcoRV sites of the pCMVSPORT 6 vector.
 Library was not normalized."

ORIGIN

Alignment Scores:
 Pred. No.: 2,42e-135 Length: 903
 Score: 1444.00 Matches: 280
 Percent Similarity: 96.27% Conservative: 4
 Best Local Similarity: 94.92% Mismatches: 11
 Query Match: 68.83% Indels: 2
 DB: 5 Gaps: 0
 US-10-801-648-2 (1-396) x BX431362 (1-903)
 Qy 92 SerProAlaProAspHisArgLeuGluArgAlaAlaSerArgAlaAenThrValArgSer 111
 Db 6 GCTCCCGCGCCACACCCCGTGGGGGGGGCGAGCCAGCCGAGCCAC- ACTGTGCGGAGC 64
 Qy 112 PheHisHisGluGluSerLeuGluLeuProGluThrSerGlyLysThrThrArgArg 131
 Db 65 TTCACCATGAGAGAAATCTTTGGAGAACTACCAAGAACGAGTGGGAAACAAACCCGGAGA 124
 Qy 132 PhePhePheAsnLeuSerSerIleProThrGluGluPheIleThrSerAlaGluLeuGln 151
 Db 125 TTCTTCTTTAATTAAAGTTCTATCCCGGAGGAGTTTATCACCTCAGCAGAGCTTTCAG 184
 Qy 152 ValPheArgGluGlnMetGlnAspAlaLeuGlyAsnAsnSerSerPheHisHisArgIle 171
 Db 185 GTTTCGAGACAGATGCAAGATGCTTTAGGAAACAATAAGCAGTTTCCATCACCGAATT 244
 Qy 172 AsnIleTyrGluIleIleLysProAlaThrAlaAsnSerLysPheProValThrArgLeu 191
 Db 245 AATATTTATGAATCATAAACCTGCAACAGCCACTCGAAATTCCTCCGTGACCATGCTT 304
 Qy 192 LeuAspThrArgLeuValAsnGlnAsnAlaSerArgTrpGluSerPheAspValThrPro 211
 Db 305 TTGGACACCAAGTGTGGTGAATCAGATGCAAGAGGTGGGAAAGTTTGTATGTCAACCC 364
 Qy 212 AlaValMetArgTrpThrAlaGlnGlyHisAlaAsnHisGlyPheValValGluValAla 231
 Db 365 GCTGTGTATGCGGTGGACTGCACAGGGACACGCCAACCATGATTCGTGGTGGAGTGGCC 424
 Qy 232 HisLeuGluGluLysGlnGlyValSerLysArgHisValArgIleSerArgSerLeuHis 251
 Db 425 CACTTGGAGGAGAAACAAGGTGTCTCCAGAGACATGTTAGGATTAACAGAGTCTTTGAC 484
 Qy 252 GlnAspGluHisSerTrpSerGlnIleArgProLeuLeuValThrPheGlyHisAspGly 271
 Db 485 CAAGATGAACACAGCTGTGTACAGATAAGGCCATTGCTAGTAACCTTTTGGCCATGATGGA 544
 Qy 272 LysGlyHisProLeuHisLysArgGluLysArgGlnAlaLysHisLysGlnArgLysArg 291
 Db 545 AAAGGGCATCTCTCCCAAAAAGAGAAAAACGTCAGCCCAACCAACCAACCGGAAACGC 604
 Qy 292 LeuLysSerSerCysLysArgHisProLeuTyrValAspPheSerAspValGlyTrpAsn 311

Db 605 CTTAAGTCCAGCTGTAAAGAGACACCCCTTTGTACGTGGAGCTTCAGTGACGTGGGGTGAAT 664
 Qy 312 AspTPIIleValAlaProGlyTyrHisAlaPheTyrCysHisGlyGluCysProPhe 331
 Db 665 GACTGGATTGGCTCCCGGGGATCACGCCCTTTTACTGCCAGGAGATGCCCTTTT 724
 Qy 332 ProLeuAlaAspHisLeuAsnSerThrAsnHisAlaIleValGlnThrLeuValAsnSer 351
 Db 725 CCTCGGCTGATCATCTCAACTCCACTTAATCATGCCATTGNTCAGACGTTGGTCACTCT 784
 Qy 352 ValAsnSerLysIleProLysAlaCysCysValProThrGluLeuSerAlaIleSerMet 371
 Db 785 GTTAACTTAAGATTCCTAAGCATGCTGTGTCCGACAGAACTCAGTGTCTATCTCGATG 844
 Qy 372 LeuTyrLeuAspGluAsnGluLysValValLeuLysAsnTyrGln 386
 Db 845 CTGTACCTTTGACGAGATGA-AAGGTTGTATTAAAGAACTTCAGA 888

RESULT 5
 DN117475/c
 LOCUS DN117475 841 bp mRNA linear EST 15-FEB-2005
 DEFINITION 1117145 MARC 4PIG Sus scrofa cDNA 3', mRNA sequence.
 ACCESSION DN117475
 VERSION DN117475.1 GI:59811735
 KEYWORDS EST.

SOURCE
 ORGANISM Sus scrofa (pig)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suidae;
 Sus.

REFERENCE 1 (bases 1 to 841)
 Smith,T.P.L., Freking,B.A., Ford,J.J., Vallet,J.L., Wise,T.A.,
 Nonneman,D.J., Wray,J.E. and Keele,J.W.
 TITLE Porcine EST collection using a normalized library constructed from
 embryos representing early developmental stages

JOURNAL Unpublished (2003)
 COMMENT Contact: Smith TPL
 USDA, ARS US Meat Animal Research Center
 PO Box 166, Clay Center, NE 68933-0166, USA
 Tel: 402 762 4366
 Fax: 402 762 4390
 Email: smith@email.marc.usda.gov
 Single pass sequencing. Bases called with phred v0.020425.c and
 trimmed with the aid of the trim_alt option. Vector identified with
 cross_match v0.990329.
 Plate: HHY8017 row: A column: 20
 Seq primer: TAGAAGGCACAGTCGAGG.

FEATURES
 Location/Qualifiers
 1..841
 /organism="Sus scrofa"
 /mol_type="mRNA"
 /db_xref="taxon:9823"
 /tissue_type="pooled"
 /lab_host="DH10B"
 /clone_lib="MARC 4PIG"
 /note="Vector: pcDNA3.1; Site 1: EcoRI; Site 2: NotI;
 Library made with combined RNA from day-10, day-13,
 day-15, day-25, and day-30 whole embryos."

ORIGIN

Alignment Scores:
 Pred. No.: 9,45e-125 Length: 841
 Score: 1339.00 Matches: 248
 Percent Similarity: 95.83% Conservative: 5
 Best Local Similarity: 93.94% Mismatches: 11
 Query Match: 63.82% Indels: 0
 DB: 8 Gaps: 0

US-10-801-648-2 (1-396) x DN117475 (1-841)

Qy 133 PhePheAsnLeuSerIleProThrGluGluPheIleThrSerAlaGluLeuGlnVal 152
 Db 839 TTTTAAATTAACTTCTGTCTCCCGAGGAGTTTATCACTTCAGCAGAACTTCAGGTC 780

Qy 153 PheArgGluGlnMetGlnAspAlaLeuGlyAsnAsnSerSerPheHisHisArgIleasn 172
 Db 779 TTTTCGGACACAGACACAGGAGACTTTGGATAACAGTAGACGTTTCCATCACCAGTAATAAT 720
 Qy 173 IleTyrGluIleIleLysProAlaThrAlaAsnSerLysPheProValThrArgLeuLeu 192
 Db 719 ATNTATGAATCATCAAACTGCAACCACTCCAACTCCAACTCCAACTCCAACTCCAACTCC 660
 Qy 193 AspThrArgLeuValAsnGlnAsnAlaSerArgTTPGluSerPheAspValThrProAla 212
 Db 659 GACACCAAGTTGGTGACTCCGAATGCCAGAGGTGGAGAGCTTCGAGCTCACCCCGCT 600
 Qy 213 ValMetArgTTPThrAlaGlnGlyHisAlaAsnHisGlyPheValValGluValAlaHis 232
 Db 599 GTGATGCGGTGAGCTGCACACGGGTGCCAACACCGGGTTCGTGGTGGAGTGGCCAC 540
 Qy 233 LeuGluGluLysGlnGlyValSerLysArgHisValAlaIleSerArgSerLeuHisGln 252
 Db 539 CCGGAGGACACCGCGGAGGTCTCCAAGAGGATGTGCGGATTAGCAGGTCTTTGCACCA 480
 Qy 253 AspGluHisSerTTPSerGlnIleArgProLeuLeuValThrPheGlyHisAspGlyLys 272
 Db 479 GATGAGCACAGCTGGTCAAAATAGACCCCTTGTCTAGTCACCTTTTCGGCCACGATGGGAA 420
 Qy 273 GlyHisProLeuHisLysArgGluLysArgGlnAlaLysHisLysGlnArgLysArgLeu 292
 Db 419 GGACACCTCTGCACAAAGGAGGAGGTCAGCAAAACACAAACACGCGCAAGCGCTG 360
 Qy 293 LysSerSerCysLysArgHisProLeuTyrValAspPheSerAspValGlyTTPAsnAsp 312
 Db 359 AAATCCAGCTGCAAGAGACACCCCTTTGTACGTGGACTTCAGTGATGTGGCTGGGAATGAC 300
 Qy 313 TrpIleValAlaProGlyTyrHisAlaPheTyrCysHisGlyGluCysProPhePro 332
 Db 299 TGGATCGTAGCCCCCGGGGTATCATGCCCTTTTACTCCACGGGAGTGCCCTTTTCCCC 240
 Qy 333 LeuAlaAspHisLeuAsnSerThrAsnHisAlaIleValGlnThrLeuValAsnSerVal 352
 Db 239 CTGGCTGATCACTGAATCCACGATCAGCCATCGTCCAGACCTTGGTCAACTCCGTT 180
 Qy 353 AsnSerLysIleProLysAlaCysCysValProThrGluLeuSerAlaIleSerMetLeu 372
 Db 179 AACTCTAAGATCCCAAGCGGTGCTGTCTCCCAACAGAACTCAGTGCCTCATCTGCTG 120
 Qy 373 TyrIleAspGluAsnGluLysValValLeuLysAsnTyrGlnAspMetValValGluGly 392
 Db 119 TACCTTGACGAGAACGAAAGGTGTATTAAAGAACTACAGGACATGTTGTGGAGGT 60
 Qy 393 CysGlyCysArg 396
 Db 59 TGTGGTGTGCT 48

RESULT 6
 AY409113 1227 bp DNA linear GSS 16-DEC-2003
 LOCUS AY409113
 DEFINITION Homo sapiens BMP4 gene, VIRTUAL TRANSCRIPT, partial sequence,
 genomic survey sequence.
 ACCESSION AY409113
 VERSION AY409113.1 GI:39765081
 KEYWORDS GSS.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homidae; Homo.
 REFERENCE 1 (bases 1 to 1227)
 AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
 Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
 Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,
 Adams,M.D. and Gargill,M.

TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
 gene trios

```

JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 1227)
AUTHORS Clark,A.G., Gianowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
source Location/Qualifiers
1..1227
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
<1..>1227
/gene="BMP4"
/locus_tag="HCM3449"
ORIGIN
Alignment Scores:
Pred. No.: 2,04e-117 Length: 1227
Score: 1269,00 Matches: 258
Percent Similarity: 73.9% Conservative: 45
Best Local Similarity: 62.32% Mismatches: 87
Query Match: 60.49% Indels: 24
DB: 10 Gaps: 10
US-10-801-648-2 (1-396) x AY409113 (1-1227)
Qy 1 MetValAlaGlyThrArgCysLeuLeuAlaLeuLeuProGlnValLeuLeuGlyGly 20
Db 1 ATGATTCCTGTAACCGAATCTGATGTCGCTTTTATTTATGCAAGTCCTGCTAGGAGGC 60
Qy 21 Ala-----AlaGlyLeuValProGluLeuGlyArgArgLysPheAla- 35
Db 61 GCGAGCCATGCTAGTTTGATACCTTGAGACGGGGGAGAAAGATCGCCGAGATTCAGGGC 120
Qy 36 AlaSerSerGlyArgProSerSerGlnProSerAspGluLeuValLeuSerGluPheGluLeu 55
Db 121 CACGGGGAGGAGCGCGCTCAGGCAG---AGCCATGAGCTCCTCGGGACTTCGAGGCG 177
Qy 56 ArgLeuLeuSerMetPheGlyLeuLysGlnArgProThrProSerArgAspAlaValVal 75
Db 178 ACACCTTCGCAGATGTTTGGGCTGCGCGCGCGCCGAGCCTAGCAAGAGTGCCTCATTT 237
Qy 76 ProProTyrMetLeuAspLeuTyrArgArgHisSerGlyGln----- 89
Db 238 CCGGACTACATCGGGGATCTTTTACCGGCTTCAGTCTGGGGAGAGGAGGAGAGACAGATC 297
Qy 90 -----ProGlySerProAlaProAspHisArgLeuGluArgAlaAlaSerArgAlaAsn 107
Db 298 CACAGCACTGCTCTGAGATATCTT-----GAGCGCCCGCGCAGCGCGGCCAC 345
Qy 108 ThrValArgSerPheHisGluGluSerLeuGluGluLeuProGluThrSerGlyLys 127
Db 346 ACCGTGAGGAGCTTCCACACGAGAACATCTGGAGAACATCCCGAGGACCAAGTGAAGAAC 405
Qy 128 ThrThrArgArgPhePheAsnLeuSerSerIleProThrGluGluPheIleThrSer 147
Db 406 TCTGCTTTTCTTCTCTTTAACTCAGCAGCATCCCTGAGACGAGGTGATCTCTCT 465
Qy 148 AlaGluLeuGlnValPheArgGluGlnMetGlnAspAlaLeuGlyAsnAsnSerSerPhe 167
Db 466 GCAGAGCTTCGGCTCTCCGGGAGCAGGTGACACCGGCCCTGATTGGGAAGGGGCTTC 525
Qy 168 HisHisArgIleAsnIleTyrGluIleLys---ProAlaThrAlaAsnSerLysPhe 186
Db 526 ---CACCGTATAAACATTTATGAGTTATGAAGCCCGCCAGCAGAAGTGGTGCCTGGGCAC 582
Qy 187 ProValThrArgLeuLeuAspThrArgLeuValAsnGlnAsnAlaSerArgTyrGluSer 206

```

```

Db 583 CTATCATCAGCAGCTACTGGACAGAGACTGGTCACCAATGTGACACGGTGGAAACT 642
Qy 207 PheAspValThrProAlaValMetArgTyrThrAlaGlnGlyHisAlaAsnHisGlyPhe 226
Db 643 TTTGATGTGAGCCCTCGGTCCTTGGCTGGACCGGGAGAACGACCAACTATGGGCTA 702
Qy 227 ValValGluValAlaHisLeuGluGlyGlnGlyValSerLysArgHisValArgIle 246
Db 703 GCCATTGAGGTGATCTACCTCCATCAGACTCGGACCCACGAGGCCAGCAGTGTGAGATT 762
Qy 247 SerArgSerLeuHisGlnAspGluHisSerTyrSerGlnIleArgProLeuLeuValThr 266
Db 763 AGCGATCGTTACTCTCAAGGAGTGGGAATGGCCAGCTCCGCCCTCTCTGGTCAAC 822
Qy 267 PheGlyHisAspGlyLysGlyHisProLeu-----HisLysArgGluLysArgGlnAla 284
Db 823 TTTGGCCATGATGCGCGGGCCATGCTTGACCCGACGCGCGGAGGCCAAGCGTAGCCCT 882
Qy 285 Lys---HisLysGlnArgLysArgLeuLysSer---SerCysLysArgHisProLeuTyr 302
Db 883 AAGCATCACTCACAGCGCGGCCAGGAGAGAATAAGAACTGCGCGGCCACTCGCTCTAT 942
Qy 303 ValAspPheSerAspValGlyTyrAsnAspTyrIleValAlaProProGlyTyrHisAla 322
Db 943 GTGGACTTCAGCGATGTGGGCTGGAATGACTTGGATTGTGCCCCACCAAGGCTACAGGCC 1002
Qy 323 PheTyrCysHisGlyGluCysProPheProLeuAlaAspHisLeuAsnSerThrAsnHis 342
Db 1003 TTCTACTGCCATGCGGGACTGCCCTTTTCCACTGGCTGACCACTCAACTCAACCAACCAT 1062
Qy 343 AlaIleValGlnThrLeuValAsnSerValAsnSerLysLysIleProLysAlaCysCysVal 362
Db 1063 GCCATTGTGCAGACCCCTGGTCAATTCTGTCAATTCACAGTATCCCAAAGCGCTGTGTGTG 1122
Qy 363 ProThrGluLeuSerAlaIleSerMetLeuTyrLeuAspGluLeuValValValLeu 382
Db 1123 CCCACTGACTGATGTCGCACTCTCCATGCTGTACTGATGATGATGATGATGATGATGATG 1182
Qy 383 LysAsnTyrGlnAspMetValValGluGlyCysGlyCysArg 396
Db 1183 AAAAAATTATCAGGAGATGGTAGTAGAGGATGTGGGTGCCGC 1224
RESULT 7
CR595138 1676 bp mRNA linear HTC 21-JUL-2004
LOCUS full-length cDNA clone CSODI042YJ24 of Placenta Cot 25-normalized
DEFINITION of Homo sapiens (human).
ACCESSION CR595138
VERSION CR595138.1 GI:50475945
KEYWORDS HTC; CNSLT_cDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 1676)
AUTHORS Li,W.B., Gruber,C., Jesses,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue
REFERENCE 2 (bases 1 to 1676)
GENOSCOPE Genoscope.
DIRECT SUBMISSION Direct Submission
SUBMITTED (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : sequef@genoscope.cns.fr)
COMMENT - Web : www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a

```



```

division of Invitrogen.
FEATURES
  Location/Qualifiers
    1..1676
      /organism="Homo sapiens"
      /mol_type="mRNA"
      /db_xref="taxon:9606"
      /clone="CSODI042YJ24"
      /tissue_type="Placenta"
      /plasmid="pCMVSPORT_6"
ORIGIN
Alignment Scores:
Pred. No.:      3.22e-117      Length:      1676
Score:          1269.00      Matches:    258
Percent Similarity: 73.19%      Conservative: 45
Best Local Similarity: 62.32%      Mismatches: 87
Query Match:      60.49%      Indels:     24
DB:                4          Gaps:        10
US-10-801-648-2 (1-396) x CR595138 (1-1676)
Qy      1 MetValAlaGlyThrArgCysLeuLeuAlaLeuLeuProGlnValLeuLeuGlyGly 20
Db      184 ATGATTCTCTGTAAACCGAATGCTGATGTCGTCTTTATTATGCCAAGTCTCTAGGAGGC 243
Qy      21 Ala-----AlaGlyLeuValProGluLeuGlyArgArgLysPheAla-----Ala 35
Db      244 CGGAGCCATGCTAGTTGATACCTGAGACGGGGAGAAAAGTCGCCGAGATTCAGGGC 303
Qy      36 AlaSerSerGlyArgProSerSerGlnProSerAspGluValLeuSerGluPheGluLeu 55
Db      304 CACGGGGAGGAGCGCGCTCAGGGCAG--AGCCATGAGCTCTCTGGGGACTTCGAGGCG 360
Qy      56 ArgLeuLeuSerMetPheGlyLeuLysGlnArgProThrProSerArgAspAlaValVal 75
Db      361 ACACCTTCGTCAGATGTTTGGGCTGGCGCGCGCGCGAGCTAGCAGAGTGCCTGTCATT 420
Qy      76 ProProTyrMetLeuAspLeuTyrArgArgHisSerGlyGln----- 89
Db      421 CCGGACTACATGCGGGATCTTTACCGCTTCAGTCTGGGGAGGAGGAGGAGAGCAGATC 480
Qy      90 -----ProGlySerProAlaProAspHisArgLeuGluArgAlaAlaSerArgAlaAsn 107
Db      481 CACAGCAGCTGCTTGTAGTATCCT-----GAGCGCGCGCGCGCGCGCGCGCAAC 528
Qy      108 ThrValArgSerPheHisGlyGluSerLeuGluLeuProGluThrSerGlyLys 127
Db      529 ACCGTGAGGAGCTTCACACGAGAACATCTGGAGAACATCCCGAGGAGCCAGTGAAAC 588
Qy      128 ThrThrArgArgPhePheAsnLeuSerSerIleProThrGluGluPheIleThrSer 147
Db      599 TCTGCTTTTCGTTCTCTTTAACTCAGCAGCATCCCTGTGAGACAGAGTGATCTCTCT 648
Qy      148 AlaGluLeuGlnValPheArgGluGlnMetGlnAspAlaLeuLeuGlyAsnAsnSerSerPhe 167
Db      649 GCAGAGCTTCGGCTCTCCGGGAGCAGGTGGACACGAGCGCTGATTGGGAAAGGGGCTTC 708
Qy      168 HisHisArgIleAsnIleTyrGluIleIleLys---ProAlaThrAlaAsnSerLysPhe 186
Db      709 ---CACCGTATAAACATTATGAGGTTATGAGCCCGCCAGCAGAGAGTGGTCCCTGGGCAC 765
Qy      187 ProValThrArgLeuLeuAspThrArgLeuValLeuGlnAsnAlaSerArgTyrGluSer 206
Db      766 CTCATCACACGACTACTGACACGAGACTGGTCCACCAATGTGACACGCGTGGGAAACT 825
Qy      207 PheAspValThrProAlaValMetArgTyrThrAlaGlnGlyHisAlaAsnHisGlyPhe 226
Db      826 TTTGATGTGAGCCCTTCGGGTCTCTCGCTGGACCGGGAGAGACGACCCAACTATGGGCTA 885
Qy      227 ValValGluValAlaHisLeuGluGlyValSerLysArgHisValArgIle 246
Db      886 GCCATTGAGGTGACTCACCTCCATCAGACTCGGAGCCACCGAGCGGCGCAGCATGTCAAGATT 945
247 SerArgSerLeuHisGlnAspGluHisSerTrpSerGlnIleArgProLeuLeuValThr 266
946 AGCCGATCGTTACCTCAAGGGAGTGGGAATTTGGGCCAGCTCCGCCCTCTCTGGTCAAC 1005
267 PheGlyHisAspGlyLysGlyHisProLeu-----HisLysArgGlyLysArgGlnAla 284
1006 TTTGGCCATGATGCCCGGGGCCATGCTTGACCCGACGCGCGAGGGGCCAACGCTAGCCCT 1065
285 Lys---HisLysGlnArgLysArgLeuLysSer---SerCysLysArgHisHisProLeuTyr 302
1066 AAGCATCACTCACAGCGGGCCAGGAGAGAGATAGAACTGCCCGGCCCATCTCGTCTAT 1125
303 ValAspPheSerAspValGlyTrpAsnAspTrpIleValAlaProProGlyTyrHisAla 322
1126 GTGGACTTCAGCGATGTGGCTGCAATGACTGGATTGTGGCCACCAAGCTTACCAAGGCC 1185
323 PheTyrCysHisGlyGluCysProPheProLeuAlaAspHisLeuAsnSerThrAsnHis 342
1186 TTCTACTGCCATGGGAGTGCCTTTCCATGCTGCTGACCACTCAACTCAACCAACCAT 1245
343 AlaIleValGlnThrLeuValAsnSerValAsnSerLysIleProLysAlaCysCysVal 362
1246 GCCATTGTGCAGACCTTGGTCAATCTGTCAATTCAGTATCCCAAGCTTGTGTGTG 1305
363 ProThrGluLeuSerAlaIleSerMetLeuTyrLeuAspGluAsnGlyValValLeu 382
1306 CCCACTGAAGTGTGATGCTCCATGCTGATGATGATGATGATGATGATGATGATGATG 1365
383 LysAsnTyrGlnAspMetValValGluGlyCysGlyCysArg 396
1366 AAAAAATTATCAGGAGATGTTAGTAGAGGATGTGGTGGCCGC 1407
RESULT 8
CONSULT118E      1692 bp      mRNA      linear      HTC 28-JAN-2003
LOCUS      human full-length cDNA clone CSODI018YL16 of Placenta of Homo
DEFINITION      sapiens (human).
ACCESSION      BX161438
VERSION      BX161438.1 GI:28071055
KEYWORDS      HTC.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE      1 (bases 1 to 1692)
AUTHORS      Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE      Full-length cDNA libraries and normalization
JOURNAL      Unpublished
REMARK      Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Paradise Avenue PO Box 6482 Carlsbad, California, 92008 Phone : +1
760 603-7200
REFERENCE      2 (bases 1 to 1692)
AUTHORS      Genoscope.
TITLE      Direct Submission
JOURNAL      BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
COMMENT      - Web : www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
FEATURES      Location/Qualifiers
      1..1692
        /organism="Homo sapiens"
        /mol_type="mRNA"
        /db_xref="taxon:9606"
        /clone="CSODI018YL16"
        /tissue_type="Placenta"
        /plasmid="pCMVSPORT_6"
        /note="Cot 25-normalized"

```



```

/clone="CSODC002YH22"
/tissue type="Neuroblastoma"
/plasmid="pCMVSPORT 6"
/notes="Cot 25-normalized"
188..1414

```

CDS

```

/note="unnamed protein product"
/codon start=1
/protein id="CAD61876.1"
/db xref="GI:28070990"
/translation="MIPGNRMLMVLLCQVLLGGASHSLIPETGKKVARIQHGAG
RRSGSHLLDFRATLQMFGLRRRPPQSKSAVTPDMRDLYRLQSGEEREEQIHST
GLEYPERSANTVRSFPHLEHLENIPTGSNSAPFLNLSIPENVEISSAELRL
FREVDQDQWERGFHRIINIEYVMKPAEYVPGHLITLRLDLRVHNNVLRWTFEDVS
PAVLRTREKQPNGLALEVTHLQTRTHOQHVRISRLPQSGSNWAOLRPLLVTFG
HDGCHALTREARRKSPKHSQARKKNKRBSLYVDFSDVGNWDMIVAPPGYQA
FYCHGDCFFPLADHLNLSNHALVQTLVNSVNSIPKACCVFELSLSMLYLDYDKV
VLKNYQEMVVEGCGR"

```

ORIGIN

```

Alignment Scores:
Pred. No.: 3,3e-117 Length: 1705
Score: 1269.00 Matches: 258
Percent Similarity: 73.19% Conservative: 45
Best Local Similarity: 62.32% Mismatches: 87
Query Match: 60.49% Indels: 24
DB: 4 Gaps: 10

```

US-10-801-648-2 (1-396) x CNSLTI18D (1-1705)

```

QY 1 MetValAlaGlyThrArgCysLeuLeuAlaLeuLeuProGlnValLeuLeuGlyGly 20
Db 188 ATGATCTCTGGTAACCGAATGCTGATGTCGTGTTTATTATGCAACATCTCTGTCAGGAGC 247
QY 21 Ala-----AlaGlyLeuValProGluLeuGlyArgArgLysPheAla-----Ala 35
Db 248 GCGAGCCATGCTAGTTGATACCTCAGACGGGGAAGAAAAAGTCGCGGAGATTTCAGGCG 307
QY 36 AlaSerSerGlyArgProSerSerGlnProSerAspGluValLeuSerGluPheGluLeu 55
Db 308 CACGCGGAGGAGCGCGCTCAGGCGAG---AGCCATGAGCTCTCTCGGAGACTTCGAGGCG 364
QY 56 ArgLeuLeuSerMetPheGlyLeuLysGlnArgProThrProSerArgAspAlaValVal 75
Db 365 ACACCTCTGCAGATGTTGGGTGGCGCGCGCGCGAGCTTAGCAAGAGTGCCTCAT 424
QY 76 ProProTyrMetLeuAspLeuTyrArgArgHisSerGlyGln----- 89
Db 425 CCGGACTACATCGCGGATCTTTACCGGCTTCAGTCTGGGGAGGAGGAGGAGGAGCAGATC 484
QY 90 -----ProGlySerProAlaProAspHisArgLeuGluArgAlaAlaSerArgAlaLen 107
Db 485 CACAGCAGCTGCTTTGAGTATCT-----GAGCGCGCGCGCGAGCGCGGCGCAAC 532
QY 108 ThrValArgSerPheHisGluGluSerLeuGluLeuProGluThrSerGlyLys 127
Db 533 ACCGTGAGAGAGCTTCACCCAGCAGAGACATCTGGAGACATCCCGAGGACGAGTGAAC 592
QY 128 ThrThrArgArgPhePheAsnLeuSerSerIleProThrGluPheIleThrSer 147
Db 593 TCTGCTTTTTCGTTCTCTTTAACTTCAGCAGCATCCCTTGAGACGAGGTGATCTCTCT 652
QY 148 AlaGluLeuGlnValPheArgGluGlnMetGlnAspAlaLeuGlyAsnAsnSerPhe 167
Db 653 GCAGAGCTTCGCTCTTCGCGGAGCAGGTGGACCGAGCGCCCTGATTTGGGAAGGGCGCTTC 712
QY 168 HisHisArgIleAsnIleTyrGluIleIleLys---ProAlaThrAlaAsnSerLysPhe 186
Db 713 ---CACCGTATAAACATTATGAGGTATGAGGCCCGCCAGCAGAGTGTGCTGGGCAC 769
QY 187 ProValThrArgLeuLeuAspThrArgLeuValAsnGlnAsnAlaSerArgTrpGluSer 206
Db 770 CTCATCACAGGACTACTGCAGCAGGAGACTGGTCCACCAATGTGACACGGTGGGAAACT 829

```

```

QY 207 PheAspValThrProAlaValMetArgTrpThrAlaGlnGlyHisAlaAsnHisGlyPhe 226
Db 830 TTTGATGTGAGCCCTGCGGCTCTTCTGCGTGGACCGGAGAGCAGCAGCAACTATGGGCTA 889
QY 227 ValValGluValAlaHisLeuGluGlyGlnGlyValSerLysArgHisValArgIle 246
Db 890 GCCATTGAGGTGACTACCTCCATCAGACTCGGACCCACCGAGGCCAGCAGTGTGAGGATT 949
QY 247 SerArgSerLeuHisGlnAspGluHisSerTrpSerGlnIleArgProLeuLeuValThr 266
Db 950 AGCCGATCGTTACTCAAGGAGTGGGAATTTGGGCCAGCTCCGCGCCCTCTCTGGTCACC 1009
QY 267 PheGlyHisAspGlyLysGlyHisProLeu-----HisLysArgGluLysArgGlnAla 284
Db 1010 TTTGGCCATGATGCGCGGGCCATGCTTTCACCGACGCGCGAGGGCCAGCGTAGCCCT 1069
QY 285 Lys---HisLysGlnArgLysArgLeuLysSer---SerCysLysArgHisProLeuTyr 302
Db 1070 AAGCATCACTCACAGCGCGGCCAGGAAGAAATAAGAACTCGCGCGCCACTCGCTCTAT 1129
QY 303 ValAspPheSerAspValGlyTrpAsnAspTrpIleValAlaProProGlyTyrHisAla 322
Db 1130 GTGGACTTCACGATGTCGCTGGAATGACTGGATTTGGGCCACCAAGGCTTACCAGGCC 1189
QY 323 PheTyrCysHisGlyGluCysProPheProLeuAlaAspHisLeuAsnSerThrAsnHis 342
Db 1190 TTTCTACTGCCATGGGAGCTGCCCTTTTCCACTGCTGCTGACCACTCAACTCAACCAACCAT 1249
QY 343 AlaIleValGlnThrLeuValAsnSerValAsnSerLysIleProLysAlaCysCysVal 362
Db 1250 GCCATTGTGCAGACCCCTGGTCAATCTGTCAATTCAGATATCCCAAGCCCTGTTGTGTG 1309
QY 363 ProThrGluLeuSerAlaIleSerMetLeuTyrLeuAspGluAsnGluLysValValLeu 382
Db 1310 CCCACTGAACAGAGTGCCATCTCCATGCTGACCTGGATGATGATGATGATGATGATGATG 1369
QY 383 LysAsnTyrGlnAspMetValValGluGlyCysGlyCysArg 396
Db 1370 AAAAATTATCAGGAGATGTTAGTAGAGGATGTTGGTGCGCGC 1411
RESULT 10
AY409115 1227 bp DNA linear GSS 16-DEC-2003
LOCUS Mus musculus BMP4 gene, VIRTUAL TRANSCRIPT, partial sequence,
DEFINITION genomic survey sequence.
ACCESSION AY409115
VERSION AY409115.1 GI:39765083
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidae; Muridae; Murinae; Mus.
REFERENCE
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
Inferred nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
Direct Submision
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
Location/Qualifiers

```

```

source      1. .1227
             /organism="Mus musculus"
             /mol_type="genomic DNA"
             /db_xref="taxon:10090"
gene        <1..>1227
             /gene="BMP4"
             /locus_tag="HMC3449"

ORIGIN
Alignment Scores:
Pred. No.:      2,57e-117      Length:      1227
Score:          1268.00        Matches:      258
Percent Similarity: 72.95%      Conservative: 44
Best Local Similarity: 62.32%    Mismatches:   88
Query Match:     60.44%        Indels:       24
DB:              10           Gaps:        10

US-10-801-648-2 (1-396) x AY409115 (1-1227)

QY 1 MetValAlaGlyThrArgCysLeuLeuAlaLeuLeuProGlnValLeuGlyGly 20
D 1 ATGATTCCTGTGAACCGAATCCTGATGCTGCTTTATTATGCCCAAGTCTCTGTAGGAGGC 60
QY 21 Ala-----AlaGlyLeuValProGluLeuGlyArgArgLysPheAla-----Ala 35
D 61 GCGAGCCATGCTAGTTTGTATCTAGACCGCGGAGAAAGTCCGCGAGATTCAGGCG 120
QY 36 AlaSerSerGlyArgProSerSerGlnProSerAspGluValLeuSerGluPheGluLeu 55
D 121 CACGCGGGAGGACCGCGCTCAGGGCAG---AGCCATGAGCTCCTCGCGGACTTCGAGGCG 177
QY 56 ArgLeuLeuSerMetPheGlyLeuLysGlnArgProThrProSerArgAspAlaValVal 75
D 178 ACACCTTCTACAGATGTTTGGCTCGCGCGCTCCGAGCGCTAGCAAGAGCGCGTCAATT 237
QY 76 ProProTyrMetLeuAspLeuTyrArgArgHisSerGlyGln-----89
D 238 CCGGATTACATGAGGATCTTTACCGCTCCAGTCTGGGAGGAGGAGGAGAGAGCAG 297
QY 90 -----ProGlySerProAlaProAspHisArgLeuGluArgAlaAlaSerArgAla 106
D 298 AGCCAGGAGAACCGGCTTGAGTACCG-----GAGCGTCCCGCGCAGCGAGCC 345
QY 107 AsnThrValArgSerPheHisHisGluGluSerLeuGluGluLeuProGluThrSerGly 126
D 346 AACACTGTGAGGAGTTTCCATCAGCAAGAACATCTGAGAGAACATCCCGAGGACAGTGAG 405
QY 127 LysThrThrArgArgPhePheAsnLeuSerSerIleProThrGluGluPheIleThr 146
D 406 AGCTCTGCTTTTCGTTTCTCTTCCACTCAGCAGCATCCAGAAATGAGGTGATCTCC 465
QY 147 SerAlaGluLeuGlnValPheArgGluGlnMetGlnAspAlaLeuGlyAsnAsnSerSer 166
D 466 TCGGCGAGAGCTCCGGCTCTTTCCGGGAGCAGGTGGACACCGGCCCTGACTGGGAACAGGC 525
QY 167 PheHisHisArgIleAsnIleTyrGluIleIleLys---ProAlaThrAlaAsnSerLys 185
D 526 TTC---CACCGTATAAATATTATGAGGTTATGAGGCTTATGAGGCCCGCCAGCAAGATGTTCTCGGA 582
QY 186 PheProValThrArgLeuLeuAspThrArgLeuValAsnGlnAsnAlaSerArgTyrTyrGlu 205
D 583 CACCTCATCAGACGACTACTGGACACCGACTAGTCTCATCTCATGTGACACGGTGGGAA 642
QY 206 SerPheAspValThrProAlaValMetArgTyrThrAlaGlnGlyHisAlaAsnHisGly 225
D 643 ACTTTCGATGTGAGCCCTCGAGTCTTCTCGTGGACCGGGAAAGCAACCAATTATGGG 702
QY 226 PheValValGluValAlaHisLeuGluGlyGlnGlyValSerLysArgHisValArg 245
D 703 CTGGCCATTGAGGTGACTCACCTCCACGACACGAGCCACCGAGGCGGCGCATGTGCGA 762
QY 246 IleSerArgSerLeuHisGlnAspGluHisSerTrpSerGlnIleArgProLeuLeuVal 265

```

```

Db 763 ATCAGCCGATCGTTACTCCTCAAGGAGTGGAGATTGGCCCAACTCCGGCCCTCTCGTC 822
QY 266 ThrPheGlyHisAspGlyLysGlyHisProLeu---HisLysArgGluLysArgGlnAla 284
D 823 ACTTTTGGCCATGATGGCCGCGGCATACCTTGACCCGAGGAGGCGCAACGAGTAGTCCC 882
QY 285 Lys---HisLysGlnArgLysArgLeuLysSer---SerCysLysArgHisProLeuTyr 302
D 883 AAGCATCACCCACAGCGGTCGAGGAAGAAGAACTGCCGTCGCCATTCATCTATAC 942
QY 303 ValAspPheSerAspValGlyTyrAsnAspTyrIleValAlaProProGlyTyrHisAla 322
D 943 GTGGACTTTCAGTGCAGCTGGGCTGGAATGATTTGGTGGCCCAACCGCTACCGGCC 1002
QY 323 PheTyrCysHisGlyGluCysProPheProLeuAlaAspHisLysLeuAsnSerThrAsnHis 342
D 1003 TTCTACTGCCATGGGACTGTCCTTTCCATCGCTGATCACCTCAACTCAACCAACCAT 1062
QY 343 AlaIleValGlnThrLeuValAsnSerValAsnSerLysIleProLysAlaCysCysVal 362
D 1063 GCCATTGTGCAGACCCCTAGTCAACTCTGTAAATCTAGTATCCCTAAGGCTGTGTGTC 1122
QY 363 ProThrGluLeuSerAlaIleSerMetLeuTyrLeuAspGluAsnGluLysValValLeu 382
D 1123 CCCACTGAACCTGAGTGCCATTTCCATGTTGTTACTGATGATGATGACAGGTGGTGTG 1182
QY 383 LysAsnTyrGlnAspMetValValGluGlyCysGlyCysArg 396
D 1183 AAAAAATTATCAGGAGATGGTGTAGAGGGGTGTGGATGCCGC 1224

RESULT 11
CX354839 1636 bp mRNA linear EST 13-JUL-2005
DEFINITION ssalrbs36157_rev_0 mixed_tissue Salmo salar cDNA, mRNA sequence.
ACCESSION CX354839
VERSION CX354839.2 GI:70788043
KEYWORDS EST.
SOURCE Salmo salar (Atlantic salmon)
ORGANISM Salmo salar
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
1 (bases 1 to 1636)
Rise,M.L., von Schalbun,K.R., Brown,G.D., Mawer,M.A., Devlin,R.H.,
Kuipers,N., Busby,M., Beetz-Sargent,M., Alberto,R., Gibbs,A.R.,
Hunt,P., Shukin,R., Zelnik,J.A., Nelson,C., Jones,S.R.,
Smailus,D.E., Jones,S.J., Schein,J.E., Marra,M.A.,
Butterfield,Y.S., Stott,J.M., Ng,S.H., Davidson,W.S. and Koop,B.F.
Development and application of a salmonid EST database and cDNA
microarray: data mining and interspecific hybridization
Characteristics
Genome Res. 14 (3), 478-490 (2004)
14962987
On Jan 5, 2005 this sequence version replaced gi:57123398.
Contact: Koop BF
Centre for Biomedical Research
University of Victoria
PO Box 3020 STN CSC, Victoria BC, V8W 3N5, Canada
Tel: 250 472 4067
Fax: 250 472 4075
Email: bkoop@uvic.ca
Genome Sciences Centre, BC Cancer Agency
cDNA preparation, sequencing and bioinformatics: Y Butterfield, R
Kirkpatrick, J Asano, N Gilm, R Guin, D Lee, S Lee, T Olson, P
Pandoh, A Prabhu, D Smailus, L Spence, J Stott, S Taylor, G Yang, J
Schein, S Jones and M Marra.
Location/Qualifiers
1. .1636
/organism="Salmo salar"
/mol_type="mRNA"
/strain="McConnell"
/db_xref="taxon:8030"
/clone_lib="mixed_tissue"

FEATURES
source

```

/note=Vector: pQW6port6; Library Creator: Research Genetics ; Atlantic salmon tissue contributors: Carlo Biagi, Mitch Uh, and Robert Devlin (DFO, Vancouver, B.C.), Simon Jones (PBS, Nanaimo, B.C.), Seaspring Hatchery (Crofton, B.C.), Rachel Roper (University of Victoria)"

ORIGIN

Alignment Scores:
Pred No.: 9.15e-116 Length: 1636
Score: 1254.50 Matches: 252
Percent Similarity: 73.19% Conservative: 51
Best Local Similarity: 60.87% Mismatches: 86
Query Match: 59.80% Indels: 25
DB: 8 Gaps: 11

US-10-801-648-2 (1-396) x CX354839 (1-1636)

```
Qy 1 MetValAlaGlyThrArgCysLeuLeuAlaLeuLeuProGlnValLeuLeuGlyGly 20
Db ATGATTCCTGTAATCGAATCGATGCTGATGCTCATTTTATTATGCCAAGTCTCTGCGGAGAG 457
Qy 21 Ala-----AlaGlyLeuValProGluLeuGlyArgArgGlyPheAlaAlaSerSer 38
Db AGCAACCATGCTAGTCTGATACCTGAGGAAGGGAAGAGAA--GCAACCGGGGCTGCGAG 514
Qy 39 GlyArgProSerSerGlnProSerAspGluValLeuSerGluPheGluLeuArgLeuLeu 58
Db AGCCGGAGCTGCTGCTGAG--AGCCATGACTGCTGCGGAGCTTTGAGGCCACGCTGCTA 571
Qy 59 SerMetPheGlyLeuLeuGlnArgProThrProSerArgAspAlaValProProFyr 78
Db CACATGTTTGACTGACAGGCGAGCGCGGCCAGTCTGCGCCACTGTGCCACGGTAC 631
Qy 79 MetLeuAspLeuYrArgArgHisSerGlyGlnProGlySerProAlaProAspHisArg 98
Db CTGCTGGACCTCTACCGCTGCTGCGGCGAG--GCTGAGGAGCGCGGACCCACCGAC 688
Qy 99 Leu-----GluArgAlaAlaSerArgAlaAenThrValArgSerPheHis 113
Db ACCGCTTTGAGTACCCGAGGCTGCTGAGCGGAGCTGAGCGGCGCACACCGTGGGGCTTCCAC 748
Qy 114 HisGluLeuSerLeuGluGluLeuProGluThrSerGlyLysThrArg----- 130
Db CACGAGAGACATGAGCCGGTTCATCCGGCGAGTCTCAGACGAGAACGAGAGGCC 808
Qy 131 -----ArgPhePheAsnLeuSerSerIleProThrGluGluPheIleThrSer 147
Db ATCCCACTGCGCTTCTCTCAATCTCAGCAACATCCCGAGGAGCGAGCTGCTCTCGTCG 868
Qy 148 AlaGluLeuGlnValPheArgGluGlnMetGlnAspAlaLeu-----GlyAsn 163
Db GCGGAGCTGCGTCTGCTCCGAGCAGATCGACGAGGCGCATTCGGAAGCGAGGCGGAC 928
Qy 164 AsnSerSerPheHisArgIleAsnIleYrGluIleIleLysProAlaThrAlaAsn 183
Db AAGGATCAGCTC--CACCGATAACTGTACGAGGTGCTGACGCCCGCGGGCGGG 985
Qy 184 SerLysPheProValThrArgLeuLeuAspThrArgLeuValAsnGlnAsnAlaSerArg 203
Db ATCAGCGGCTTTTGGACACACGCGTGTGTCACCATACGATACGCGCTCGCGC 1039
Qy 204 TrpGluSerPheAspValThrProAlaValMetArgTrpThrAlaGlnGlyHisAlaAsn 223
Db TGGGAGAGCTTTGAGCTGAGCCCCCGCTGCTGCGCTGACACGCGGCGGCTGCGCCAAC 1099
Qy 224 HisGlyPheValValGluValAlaHisLeuGluGluLysGlnGlyValSerLysArgHis 243
Db TACGGGCTGGCGCTGAGTCCAGCCTCAACACGACACCGCCACCGAGGCGCGCCAC 1159
Qy 244 ValArgIleSerArgSerLeuHisGlnAspGlu---HisSerTrpSerGlnIleArgPro 262
Db CTGCGCATCAGCGCTGCTGCTGACGAGGCGCGGGGAGGACTGGGAGCAGCTACGCCCC 1219
```

```
Qy 263 LeuLeuValThrPheGlyHisAspGlyLysGlyHisProLeuHisLysArgGluLysArg 282
Db CTGCTGCTACCTTCGCGCCATGACGCGCAAGGGCCACCGTTGACGCGTGGCAAGCGC 1279
Qy 283 GlnAlaLysHisLysGlnArgLysArgLeuLysSerSerCysLysArgHisProLeuYr 302
Db AGCCAAAGCAGCGGGGGCGTAAGCGC---AACCGCAACTGTGCGCGTCATGCTCTCTAC 1336
Qy 303 ValAspPheSerAspValGlyTrpAsnAspTrpIleValAlaProProGlyLysHisAla 322
Db GTGGACTTCAGCGATGTAGGCTGGATGACTGGATGATGGCGCCGCCAGGTACCGACA 1396
Qy 323 PheYrCysHisGlyGluCysProPheProLeuAlaAspHisLysLeuAsnSerThrAsnHis 342
Db TACTACTGCCATGGGAATGTCCCTTCCCTGCGCAGACCACTTCCAAACCCAC 1456
Qy 343 AlaIleValGlnThrLeuValAsnSerValAsnSerLysIleProLysAlaCysCysVal 362
Db GCCATGTTTCAAGCGTTGGTGAATCCGGTGAACCAACCATTTCCCAAGGCTGCTGCGTG 1516
Qy 363 ProThrGluLeuSerAlaIleSerMetLeuYrLeuAspGluAsnGluLysValValLeu 382
Db CCCAGGAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1576
Qy 383 LysAsnYrGlnAspMetValValGluGlyCysGlyCysArg 396
Db AAAAATACCAGGAATGTTGTTGGAAGGTTGCTGCGC 1618
RESULT 12
CV804617 724 bp mRNA linear EST 15-NOV-2004
LOCUS AGENCOURT 36361580 NIH MGC 280 Homo sapiens cDNA clone
DEFINITION IMAGE:7503800 5', mRNA sequence.
ACCESSION CV804617.1 GI:55747583
VERSION CV804617.1
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 724)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Meri Firpo
cDNA Library Preparation: Express Genomics
cDNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLM15873 row: h column: 06
High quality sequence stop: 598.
Location/Qualifiers
1. 724
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:7503800"
/tissue_type="pluripotent cell line derived from
blastocyst inner cell mass"
/lab_host="DH10B"
/clone_lib="NIH MGC_280"
/note="Organ: Blastocyst; Vector: pExpress-1; Site:1:
EcoRV; Site 2: NotI; RNA obtained from pluripotent cell
line derived from blastocyst inner cell mass (cell line
HSP-6, NIH Registry designation UC06. Positive for OCT4
```

expression by rtPCR, positive for SSRA-3, SSRA-4, Tra-1-81, Tra-1-60 by immunofluorescence. Negative for SSRA-1 by immunofluorescence Passage 62. cDNA was primed using oligo-dT primer:
5'-pGACTAGTCTAGATCGGAGCGCGCC(T)25-3' and cloned into the EcoRV/NotI sites of pExpress-1. Size-selection >1.25 kb resulted in an average insert size of 1.8 kb. This primary library is non-normalized (normalized primary library is NIH MGC 281) and was constructed by Express Genomics (Frederick, MD). Note: this is a Mammalian Gene Collection library."

ORIGIN

Alignment Scores:
Pred. No.: 3, 29e-114 Length: 724
Score: 1234.00 Matches: 236
Percent Similarity: 97.93% Conservative: 0
Best Local Similarity: 97.93% Mismatches: 5
Query Match: 58.82% Indels: 1
DB: 8 Gaps: 0

US-10-801-648-2 (1-396) x CV804617 (1-724)

Qy 85 ArgHisSerGlyGlnProGlySerProAlaProAspHisArgLeuGluArgAlaAlaSer 104
Db 1 AGGCACCTCGGTCAGCGGGCTCACCGCCACAGCCCGTTGGAGAGCGCAGCCAGC 60

Qy 105 ArgAlaSerThrValArgSerPheHisHisGluSerLeuGluLeuProGluThr 124
Db 61 CGAGCCCAACACTGTGCGCAGCTCCACCATGAAGATCTTTGGAGAACTACCAAGAACG 120

Qy 125 SerGlyLysThrThrArgArgPhePheAsnLeuSerSerIleProThrGluGluPhe 144
Db 121 AGTGGAAACACCCCGAGATCTTCTTAATTAAGTCTATCCCCACGAGAGGTTT 180

Qy 145 IleThrSerAlaGluLeuGlnValPheArgGluGlnMetGlnAspAlaLeuGlyAsnAsn 164
Db 181 ATCACTCAGCAGAGCTTCAGGTTTTCGAGAACAGATGCAAGATGCTTTAGGAAACAAT 240

Qy 165 SerSerPheHisHisArgIleAsnIleTyrgluilelelyserProAlaThrAlaAsnSer 184
Db 241 AGCAGTTTCCATCACCCGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 300

Qy 185 LysPheProValThrArgLeuLeuAspThrArgLeuValAsnGlnAsnAlaSerArgTyrp 204
Db 301 AAATCCCGTGACAGCTCTTTTGACACCCAGGTGGTGAATCAAGATGCAAGCAGGTGG 360

Qy 205 GluSerPheAspValThrProAlaValMetArgTyrThrAlaGlnGlyHisAlaAsnHis 224
Db 361 GAAAGTTTGTATGTCACCCCGCTGTGTGCGGTGGACTGCACAGGACACGCCAACCAT 420

Qy 225 GlyPheValValGluValAlaHisLeuGluGluLysGlnGlyValSerLysArgHisVal 244
Db 421 GGATTCTGTGGTGAAGTGGCCCACTTGGAGAGAAACAAGGTGTCTCCAAGACATGTT 480

Qy 245 ArgIleSerArgSerLeuHisGlnAspGluHisSerTrpSerGlnIleArgProLeuLeu 264
Db 481 AGGATAGCAGGCTTTTGGACCAAGATGAACACAGCTGGTGCACAGATAAGGCCATTGCTA 540

Qy 265 ValThrPheGlyHisAspGlyLysGlyHisProLeuHisLysArgGluLysArgGlnAla 284
Db 541 GTAACCTTTGGCCATGATGGAAGGGCATCTCTCCACAAAGAGAAACGTCAGACC 600

Qy 285 LysHisLysGlnArgLysArgLeuLysSerSerCysLysArgHisProLeuTyrrValasp 304
Db 601 AAACACAAACAGCGGAACCGCTTAAGTCCAGCTGTGAAGAGACACCCCTTTGTACGTGGAC 660

Qy 305 PheSerAspValGlyTyrAsnAspTyrIleValAlaProProGlyTyrHisAlaPheTyr 324
Db 661 TTCAGTGGACGTGGTGGATGACGGATTTGTGCTCTCCCGGGGAT-CACGCCCTTTTAC 719

325 Cys 325

720 TGC 722

RESULT 13
AY418813
LOCUS
DEFINITION
Pan troglodytes BMP2 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION
AY418813
VERSION
AY418813.1 GI:39774773
SOURCE
GSS.
ORGANISM
Pan troglodytes (chimpanzee)
Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Pan.
1 (bases 1 to 711)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarival, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
Science 302 (5652), 1960-1963 (2003)
14671302
2 (bases 1 to 711)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarival, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
These sequences were made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
Location/Qualifiers
source
1..711
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
gene
<1..>711
/gene="BMP2"
/locus_tag="HCM682"

ORIGIN

Alignment Scores:
Pred. No.: 5, 11e-114 Length: 711
Score: 1232.00 Matches: 230
Percent Similarity: 97.88% Conservative: 1
Best Local Similarity: 97.46% Mismatches: 5
Query Match: 58.72% Indels: 0
DB: 10 Gaps: 0

US-10-801-648-2 (1-396) x AY418813 (1-711)

Qy 117 SerLeuGluGluLeuProGluThrSerGlyLysThrArgArgPhePheAsnLeu 136
Db 3 TCTTTGGAGAGCTTACAGAAACGAGTGGGAAACACCCGAGATCTCTTCAATTTA 62

Qy 137 SerSerIleProThrGluGluPheIleThrSerAlaGluLeuGlnValPheArgGluGln 156
Db 63 AGTTCTATCCCCGAGGAGTCTATCACCTCAGCAGAGCTTCAGGTTTTTCGAGAACAG 122

Qy 157 MetGlnAspAlaLeuGlyAsnAsnSerSerPheHisHisArgIleAsnIleTyrrGluile 176
Db 123 ATGCGAGATGCTTTAGGAAACAATAGCAGTTTCATCACCAGGATTTTATGAAATC 182

Qy 177 IleLysProAlaThrAlaAsnSerLysPheProValThrArgLeuLeuAspThrArgLeu 196
Db 183 ATAAACCTCAACAGCAACTCGAAATTCCTGTCACAGACTTTTGGACACAGGTTG 242

Qy 197 ValAsnGlnAsnAlaSerArgTyrGluSerPheAspValThrProAlaValMetArgTyrp 216
Db 243 GTGAATCAGAATGCAAGCAGGTGGGAAAGTTTTTGATGTACCCCGCTGTGATCGGTGG 302

was blunted, ligated to NotI adapters, digested with EcoRI, size-selected, and cloned into the NotI and EcoRI compatible sites of a custom modified MCS of the pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS (1994) 91: 9228-9232 and Bernaldo et al., Genome Research 6 (1996): 791, except that a significantly longer reannealing hybridization was used."

ORIGIN

Alignment Scores: 1.41e-113 Length: 881
Pred. No.: 1229.00 Matches: 234
Score: 1229.00
Percent Similarity: 90.58% Conservative: 16
Best Local Similarity: 84.78% Mismatches: 23
Query Match: 58.58% Indels: 3
DB: 5 Gaps: 0

US-10-801-648-2 (1-396) x BU444424 (1-881)

QY 124 ThrSerGlyLysThrThrArgArgPhePheAenLeuSerSerIleProThrGluGlu 143
Db 5 ACAAGTGGGAAACAGCAGCAGCTTCCTTTTAATTAATTCATCCCTAATGAGAG 64
QY 144 PheIleThrSerAlaGluLeuValPheArgGluMetGlnAenAlaLeuGlyAen 163
Db 65 TCTGTCACTCAGCTGAACCTCCAGATTTTCGGGAGCAGGTGCAGAGCCCTTTGAGAGC 124
QY 164 AenSerSerPheHisHisArgIleAenIleTyrglullelleLysProAlaThrAlaAen 183
Db 125 AACAGCAGCTACCATCCCGTATTATATTTATGAAATTTATGAAGCCAGCCAGCCACC 184
QY 184 SerLysPheProValThrArgLeuLeuAspThrArgLeuValAenGlnAenAlaSerArg 203
Db 185 TCCAGGACCTCTGCAGAGACTTTTGACACAGGTGGTGGTGCATATATGCAAGTAAA 244
QY 204 TrpGluSerPheAspValThrProAlaValMetArgTrpThrAlaGlnGlyHisAlaAen 223
Db 245 TGGGAAAGTTTGTATGATTAACGCCAGCTGTTTGTAGGTGGATTGCACAGCAACCTAAC 304
QY 224 HisGlyPheValValGluValAlaHisLeuGluLysGlnGlyValSerLysArgHis 243
Db 305 CATGGTGTGGTGGAGGTGTTCACTTGACAAAGAGAACAGTGCCTCCAAAGGGCAC 364
QY 244 ValArgIleSerArgSerLeuHisGlnAspGluHisSerTrpSerGlnIleArgProLeu 263
Db 365 GTTAGGATTAGCAGGTCTTTACATCAGATGAAGTAGCTGCTCAGCTCAGGCCGTG 424
QY 264 LeuValThrPheGlyHisAspGlyLysGlyHisProLeuHisLysArgGlyLysArgGln 283
Db 425 TTAGTGACGTTGGGCATGATGGCAGGACACCGCTCCACAAAGAGAAAGAGGTCAA 484
QY 284 AlalyHisLysGlnArgLysArgLeuLysSerSerCysLysArgHisProLeuTyVal 303
Db 485 GCGAAACACAAACAGCGTAAGCGCACAAATACAGTTTGCAAAAGAGCATCCCGTGTATGTG 544
QY 304 AspPheSerAspValGlyTrpAsnAspTrpIle-ValAlaProProGlyTyThrHisAlaPh 323
Db 545 GACTTCAATACGTTGGGGTGNAAATGACTGGATTGTTGCCCCCGGGGTACAGTGCCTT 604
QY 323 eTyrcys-HisGlyGluCysProPheProLeuAlaAspHisLeuAenSerThrAenHisA 343
Db 605 TTATCGCCATGGGGAATGTCCTTTTCGCTGGCAGATCACCTAAATCAACAAACCATG 664
QY 343 lalleValGlnThrLeuValAenSerValAenSerLysIleProLysAlaCysCysValP 363
Db 665 CCATTGTTCACTTTGGTCAATTCCGTGAATTCGAAATCCAAATCCCAAGGCTGTGTGTG 724
QY 363 roThrGluLeuSerAlaIleSerMetIleTyTrpLeuAspGluAenGluLysValValLeu 383
Db 725 CGACAGAACTCAGTGTCTATCTCAATGCTCTACCTTGCAGAGAACGAAAGGTGCTACTAA 784
QY 383 ysAenTyrcGlnAspMetValValGluGlyCys-GlyCysArg 396

217 ThrAlaGlnGlyHisAlaAenHisGlyPheValValGluValAlaHisLeuGluGluLys 236
Db 303 ACTGCACAGGAGCAGCCACCATGGATTCTGTGTGGAGTGGCCACTTGGAGAGAGAA 362
QY 237 GlnGlyValSerLysArgHisValArgIleSerArgSerLeuHisGlnAspGluHisSer 256
Db 363 CAAGTGCTCTCAAGAGACATGTTAGGATAAGCAGGTCTTTGCAACCAAGATGAACACAGC 422
QY 257 TrpSerGlnIleArgProLeuLeuValThrPheGlyHisAspGlyLysGlyHisProLeu 276
Db 423 TGGTCACAGATAAGCCATTCCTAGTAACTTTTGCCCATGATGAAAGAGGCATCCCTCTC 482
QY 277 HisLysArgGluLysArgGlnAlalyHisLysGlnArgLysArgLeuLysSerSerCys 296
Db 483 CACAAAGAGAAACAGTCAAGCCCAACACACAGCGGAAACGCTTAACTCAGCTGT 542
QY 297 LysArgHisProLeuTyValAspPheSerAspValGlyTrpAsnAspTrpIleValAla 316
Db 543 AAGAGACACCTTTGTACGTGGACTTCAGTCAGCTGGGTGGATGACTGATTTGTGGCT 602
QY 317 ProProGlyTyThrHisAlaPheTyrcHisGlyGluCysProPheProLeuAlaAspHis 336
Db 603 CCCCCGGGTATCAGCCCTTTTACTGCCAGGNNATGCCCTTTTCTCTGGCTGATCAT 662
QY 337 LeuAenSerThrAenHisAlaIleValGlnThrLeuValAenSerVal 352
Db 663 CTGAACCTCANNNTNATCATGCCATTGTCAGAGCTTGGTCAACTCTGTT 710

RESULT 14
BU444424
LOCUS
DEFINITION 881 bp mRNA linear EST 29-NOV-2002
603213309P1 CSEQBEN13 Gallus gallus cdna clone CHEST196a3 5', mRNA
sequence.
ACCESSION BU444424
VERSION BU444424.1 GI:25933735
KEYWORDS EST.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 881)
Boardman, P. E., Sanz-Ezquerro, J., Overton, I. M., Burt, D. W., Bosch, E.,
Pong, W. T., Tickle, C., Brown, W. R. A., Wilson, S. A. and Hubbard, S. J.
A Comprehensive Collection of Chicken CDNAS
Curr. Biol. 12 (22), 1965-1969 (2002)
12445392
Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
(UMIST)
PO Box 88, Manchester, M60 1QD, UK
Tel: 0161208930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.
Location/Qualifiers
1. :881
/organism="Gallus gallus"
/mol_type="mRNA"
/strains="Layer"
/db_xref="taxon:9031"
/clone="CHEST196a3"
/sex="Female"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="CSEQBEN13"
/note="Organ: ovary; Vector: pBluescript II KS(+); Site_1:
EcoRI; Site_2: NotI; This normalized library was
constructed from 1 million independent clones. cdna
synthesis was initiated using an oligo(dT) primer, using
methylated C in the first strand synthesis reaction.
Following this first strand reaction, double-stranded cdna

```

Db      785 AGAACTATCAGATATGTTGTGGAGGCTCGGGTGGCGT 826
|||||
RESULT 15
BU625617/c
LOCUS
DEFINITION
  UI-H-FG1-bgn-b-18-0-UI-s1 NCI CGAP_FG1 Homo sapiens cDNA clone
  UI-H-FG1-bgn-b-18-0-UI 3', mRNA sequence.
ACCESSION
  BU625617
VERSION
  BU625617.1 GI:23291832
KEYWORDS
  EST.
SOURCE
  Homo sapiens (human)
ORGANISM
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
  Hominidae; Homo.
REFERENCE
  1 (bases 1 to 727)
  NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
  Tumor Gene Index
  Unpublished (1997)
JOURNAL
  Contact: Robert Strausberg, Ph.D.
  Email: cgapsb@mail.nih.gov
COMMENT
  Tissue Procurement: James Martin
  cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
  cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
  DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
  Clone Distribution: Clone distribution information can be obtained
  from Dr. M. Bento Soares, bento-soares@uiowa.edu
  The following repetitive elements were found in this cDNA
  sequence: 1-27, >POLY_A#Simple_repeat (matched complement) 31-61,
  >(TA)#Simple_repeat (matched complement)
  Seq primer: M13 FORWARD
  POLYA=Yes.

FEATURES
  source
    1..727
    /location="Qualifiers"
    /organism="Homo sapiens"
    /mol_type="mRNA"
    /db_xref="taxon:9606"
    /clone="UI-H-FG1-bgn-b-18-0-UI"
    /tissue_type="Cell lines"
    /dev_stage="Adult"
    /lab_host="DH10B (Life Technologies)"
    /clone_lib="NCI-CGAP_FG1"
    /note="Organ: Enchondroma; Vector: p7T3-Pac (Pharmacia)
    with a modified polylinker; Site 1: EcoR I; Site 2: Not I;
    NCI CGAP_FG1 is a normalized cDNA library obtained from a
    pool of mRNA from 2 cell lines from Enchondroma tissues.
    The library was constructed according to Bonaldo, Lennon
    and Soares, Genome Research, 6:791-806, 1996. First strand
    cDNA synthesis was primed with an oligo-dT primer
    containing a Not I site. Double stranded cDNA was ligated
    to an EcoR I adaptor, digested with Not I, and cloned
    directionally into p7T3-Pac vector. The oligonucleotide
    used to prime the synthesis of first-strand cDNA contains
    a library tag sequence that is located between the Not I
    site and the (dT)18 tail. The sequence tag for this
    library is CGGTCACTC. The cell lines were provided by Dr.
    James Martin from the University of Iowa.
    TAG_TISSUE=Enchondroma cell line (Mix of EN1 and EN2)
    TAG_L18=UI-H-FG1
    TAG_SEQ=CGGTCACTC"

ORIGIN
  Alignment Scores:
  Pred. No.:      2.03e-107      Length:      727
  Score:          1167.00      Matches:      214
  Percent Similarity: 99.08%      Conservative: 1
  Best Local Similarity: 98.62%      Mismatches: 2
  Query Match:      55.62%      Indels:      0
  DB:              5          Gaps:      0
  US-10-801-648-2 (1-396) x BU625617 (1-727)

```

Search completed: January 11, 2006, 02:09:20

Job time : 3462 secs

```

Qy      180 AlaThrAlaAsnSerLysPheProValThrArgLeuLeuAspThrArgLeuValAsnGln 199
      726 GCAACAGCCAACTCGAAATTCNCGGTGACACAGCTTTGTGAGCACCAGGTTGGTGAATCAG 667
      Qy      200 AsnAlaSerArgTrpGluSerPheAspValThrProAlaValMetArgTrpThrAlaGln 219
      Db      666 AATGCAAGCAGGTGGGAAAGTTTGTATGTCACCCCTGTGATGCGGTGACTTGCACAG 607
      Qy      220 GlyHisAlaAsnHisGlyPheValValGluValAlaHisLeuGluGluLysGlnGlyVal 239
      Db      606 GCACAGCCCAACCATGGATTTCGTGTGTAAGTGGCCCACTTGGAGGAGAAACAAGGTGTC 547
      Qy      240 SerLysArgHisValArgLleSerArgSerLeuHisGlnAspGluHisSerTrpSerGln 259
      Db      546 TCCAAGAGACATGTTAGGATAAGCAGGCTCTTTGCACCAAGATGAACACAGCTGGTTCACAG 487
      Qy      260 IleArgProLeuLeuValThrPheGlyHisAspGlyLysGlyHisProLeuHisLysArg 279
      Db      486 ATTAGGCCATTTAGTAACTTTTGGCCATGTATGAAAAGGGCATCTCTCCACAAAGA 427
      Qy      280 GluLysArgGlnAlaLysHisLysGlnArgLysArgLeuLysSerSerCysLysArgHis 299
      Db      426 GAAAAACGTCAAGCCAAACACAAACAGCGGAAACGCCCTTAAGTCCAGCTGTAAAGAGACAC 367
      Qy      300 ProLeuTrpValAspPheSerAspValGlyTrpAsnAspTrpIleValAlaProProGly 319
      Db      366 CCTTTGTACGTGGACTTTCACTGACGTGGGTGGAATGACTGGATTTGGGCTCCCGGGG 307
      Qy      320 TyrHisAlaPheTyrCysHisGlyGluCysProPheProLeuAlaAspHisLeuAsnSer 339
      Db      306 TATCACCCCTTTTACTCCACGAGGAATGCCCTTTCTCTGGCTGATCATCTGAATCC 247
      Qy      340 ThrAsnHisAlaIleValGlnThrLeuValAsnSerValAsnSerLysLysIleProLysAla 359
      Db      246 ACTAATCATGCCATTGTTTCAGACGTTGGTCACTCTGTAACTCTAAGATTCCTAAGGCA 187
      Qy      360 CysCysValProThrGluLeuSerAlaIleSerMetLeuTyrLeuAspGluAsnGluLys 379
      Db      186 TGCTGTGTCCCGACAGAACTCAGTCTATCTCGATGCTGTACCTTGCAGAGAAATGAAAAG 127
      Qy      380 ValValLeuLysAsnTyrGlnAspMetValValGluGlyCysGlyCysArg 396
      Db      126 GTTGTATTAAAGAACTATCAGGACATGGTTGTGGAGGGTTGTGGGTGTGCG 76

```